

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

m151.pep	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMDSNDLEKERGITILAKNT					
g151	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMDSNDLEKERGITILAKNT					
	10	20	30	40	50	60
m151.pep	70	80	90	100	110	120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
g151	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
	70	80	90	100	110	120
m151.pep	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDES					
g151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESS					
	130	140	150	160	170	180
m151.pep	190	200	210	220	230	240
	DMRPLFDTILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAMN					
g151	DMRPLFDTILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAMN					
	190	200	210	220	230	240
m151.pep	250	260	270	280	290	300
	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
g151	HEQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
	250	260	270	280	290	300
m151.pep	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
g151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
	310	320	330	340	350	360
m151.pep	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR					
g151	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR					
	370	380	390	400	410	420
m151.pep	430	440	450	460	470	480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
g151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
	430	440	450	460	470	480
m151.pep	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
g151	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
	490	500	510	520	530	540
m151.pep	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					
	550	560	570	580	590	600

m151.pep KLDX
 ||||
 g151 KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

a151.seq
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCACGTCG ACCACGGCAA
 51 AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
 251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
 301 CAGGAAGGCC CGATGCCGCA AACCCTTTC GTGACCAAAA AAGCCTTGCC
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAATCGAC AAACCGTCCG
 401 CCCGTCCGAG CTGGGTCATC GACCAAACCT TCGAGCTGTT CGACAACCTG
 451 GGCGGCGACG ACGAGCAGTT GGATTTCCCG ATTGTTTATG CTTCCGGTCT
 501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
 551 CGCTGTTTGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
 601 GACGAAACGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
 651 CGGCCGCCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC
 701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGCATC
 751 AACCAGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCGC TTGAAGAAGC
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATTGAAGAC ATCGGCATCG
 851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
 901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCCTT
 951 GGCAGGTACG GAAGGCAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
 1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGGTGGA AGATACCGCC
 1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GGCGAGCTGC ACCTGACCAT
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
 1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
 1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAAGC GACGGCAACG
 1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGCTTC
 1351 CAAGGCGAAT TTATGACCCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
 1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCTGGC CGCCACAACG
 1451 GCGTCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTGG
 1501 AATCTGGAAG ACCGCGGCCG TATGTTGCTA TCGCCCAACG ACAAATCTA
 1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
 1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CCGTACCGAC
 1651 GAAGCCGTTT GCCTGACCAC GCCGATTAAG CTGACGCTGG AAGGTGCGGT
 1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCACGCCG CAATCCATCC
 1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCATTTCAAA
 1801 AAGTAGATT GA

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

a151.pep
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
 51 RGITILAKNT AIDYEGYHIN IVDPGHADF GGEVERVLGM VDCVLLVDA
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQAQGR
 251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGPLMLS
 301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
 351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
 401 NLTVDPVDDN QGAVMEELGR RRGELTNMES DGNGRTRLEY HIPARGLIGF
 451 QGEFMTLTRG VGLMSHVDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
 501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDDELVEITP QSIRLRKRYL SELERRRHFK
 601 KLD*

m151/a151 99.8% identity in 603 aa overlap

10 20 30 40 50 60

434

m151.pep	MKQIRNIAIIAHVDHGKTTLV	DQLLRQSGTFRANQQVDERV	MDSNDLEKERGITILAKNT
a151	MKQIRNIAIIAHVDHGKTTLV	DQLLRQSGTFRANQQVDERV	MDSNDLEKERGITILAKNT
	10 20 30 40 50 60		
m151.pep	AIDYEGYHINIVDTPGHADFG	GEVERVLGMVDCVLLVDAQEG	PMPQTRFVTKKALALGL
a151	AIDYEGYHINIVDTPGHADFG	GEVERVLGMVDCVLLVDAQEG	PMPQTRFVTKKALALGL
	70 80 90 100 110 120		
m151.pep	KPIVVINKIDKPSARPSWVIDQ	TFFELFDNLGATDEQLDFPIV	YASGLSGFAKLEETDESN
a151	KPIVVINKIDKPSARPSWVIDQ	TFFELFDNLGATDEQLDFPIV	YASGLSGFAKLEETDESN
	130 140 150 160 170 180		
m151.pep	DMRPLFDITILKYTPAPSGSA	DETLQLQISQLDYDNYTGRLG	IGRILNGRIKPGQTVAVMN
a151	DMRPLFDITILKYTPAPSGSA	DETLQLQISQLDYDNYTGRLG	IGRILNGRIKPGQTVAVMN
	190 200 210 220 230 240		
m151.pep	HDQQIAQGRINQLLGFKGLER	VPLEEAEAGDIVIISGIEDIG	IGVTITDKDNPKGLPMLS
a151	HDQQIAQGRINQLLGFKGLER	VPLEEAEAGDIVIISGIEDIG	IGVTITDKDNPKGLPMLS
	250 260 270 280 290 300		
m151.pep	VDEPTLTMDFMVNTSPLAGTE	GKFVTSRQIRDRLQKELLTN	VALRVEDTADADVFRVSGR
a151	VDEPTLTMDFMVNTSPLAGTE	GKFVTSRQIRDRLQKELLTN	VALRVEDTADADVFRVSGR
	310 320 330 340 350 360		
m151.pep	GELHLTILLENMRREGYELAV	GKPRVVYRDIDGQKCEPYEN	LTVDVPDDNQGAVMEELGR
a151	GELHLTILLENMRREGYELAV	GKPRVVYRDIDGQKCEPYEN	LTVDVPDDNQGAVMEELGR
	370 380 390 400 410 420		
m151.pep	RRGELTNMESDGNGRTRLEY	HIPARGLIGFQGEFMTLTRG	VGLMSHVFDYAPVKPDMPG
a151	RRGELTNMESDGNGRTRLEY	HIPARGLIGFQGEFMTLTRG	VGLMSHVFDYAPVKPDMPG
	430 440 450 460 470 480		
m151.pep	RHNGVLVSQEQGEAVAYALW	NLEDRGRMFVSPNDKIYEG	MIIGIHSRDNLDVNVPLKGKK
a151	RHNGVLVSQEQGEAVAYALW	NLEDRGRMFVSPNDKIYEG	MIIGIHSRDNLDVNVPLKGKK
	490 500 510 520 530 540		
m151.pep	LTNIRASGTDEAVRLTTPIK	LTEGAVEFIDDELVEITPQ	SIRLRKRYLSELERRRHFK
a151	LTNIRASGTDEAVRLTTPIK	LTEGAVEFIDDELVEITPQ	SIRLRKRYLSELERRRHFK
	550 560 570 580 590 600		
m151.pep	KLDX		
a151	KLDX		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

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1  ATGAAAAaca aaACCAaagt ctgGGacttc cCCaccgcgc ttTTCactG
51  GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGGCTCG GGCTGCTCGT CCTTTCCTG

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g152.ppe

1	MKNKTKVWDF	PTRLFHWLLA	ASLPFMWYSA	KAGGDMLQWH	TRVGLLVFL
51	<u>LVFRLCWGIW</u>	GSDTARFSRF	VRGWAGIRGY	LKNGIPEHIQ	PGHNP <u>LGALM</u>
101	<u>VVALLAAVSF</u>	<u>QVGTGLFAAN</u>	ENTFSTNGYL	NHLVSEHTGS	LIRKIHLNFF
151	<u>KLAVFSAVH</u>	<u>IAAAYARIF</u>	KKKNLVRPMI	TGFKYIEGKT	SIRFAGKAAL
201	AAALSVAAAL	AAAILLS*			

m152.seq

1	ATGAAAAACA	AAACCAAAGT	CTGGGACCTC	CCCACCCGCC	TTTTCCA CTG
51	GCTGCTTGCC	GCGTCCCTGC	CCTTTATGTG	GTATAGCGCG	AAAGCCGGCG
101	CGCATATGCT	GCAATGGCAG	ACGCGCGCTG	GGCTGTTCTG	CCTTTTCTGT
151	CTCGTATTTC	GCCCTCTGCTG	GGGCATTTGG	GGCAGCGATA	CCGCCCGTTT
201	TTCCCCGTTT	GTCCAAGGCT	GGGCAGGCAT	ACGCGGCTAT	CTGAAAAACG
251	GTATTTCCGA	ACACATCCAG	CCCGGACACA	ACCCCTTGGG	CGCACTGATG
301	GTCGTTGCGC	TTTTGGCCGC	CGTGTCCTTC	CAAGTCGGCA	CCGGGCTTTT
351	TGCCCGCCAG	GA AAAACACCT	TCAGCACCAA	CGGCTACCTC	AACCACTTGG
401	TTTCCGAACA	TACGGGCAGC	CTTATGCGGA	AAATCCACCT	CAACTTTTTC
451	AAGCTGCTCG	CCGTTTTTTT	TGCAATCCAC	ATCGCCGCCG	TCGCCGCATA
501	CCGCGTATTC	AAAAAGAAAA	ACCTCATCCT	CCCGATGATA	ACCGGCTTCA
551	AATACATCGA	AGGCAAAACC	TCAATCCGCT	TTGCAGGCAA	AGCCGCGCTT
601	GCCGCCGCAT	TATCGGTTGC	CTCGCTTGCC	GCAGCCGCCA	TCCTGCTCCT
651	GTCCTGA				

m152.pep

1	MKNKTKVWDL	PTRLFHWLLA	ASLPFMWYSA	KAGGDMLQWH	TRVGLFVLFL
51	<u>LVFRLCWGIW</u>	GSDTARFSRF	VQGWAGIRGY	LKNGIPEHIQ	PGHN <u>PLGALM</u>
101	VVALLAAVSF	QVGTGLFAAD	ENTFSTNGYL	NHLVSEHTGS	LMRKIHLNFF
151	<u>KLAVFSAIH</u>	<u>IAAAAYRVF</u>	KKKNLILPMI	TGFKYIEGKT	SIRFAGKAAL
201	AAALSVASLA	AAAILLS*			

Homology with a predicted ORF from *N.gonorrhoeae*

m152/q152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFHWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVLFLLVFRLCWGIW					
	:					
g152	MKNKTKVWDFPTRLFWHLLAASLPFMWYSAKAGGDMQLQWHTRVGLLVLFLLVFRLCWGIW					
	10	20	30	40	50	60

	70	80	90	100	110	120
m152.pep	GSDTARFSRFRVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:					
g152	GSDTARFSRFRVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN					
	70	80	90	100	110	120

436

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS AIHIAAVAAYRVFKKKNLILPMI					
	: : : :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFS AVHIAAVAAYRIFKKKNLVLRPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVASLAAAAI LLSX			
	:			
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAI LLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

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a152.seq
1   ATGAAAAACA AAACCAAGT CTGGGACTTC CCCACCGGCC TTTTCCACTG
51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCTG
151 CTCGTATTCC GCCTCTGCTG GGGCATTTGG GGCAGCGATA CCGCCCGTTT
201 CTCCCGTTTC GTCCGCGGAT GGTCCGGTAT CAGAGAGTAT ATGAAAAACG
251 GTATTCCCGA ACACGTCCAA CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGGCCGC CGTGTCGTTC CAAGTCGGCA CAGGGCTTTT
351 TGCCGCCGAT GTAAACACCT TCAGACCAA CGGCTACCTC AACCATTG
401 TTTCCGAACA TACGGGCAGC CTATGCGGA AAATCCATCT CAACTTTTTC
451 AAACGTGCTC CCGTTTTTTC CGCAGTCCAC ATCGCCGNCG TCGCCGCATA
501 CCGCGTGTTC AAAAAGAAAA ACCTCGTCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

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This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```

a152.pep
1   MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGGDMLQWH TRVGLFILFL
51  LVFRLCWGIW GSdTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101 VVALLAAVSE QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNEF
151 KLLAVFSAVH IAXVAAYRVF KKKNLVLPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*

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m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGDMLQWHTRVGLFVLLVFRLCWGIW					
	: : : :					
a152	MKNKTKVWDFPTRLFWLLAASLPFMWYSAKTGGDMLQWHTRVGLFILFLVFRLCWGIW					
	10	20	30	40	50	60

	70	80	90	100	110	120
m152.pep	GSdTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	: : : :					
a152	GSdTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS AIHIAAVAAYRVFKKKNLILPMI					
	: : : :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS AVHIAAXVAAYRVFKKKNLVLRPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVASLAAAAI LLSX			
	:			
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAI LLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```
g153.seq
1   atgggggtttg   cttaCAgtat   gacgtatatc   gaggtCGGGA   taccggaggc
51  ggcacccgctc   ctttCgctGC   CCGAGATgat   gcgcctgatG   GTGTTtCagg
101 attATGgTTT    TttggcCGAA   GTGATGTTTG   TGctgaCTTT   cGGCGcgcCG
151 GTTCTGTTtC    TGCTGCTGTG   CCTGTATGTC   TATGCCGCGC   TGATACGGAA
201 ACAGGCCTAT    CCTGCGCTGC   GTTGGCAAC    GCGTGTGATG   GTGCGCTTGA
251 GGCAGGCGAT    GATGGTGGAT   GTGTTTTTTG   TTTCCACTCT   GGTGGCGTAT
301 ATCAAGCTCT    CGTCTGTGGC   AAAGGTTTCG   TTCGGGCCGG   CGTTTTATCT
351 GATGTTCCGG    CTGTCCGTTA   TGCTGATTCG   GACTTCGGTA   TCGGTTCCCC
401 AGCATTGGGT    GTATTTCCAA   ATCGGGCGGC   TGACGGGGAA   TAATGCGGTT
451 CAGACGGCAT    CGGAAGGCAA   AACCTGTTGC   AGCCGCTGCC   TGTATTTccg
501 cgacAGTgccc   gaatccCCCT   GCGGGGTGTg   cgGCGcggaa   CTgtacggcg
551 gacggccgaa    aagtCTGAGt   atttCgtCGG   CGTTTCTgac   ggcggcggTT
601 GTTTTGTATT    TCCctgCcaa   TATCctgccc   attatGAttt   cgtccAATCc
651 tgccgccacg    GAGGcCAACA   CCATCTTTAG   CGGCATCGCT   TATATGTGGG
701 ACGaggcgca    CAGGCTGATT   GCGGCGGTTA   TTTTCAGCGC   GAGTATTTTG
751 GTGCCGGTGC    TGAAGATTGC   GGCAATGTCG   GTTTTGATTG   CGGCGGCACG
801 GTTCGCTTTG    CCGGCGGGCG   CAAAGAAATT   GTCGCACCTC   tacCGCATCA
851 CCGAAGCGGT    CGGCCGCTGG   TCGATGATTG   ATATTTTTGT   GATTATTATT
901 TTGATGTGTT    CGTTCacac   TTATGCCCGC   CGCGTCATTC   CGGGCAGTGC
951 GGCAGTCTAT    TTCTGCCTGG   TCGTGATTCT   GACGATGCTG   TCCGCCTATT
1001 ATTTGACCCC    GCGCCTGCTT   TGGGACAAAC   GCGCTTCAGA   CGGCATTGCT
1051 TTCAACGAAA    CGGAAAAATA   TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```
g153.pep
1   MGFAYSMTYI   EVGIPEASV   LSLPEMMRLM   VFQDYGFLAE   VMFVLTFGAP
51  VLFLLLCLYV   YAALIRKQAY   PALRLATRV   VRLRQAMMVD   VFFVSTLVAY
101 IKLSSVAKVR   GPAPFYLMPA   LSVMLIRTSV   SVPQHWVYFO   IGRLTGNNAV
151 QTASEGKTCC   SRCLYFRDSA   ESPCGVCGAE   LYGGRPKSLs   ISSAFLTAAV
201 VLYFPANILP   IMISSNPAAT   EANTIFSGIA   YMWDEGDRLI   AAVIFSASIL
251 VPVLKIAAMS   VLIAAARFAL   PAGAKKLSHL   YRITEAVGRW   SMIDIFVII
301 LMCSFHTYAA   RVIPGSAAVY   FCLVVILTML   SAYYFDPRL   WDKRASDGIA
351 FNETEKYD*
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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```
m153.seq
1   ATGGCGTTTG   CTTACGGTAT   GACGTATATC   GAGGTCGGGA   TACCGGGTGC
51  GGCATCCGTC   CTTTCGCTGC   CCGAGATGAT   GCGCCTGATG   GTGTTTCAGG
101 ATTATGTTTT   TTTGGCCGAA   GTGATGTTTG   TGCTGACTTT   CGGCGCGCCG
151 GTTCTGTTTC   TGCTGCTGTG   CCTGTATGTC   TATGCCGCGC   TGATACGGAA
201 ACAGGCGTAT   CTTGCGCTGC   GTTGGCAAC    GCGTGTGATG   GTGCGCTTGA
251 GACAGGCGAT   GATGGTGGAT   GTGTTTTTTG   TTTCCACTTT   GGTGGCGTAT
301 ATCAAGCTCT   CGTCTGTGGC   AGAGGTTTCG   TTCGGGCCGG   CGTTTTATCT
351 GATGTTCCGG   CTGTCACTTA   TGCTGATTCG   GACTTCGGTA   TCGGTTCCCC
401 AGCATTGGGT   GTATTTTCAA   ATCGGGCGGC   TGACGGGGGA   TAATGCGGTT
451 CAGACGGCAT   CGGAAGGTAA   AACCTGTTGC   AGCCGCTGCC   TGTATTTCCG
501 CGACAGTGCC   GAATCCCCCT   GCGGCGTGTG   CGGTGCGGAA   CTGTACCGCC
551 GACGGCCGAA   AAGTCTGAGT   ATTTCGTCGG   CGTTTCTGAC   GCGGCGGGTT
601 ATTTTGATT    TCCCTGCCAA   TATCCTGCCG   ATTATGATT    CGTCCAATCC
651 TGCCGCCACG   GAGGTCAATA   CCATCCTTAA   CGGCATCGCT   TATATGTGGG
701 ACGAGGGCGA   CAGGCTGATT   GCGGCGGTTA   TTTTCAGCGC   GAGTATTTTG
751 GTGCCGGTAC   TGAAGATTGC   GGCAATGTCG   GTTTTGATTG   CGTCCGCCCG
801 CTTGCTTTG    CCAACGGGTG   CAAAGAAATT   GTCGCACCTC   TACCGCATCA
851 CCGAAGCGGT    CGGCCGCTGG   TCGATGATTG   ATATTTTTGT   GATTATTATT
901 TTGATGTGTT    CGTTCACAC   TTATGCCCGC   CGCGTCATTC   CGGGCAGTGC
951 GGCAGTCTAT    TTCTGCCTGG   TCGTGATTCT   GACGATGCTG   TCCGCCTATT
1001 ATTTGACCCC    GCGCCTGCTT   TGGGACAAAC   GCGCTTCAGA   CGGCATTGCT
1051 TTCAATGAAA    CGGAAAAACA   TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```
m153.pep
1   MAFAYGMTYI   EVGIPGAASV   LSLPEMMRLM   VFQDYGFLAE   VMFVLTFGAP
51  VLFLLLCLYV   YAALIRKQAY   PALRLATRV   VRLRQAMMVD   VFFVSTLVAY
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101	<u>IKLSSVAEVR</u>	<u>FGPAFYLMFA</u>	<u>LSVMLIRTSV</u>	SVPQHWVYFQ	IGRLTGDNAV
151	QTASEGKTC	SRCLFYRDSA	ESVPTGCGAE	LYRRRPKSL	ISSAFLTAAL
201	<u>ILYFPANILP</u>	<u>MISSNPAA</u>	<u>EVNITLNGA</u>	YMWDEGRLL	AAVIFSALIV
251	<u>VPVLKIAAMS</u>	<u>VLIASARFAL</u>	<u>PTGAKKLSHL</u>	<u>YRITEAVGRW</u>	<u>SMIDIFVII</u>
301	<u>LMCSFHTYAA</u>	<u>RVIPGSAAVY</u>	<u>FCLVVILTML</u>	SAYYFDPRL	WDKRASDGI
351	FNTEKH*				

m153 / g153 96.1% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPENMRLMVFDYGFGLAEVMFVLTFGAPVLFLLCLYV					
g153	MGFAYSMTYIEVGIPGAASVLSLPENMRLMVFDYGFGLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMVRLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
g153	YAALIRKQAYPALRLATRVMVRLRQAMMVDVFFVSTLVAYIKLSSVAKVRFGPAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVPPQHWWYFQIGRLTGDNNAVQTASEGKTCCSRCLYFRDSDAESPCGVCGAE					
g153	LSVMLIRTSVSVPPQHWWYFQIGRLTGNNNAVQTASEGKTCCSRCLYFRDSDAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSLISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
g153	LYGGRPKSLSLISSAFLTAAVVLYFPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASII LVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVII					
g153	AAVIFSASII LVPVLKIAAMSVLIAARFALPAGAKKLSHLRYRITEAVGRWSMIDIFVII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHTYAAARVIPGSAAVYFCLVVIILTMSAYYFDPRLLLWDKRASDGI AFNETEKHDX					
g153	LMCSFHTYAAARVIPGSAAVYFCLVVIILTMSAYYFDPRLLLWDKRASDGI AFNETEKYDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 629>:

```

a153.seq
1  ATGGCGTTTG  CTTACGGTAT  GACGTATATC  GAGGTCGGGA  TACCGGGTGC
51  GGCATCCGTC  TTTTCGCTGC  CCGAGATGAT  GCGCCTGATT  GTGTTTCAGG
101 ATTATGGTTT  CTTTGGCGAA  GTGATGTTTG  TGCTGACCTT  CGGCGCGCCG
151 GTTCTGTTTC  TGCTGCTGTG  CCTGTATGTC  TATGCCGCGC  TGATACGGAA
201 ACAGGCGTAT  CCTGCGCTGC  GTTTGGCAAC  GCGTGTGATG  GTGCGCTTGA
251 GACAGGCGAT  GATGGTGGAT  GTGTTTTTTG  TTTCCACTTT  GGTGGCGTAT
301 ATCAAGCTCT  CGTCTGTGGC  AGAGGTTCCG  TTCGGATCGG  CGTTTTATCT
351 GATGTTCCGC  CTGTCGGTTA  TGCTGATTCT  GACTTCGGTA  TCGGTTCCCC
401 AGCATTGGGT  GTATTTTCAA  ATCGGGCGGC  TGACGGGGGA  TAATGCGGTT
451 CAGACGCGAT  CGGAAGGTAA  AACCTGTTGC  AGCCGCTGCC  TGTATTTCCG
501 CGACAGTGCC  GAATCCCCCT  GCGGCGGTGT  CGGTGCGGAA  CTGTACCGCC
551 GACGGCCGAA  AAGTCTGAGT  ATTCGTCGG  CGTTTCTGAC  CGGCGCGGTT
601 ATTTTGTATT  TCCCTGCCAA  TATCCTGCCG  ATTATGATTT  CGTCCAATCC
651 TGCCGCCACG  GAGGTCAATA  CCATCCTTAA  CGGCATCGCT  TATATGTGGG
701 ACGAGGGCGA  CAGGCTGATT  GCGGCGGTTA  TTTTTCAGCG  GAGTATTTTG
751 GTGCCGGTAC  TGAAGATTGC  GGCAATGTCG  GTTTTGATTG  CGTCCGCCCG
801 CTTTCGTTTG  CCAACGGGTG  CAAAGAAATT  GTGCGACCTC  TACCGCATCC

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851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTCGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
  1 MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
 51 VLFLLCLYV YAALIRKQAY PALRLATRV MRLRQAMMVD VFFVSTLVAY
101 IKLSSVAEVR FGSAYFLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSLS ISSAFLTA
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHXYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL WDKRASDGIA
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

m153.pep	10	20	30	40	50	60
	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
m153.pep	70	80	90	100	110	120
	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
m153.pep	130	140	150	160	170	180
	LSVMLIRTSVSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
a153	LSVMLIRTSVSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
m153.pep	190	200	210	220	230	240
	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
a153	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
	190	200	210	220	230	240
m153.pep	250	260	270	280	290	300
	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
m153.pep	310	320	330	340	350	359
	LMCSFHXYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
a153	LMCSFHXYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
  1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCTCAAG CACGCGTCCG
 51 CAAAAACAAC accttctctCT CGGCCGTCTG GCTGGTCCCG CTGATCGCGC
101 TGATTGCCG CGGCTGGCTT TGGGTAAAGG AAATCCGCAA CAGGGGCGCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCATTAAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTTA CTGCCAACT CAATGCGGAC
301 GTATCCGCGC TCATCCGCAG CGATACCCAG TTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

```

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401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGcg GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGAcCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCCTCT GCCTGCCCTG
751 CTGTCAGGCG CGATTTCAAT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCCT GTcgaATACA AAGGGCtgaA
951 TGTcggCATG GTTTCCGATG TCCCTTATTT TGACCGCAAt gacagCCTGC
1001 ACctgtTTGA aaacggctgg aTTcccGtac gCATCCGCAT cgagccTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAAACAACA
1101 ATTCCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGCGCGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGCG GCGGTTTGG ATGACTTGCA GGTCAAATTG GCGGATTGCG
1301 TGGACaaatT CAACAATCTG CCATTggata aAACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaaTCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACCTG AAAGAGTTGC GCATAACCCT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGAgacgta caAAATAcgc tgCaAAGTTT
1551 GGACAAAACC TTAaagacg TtcaACCGT CATTAACACT TTGAaAGAAa
1601 aacCCaaCgc actGATTTtc aacaACAGCA GCAAAGAccc tATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

```

g154.pep
1  MTDNSPPPNQ HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGLTL SGSYIAFTPG KSGEAKDVFQ
151 VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV GQIESAHFDP
201 LSDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGATISFDSF KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATRG GGLDDLQVKL ADLLDKFNNL PLDKTVAEIN
451 GSLAELKSAL KSANAALSSI DKLVGNPQTQ NIPNELNQLT KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSSKDPIPK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

```

m154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAACAAC ACCTTCCTCT CTGCCGCTCG GCTGGTTCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTAAAG AAATCCGCA CAGGGGGCCT
151 GTGATTCAGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTACATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TCGCGGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCACT CAATGCGGAC
301 GTATCCGGCC TCATCCGAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGTTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTGC AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTCAAT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTGCGCC GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCCGAGC TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTTTCAGAC GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

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1201 TCACCTAAGC TGCAGCCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GGCGGTTTGG ACGATTGTCG GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAATACGCG TGCAAAGTTT
1551 GGACAAAAC TTTAAAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

```

m154.pep
1  MTDNSPPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLL SGSYIAFTPG KSDEAKDVFQ
151 VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAELKSTL KSANAALSSI DKLVGKPQTQ NIPNELNQT LKELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
g154	10	20	30	40	50	60
	MTDNSPPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
m154.pep	70	80	90	100	110	120
	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
g154	70	80	90	100	110	120
	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
m154.pep	130	140	150	160	170	180
	SGVTGLGTLLSGSYIAFTPGKSDEAKDVFQVQDIPPVTAIGQSGRLRLNLIGKNDRIILNVN					
g154	130	140	150	160	170	180
	SGVTGLGTLLSGSYIAFTPGKSDEAKDVFQVQDIPPVTAIGQSGRLRLNLIGKNDRIILNVN					
m154.pep	190	200	210	220	230	240
	SPVLYENFMV GQVESAHFDP SDQSVHYTIFIQSPNDKLIH SASRFWLESG INIETTSGSI					
g154	190	200	210	220	230	240
	SPVLYENFMV GQIESAHFDP SDQSVHYTIFIQSPNDKLIH SASRFWLESG INIETTSGSI					
m154.pep	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ					
g154	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ					
m154.pep	310	320	330	340	350	360
	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGWIPVRIRIEPS RLEINADEQS					
g154	310	320	330	340	350	360
	SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGWIPVRIRIEPS RLEINADEQS					
m154.pep	370	380	390	400	410	420
	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
g154	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATRG					

442

	370	380	390	400	410	420
	430	440	450	460	470	480
m154 . pep	GGLDDLQVKLADLLDKFDKPLDKTVAEIENGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
g154	GGLDDLQVKLADLLDKFNNLPLDKTVAEIENGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154 . pep	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
g154	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154 . pep	NSSSKDPIPKGSRX					
	:					
g154	NNSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCATCAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGCG AAAAGCGACG AGGCAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTA AAAACG ACCGCATCCT CAACGTC AAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCAATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTCTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTCAAT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTTCGCCT GTCGAGTACA AAGGGCTGAA
951 TGTCGGCGTG GTTTCCGATG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCGCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGA AAATGCCGA CGAACAAGC AAAGAACATT GGAAACAACA
1101 ATTTTCAGAC GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTTGCA GGTCAAATTG GCGGATTTGC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAACCCCTG AAAGAGTTGC GCACAACCCT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAACC TTAAAAGACG TTCAACCCGT CATTAACTT TTGAAAGAAA
1601 AACCCAAACG GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154 . pep
1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFO

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151 VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAELKSTL KSANAALSSI DKLVGKPQTQ NIPNELNQTQ KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154/a154 100.0% identity in 553 aa overlap

	10	20	30	40	50	60
m154.pep	MTDNSPPPNGHAQARVRKNNFTLSAVWLVPALIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
a154	MTDNSPPPNGHAQARVRKNNFTLSAVWLVPALIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m154.pep	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDTQFVWVKPRIDQ					
a154	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDTQFVWVKPRIDQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m154.pep	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVFQVQDIPPVTAIGQSGRLRLNLIGKNDRIILNVN					
a154	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVFQVQDIPPVTAIGQSGRLRLNLIGKNDRIILNVN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m154.pep	SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTSGSI					
a154	SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTSGSI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m154.pep	KLNSAPLPALLSGAISFDSPKTKNSKNVKSSEDSTLYDSRSEVANLPDDRSLYYTAFFKQ					
a154	KLNSAPLPALLSGAISFDSPKTKNSKNVKSSEDSTLYDSRSEVANLPDDRSLYYTAFFKQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m154.pep	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
a154	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m154.pep	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
a154	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m154.pep	GGLDDLQVKLADLLDKFDKPLDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
a154	GGLDDLQVKLADLLDKFDKPLDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154.pep	NIPNELNQTQKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
a154	NIPNELNQTQKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540

444

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                    550
m154.pep      NSSSKDPIPKGSRX
              |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1   atGAAaatcg GtataCCACG CGAGTCAtta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gCCACCGTTG CCctgtggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAGgt TTGGCGGCAA GTTTggaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCCC
201 TTTAATTTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGC GCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCCCGC ATTTCCCGCG CTCAGGCCTT GGACGCTTTG TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTTTGGTG ATTGGCGCCG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GGCGGCAGCG GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTTG CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CTCCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAAACCG GCAACGGCGT GAAAATCATC GGCTACACCG ACATGGCAAA
951 CGCCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgaAATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTTCCCGCCT CCGccgaTTc aggtTTCCgc ccggccgCAG CAAAcgccgt
1151 ctgaAAAagc cgcGCCTGCC GCCAagccg AgccGaaacc tggtCCcctg
1201 tggAAAAaac tcgCGCCCGC GCcctcgCC GCCGTATTGG tgcgtgGgt
1251 cggCgcggtc gcacccgcag CATTCTTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCCTGCGT CATCGGTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGAtgtcggt aaccaaCgcc atctccGGCA tcatggtcgt
1401 cggCGCGCTG CTGCAAATCG GTCAGGGcaa cggcttcgtT TCgtGCTGT
1451 CGTTTGTTC CATCTGATT GCCGGCATCA ATATCTTCG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1   MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMVPR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFLQES GSGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAaip GKPAKLITK EMVESMKSGS VIVDLAATGG NCELTRPGEL
301 SVTNGVKII GYTDMANRLA GQSSQLYATN LVNLTKLLSP NKDGEITLDF
351 EDVIIRNMTV TRDGEITFPF PPIQVSARPQ QTPSEKAAPA AKPEPKPVPL
401 WKKLAPAAIA AVLVLWVGAV APAFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAL LQIQGNGFV SLLSFVAILI AGNIFGGFA
501 VTRRMLNMFK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1   ATGAAATCG GTATCCCACG CGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTGAAAG CGGTGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAACTG CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

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445

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301 TTGGTCGAAG CCTTGC GCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCCGCGCA
501 GGTTTTGGTG ATTGGTG CAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GCGCGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCGG GGCAAACCCG CGCCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGGC GGCAACTGCG AACTCACCCG CCCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTTGGAC
1051 TTCAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCGGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGGAAAA AACTCGCGCC CGCCGTCATC GCCCGCTCT TGGTACTGTG
1251 GGTGCGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGTGATGTC GGTAAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCGCGA TCAACATCTT CGGCGGCTTT
1501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51 QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMVPR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTQGITA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLFAEQAQEV
251 DIIITTAAP GKPAKLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QQTPEKAVP AAKPEPKPVP
401 LWKKLAPAVI AAVLVLVVGA VAPAAFLNHF IVFVLACVIG YYVWVNVSHS
451 LHTPMSVTN AISGIIVVGA LLQIGQNGF VSLLSFVAIL IAGINIFGGF
501 AVTRRMLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||
g155           MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m155.pep      AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMVPR
              |||:|||||
g155           AAVWACPLIYKVNAPSEGELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMVPR
              70      80      90      100     110     120

              130     140     150     160     170     180
m155.pep      ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPPAQVLVIGAGVAGLAA
              |||
g155           ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPPAQVLVIGAGVAGLAA

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446

	130	140	150	160	170	180
	190	200	210	220	230	240
m155.pep	IGTANSLGAVVRAFDTRLEVAEQIESMGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m155.pep	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
	250	260	270	280	290	
	310	320	330	340	350	360
m155.pep	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	300	310	320	330	340	350
	370	380	390	400	410	420
m155.pep	VTHDGEITFPPPIQVSAQPQOTPSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVWVGA					
g155	VTRDGEITFPPPIQVSARPQOTPSEKAAPAKPEPKPVPLWKKLAPAAIAAVLVLVWVGA					
	360	370	380	390	400	410
	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFVLACVIGYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
g155	VAPAAFLNHFIVFVLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
	420	430	440	450	460	470
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
	480	490	500	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAATCG GTATCCCACG TGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTGAAACCG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGGCATACCC
201 TTTAATTTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGCTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGC GCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCCGC ATTTGCGCGC GCGAGGCTTT GGACGNTTTG TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCCG CCTG.AAGTG
601 GCGGAACAAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GGCGGCAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GGCGACGGGC GGCAACTGCG AACTCACCAA ACAGGGCGAA
901 TTGTTTCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCGCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCGCGC ACGCGAAAT
1101 CACCTTCCCC CCTCCGCCGA TTCAAGTTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCAAGC CCGAACCGAA ACCCGTTCCC

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447

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1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTGCGGCGG GTCGCACCCG CAGCATTCTT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GGCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDXL SXMANISGYR AVIEAANAFG
151 RXFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDLPQES GSGDGYAKV MSDEFIAAEM KLFQAEQAKEV
251 DIIITTAaip GKPAKXXXK EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LFVTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QOTPSEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLWVGA VAPAAFLNHF IVFVLACVIG YYVWNVVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQNGF VSLLSFVAIL IASINIFGGF
501 FVTRRMLNMF RKG*

```

m155/a155 95.3% identity in 513 aa overlap

m155.pep	10	20	30	40	50	60
	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK					
a155	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK					
	10	20	30	40	50	60
m155.pep	70	80	90	100	110	120
	AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
a155	AAVWAYPLIYKVNAPSEDELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
	70	80	90	100	110	120
m155.pep	130	140	150	160	170	180
	ISRAQALDALSSMANISGYRAVIEAANAFGRFFTGQITAAGKVPPAQVLVIGAGVAGLAA					
a155	ISRAQALDXLSXMANISGYRAVIEAANAFGRXFTGQITAAGKVPPAQVLVIGAGVAGLAA					
	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLVVAEQIESMGGKFLKLDLPQESGSGDGYAKVMSDEFIAAEM					
a155	IGTANSLGAVVRVFDTRLXVAEQLESMGGKFLKLDLPQESGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLFQAEQAKEVDIIITTAaipGKPAKKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
a155	KLFQAEQAKEVDIIITTAaipGKPAKXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE					
	250	260	270	280	290	300
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
a155	LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	310	320	330	340	350	360
m155.pep	370	380	390	400	410	420
	VTHDGEITFPPIQVSAQPQOTPSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLWVGA					
a155	VTRDGEITFPPIQVSAQPQOTPSEKAAPAAKPEPKPVPLWKKLAPAXIAAVLVLWVGA					
	370	380	390	400	410	420

448

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              430      440      450      460      470      480
m155.pep      VAPAAFLNHFIVFVLACVIGYYVWNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a155           VAPAAFLNHFIVFVLACVIGYYVWNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF
              430      440      450      460      470      480

              490      500      510
m155.pep      VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX
              |||||||||||:||||||| |||||||||:|||
a155           VSLLSFVAILIASINIFGGFFVTRMLNMFRRGX
              490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

```

g156.seq
1  ATGACTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTTCTG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG ATTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGGCGG GCGGATTTCG
351 CTGCACCGTC GGA CTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

```

g156.pep
1  MTFAYWCILI ACLLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LFRLAFIWCY
101 IADKAALRSL MWAGGFACTV GLFVAAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```

m156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTTCTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC GCGCAATCG ACCATCAACA
251 CGCTTGCCCTG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAT
301 ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTTCG
351 CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

```

m156.pep
1  MTFAYWCILI ACLLPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAAQS TINTLACLFI LFRLAFIWCY
101 IADKAAMRSL MWAGGFACTV GLFVAAA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m156 / g156 96.1% identity in 127 aa overlap

```

              10      20      30      40      50      60
m156.pep      MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
g156           MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
              10      20      30      40      50      60

              70      80      90      100     110     120
m156.pep      FAPFAAAVLT AHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFACTV
              |||||||||||:|:|:| |||||||||||:|||||||||

```

```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWAGGFACTV
              70      80      90      100      110      120

m156.pep  GLFVAAAX
           |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
  1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
 51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101  ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151  CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201  CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251  CGCTTGCCGG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301  ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351  CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
  1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAARA
 51  HAAQQNGFEA FAPFAAAVLTAHATGNAGQA TVNTLAGLFI LFRFAFIWCY
101  IADKAALRSL MWVGGFVCTV GLFVVAAX*

m156/a156  90.6% identity in 127 aa overlap

              10      20      30      40      50      60
m156.pep    MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a156        MTFAYWCILIA YLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAARAHAAQQNGFEA
              10      20      30      40      50      60

              70      80      90      100     110     120
m156.pep    FAPFAAAVLTAHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFACTV
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a156        FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWVGGFVCTV
              70      80      90      100     110     120

m156.pep    GLFVAAAX
           ||||:|
a156        GLFVVAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
  1  atgaggaacg aggAAAAACg cgccctgcgc cgcggaattgC gCgGgcggcg
 51  ttgcgCAATg GGgcgagacg tGCGggCGGC GGCGgCgatA Aaaatcaacc
101  gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151  cCGATGGGCA AGGAATTGcg TTTGGGCGGc tTgtcCGCG CGGCGCAAAA
201  ACGCGGCGCA AAactctatc tgccttATAT CGAACC GCAC AC GCGGCGGA
251  TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301  GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351  GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAAG
401  GCTACCGTTT GGGGCAGGCA GGCGGCTATT ACGATGCGAC GCTTTCGGCG
451  ATGAAATACC GTTTGCAGGC GAAAACCGTG GGCGTGGGCT TTGCCTGCCA
501  GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551  TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLLKRYI KRGRKIGVYW
  51 PMGKELRLGG FVRAAQKRGK KLYLPYIEPH TRRMWFTYPY ERGMRERKR
 101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
 151 MKYRLQAKTV GVGAFACQLVD RLPREAHDL LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
  1 ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGCG
  51 TTCGCAAATG GGGCGGGACG TGCGGGCGGC GGCAACGGTA AAAATCAACC
 101 ACCTGCTCAA ACGTTATATT AAAAAAGGGC GGAAATCGG CGTGTATTGG
 151 CCGATGGGCA AGGAATGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
 201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACC CGT TCGCGGCGGA
 251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAAACAAGA ACGCAAGCGC
 301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCGGA AAAAGCGTGT
 351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTCGGTATG GACAGGCTGG
 401 GCTACCGCTT GGGACAGGCA GGCGGCTATT ACGATGCGAC GCTTTCAGCG
 451 ATGAAATACC GTTTCAGGC AAAAACCGTG GGCGTGGGCT TTGCCTGCCA
 501 GTTGGTGAC AGGCTGCCGG TCGAGGCGCA CGACCGGTCT TTGGACGGTT
 551 TTGTGTCGGA GCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAATV KINHLLKRYI KKGRKIGVYW
  51 PMGKELRLDG FVRAAQKRGK ELYLPYIEPR SRRMWFTYPY ADGVKQERKR
 101 GRAKLHVPQF AGRKKRVHDL NLLVPVVGMD RLG YRLGQA GGYDATLSA
 151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

m157.pep	10	20	30	40	50	60
	MRNEEKRALRRELGRRSQMGRDVRAAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG					
g157	MRNEEKRALRRELGRRSQMGRDVRAAAAIKINRLLKRYIKRGRKIGVYWPMGKELRLGG					
	10	20	30	40	50	60
m157.pep	70	80	90	100	110	120
	FVRAAQKRGAEYLYLPYIEPRSRMWFTYPYPADGVKQERKRGRAKLHVPQFAGRKKRVHDL					
g157	FVRAAQKRGAKLYLPYIEPHTRRMWFTYPYPERGMRERKRGRAKLHVPQFAGRKIRVHGL					
	70	80	90	100	110	120
m157.pep	130	140	150	160	170	180
	NLLLVPPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
g157	SVLLVPLVGIDREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
m157.pep	190					
	LDGFVSEAGILCFX					
g157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
  1 ATGAGGAACG AGGAAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCG
  51 CGCGCAGATG GGCATCAAG GCGGTTGGC GCGGGGCAA ACGATTAACC
```

451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACTTTATC TGCCTTATAT CGAACCCGCG TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCGTG GGCGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACCGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

```

a157.pep
  1 MRNEEKHALR RELRRARAQM GHQGRLAAGQ TINRLLKRYI KRGRKIGVYW
 51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWFTYPY ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFAQCFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

```

              10      20      30      40      50      60
m157.pep    MRNEEKRALRRELGRRSQMGRDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG
              |||||:||||| |::|||: | ||  ||:|||||:|||||
a157        MRNEEKHALRRELRRARAQMGGHQGRLAAGQTINRLLKRYIKRGRKIGVYWPMGKELRLDG
              10      20      30      40      50      60

              70      80      90      100     110     120
m157.pep    FVRAAQKRGAEKLYLPYIEPRSRMWFTYPYPADGVKQERKRGRAKLHVQFAGRKKRVHDL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a157        FVRAAQKRGAKLYLPYIEPRSRMWFTYPYPESGMERERIRGRAKLNVPQFAGRKIRVHGL
              70      80      90      100     110     120

              130     140     150     160     170     180
m157.pep    NLLLVVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS
              ::|||:|:| | |||||:|||||:|||||:|||||:|||||
a157        SVLLVPLVGIDREGYRLGQAGGYDATLAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL
              130     140     150     160     170     180

              190
m157.pep    LDGFVSEAGILCFX
              |||||:|||||
a157        LDGFVSEAGILCFX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

```

g158.seq
  1 ATGAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAAcCTGctc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTGCGCGT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCcgac TTTGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGcCT TACGGGCCGG AGAATTGGAC
451 GATTCCGGGC TGCGTGCACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```


452

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
851 TATTTTGGGA TTTTGTAGTG AAGGAACTGG GAAAAAATAT GAATAGAACG
901 AATACCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

```

g158.pep
  1 MKTNSEELTV FVQVVESGSF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFRRR QRILQEMAAA ETEMLAVHEV PQGVLRVDSA
101 MPMVLHLLAP LAAKFNERYP HIRLSLVSSE GYINLIERKV DIALRAGELD
151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE
251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNLR LRVFLDFLV KELGKNMNRRT
301 NTK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

```

m158.seq
  1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
151 AACC GCACCA CGCGGCAACT CAGTCTGACG GAAGAAGCGC CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTTGAGCGT GGATTCCGCG
301 ATGCCGATGG TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCCGAC TTTCGCTCGT TTCTTCCGAA GGCTATATCA
401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC
451 GATTCCGGGC TGCGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG
551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGATGC GCAGGGAAAT CCCTATAAGA TTTACCCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT
701 GCGGTATTGT TTGCTTATCA GATTTTGTGG TTGACAACGA CATCGCTGAA
751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
851 TATTTTGGGA TTTTGTAGTG GAGGAACTGG GAAACAATCT CTGTGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

```

m158.pep
  1 MKTNSEELTV FVQVVESGSF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFRRR QRILQEMAAA ETEMLAVHEI PQGVLSVDSA
101 MPMVLHLLAP LAAKFNERYP HIRLSLVSSE GYINLIERKV DIALRAGELD
151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN
201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE
251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNLR LRVFLDFLV EELGNLCLG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

```

          10      20      30      40      50      60
m158.pep  MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT
          |||
g158       MKTNSEELTVFVQVVESGSFSRAAEQLEMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT
          10      20      30      40      50      60

          70      80      90     100     110     120
m158.pep  EEGAQYFRRRQRILQEMAAAETEMLAHVHEIPQGVLSVDSAMPMLHLLAPLAAKFNERYP
          |||
g158       EEGAQYFRRRQRILQEMAAAETEMLAHVHEVPQGVLRVDSAMPMLHLLAPLAAKFNERYP
          70      80      90     100     110     120

```

453

	130	140	150	160	170	180
m158.pep	HIRLSLV	SEGYIN	LIERKVD	IALRAGEL	DDSGLRAR	HLFDSRFRVIASPEYLAKHGTPQ
g158	HIRLSLV	SEGYIN	LIERKVD	IALRAGEL	DDSGLRAR	HLFDSHFRVVASPEYLAKHGTPQ
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGH	QCLGFTE	PGSLNTW	AVLDAQGN	PNYKISPH	FTASSGEILRSLCLSGCGIVCLS
g158	SAEDLANH	QCLGFTE	PGSLNTW	AVLDAQGN	PNYKISPH	FTASSGEILRSLCLSSCGIACLS
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDND	IAEGKLI	PLLAEQ	TSKTHPF	NAVYYSD	KAVNLRRLRVFLDFLVEELGNNLCGX
g158	DFLVDND	ITEGKLI	PLFAEQ	TSNKTHP	NAVYYSD	KAVNLRRLRVFLDFLVKELGKNMNR
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAACCA	ATTCAGAAGA	ACTGACCGTA	TTTGTTCAAG	TGGTGGAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCGCGT	GGATTCCCGG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATTCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGCACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTTAGATGC	GCAGGGAAAT	CCCTATAAGA	TTTCACCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTTGGA	TTTTTTAGTG	GAGGAACCTG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRRA	QRILQEMAAA	ETEM LAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LA AKFNERYP	HIRLSLVSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQC	LGFTPEPSLN
201	TWAVLDAQGN	PNYKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYYSDKAVNL	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL	NRTTRQLSLT
a158	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL	NRTTRQLSLT
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRA	QRILQEMAAA	ETEM LAVHEI	PQGVLSVDS	SAMP MVLHLLAP	LA AKFNERYP
a158	EEGAQYFRRA	QRILQEMAAA	ETEM LAVHEI	PQGVLRVDS	SAMP MVLHLLAP	LA AKFNERYP
	70	80	90	100	110	120

q160.seq

1	ATGGACattc	tgGACAAact	ggtcgatCTC	GCccaATTGA	CGGGCAGTGC
51	GGATGTGcAG	TgcctTTTGG	GCGGACAATG	gcATGaaacc	TTGCAACGCG
101	AAGGGCTGGT	ACACATTGTT	ACGGCGGGCA	GCGGTTATCT	CTGCATCGAC
151	GGCGAAACTT	CCCCGCGTCC	GGTCGGCAGC	GCGGATATTG	TATTTTTCCC
201	GCGCGGCTTG	GGTCATGTGT	TGAGCCACGA	CGGAAAATAC	GGAGAAAGTT
251	TACAACCGGA	CATACGACAA	AACGGCACAT	TTATGGTCAA	ACAGTGCGGC
301	AACGGGCTGG	ATATGAGCCT	GTTTTGCGCC	CGTTTTCCGT	ACGACACCCA
351	CGCCGATTGG	ATGAACGGGC	TGCCGGA AAC	CGTTTTCTG	AACATTGCCC
401	ATCCAAGTTT	GCAGTATGTG	GTTCCAATGC	TGCAACTGGA	AAGCGAAAAA
451	CCTTTGACGG	GGACGGTTTC	CGTGGTCAAC	GCATTACCGT	CCGTCTTGCT
501	GGTGCTTATC	CTGCGCGCTC	ATCTCGAACA	GGATAAGGAT	GTGCAACTCT
551	CGGGCGTATT	GAAAGTTTGG	CAGGACA AAC	GTTTGGGACA	TTTGATCCAA
601	AAGGTGATAG	ACAAACCGGA	AGACGAATGG	AATATTGACA	AATAGTTTGC
651	GCGCGCAAT	ATCTCGCGCG	CGCAACTGAT	GCGCCGCTTC	AAAAGCCAAG
701	TCGGA CT CAG	CCCGCACGCC	TTTGTGAACC	ATATCCGCCT	GCAAAAAGGC
751	GCATTGCTCG	TGAAGAAAAA	CCCGGATTCG	GTTTTGGAGG	TCGCGCTGTC
801	GGTGGGCTTT	CAGTCGGAAA	CGCATTTCCG	CAAGGCGTTC	AAACGGCAAT
851	ATCACGTTTC	GCCGGGGCAA	TACCGGAAAG	AAGGCGGCA	AAAATAA

q160.pep

1	MDILDKLVDL	AQLTGSADVQ	CLLGGQWHET	LQREGLVHIV	TAGSGYLCID
51	GETSPRPVGT	GDIVFFPRGL	GHVLSHDGKY	GESLQDPDIR	NGTFMVKQCG
101	NLGLDMSLFA	RFRYDTHADL	MNGLPETVFL	NIAPHSLQYV	VSMGLQLESEK
151	PLTGTVSUVN	ALPSVLLVLI	LRAYLEQDKD	VELSGVLKVG	QDKRLHGLIQ
201	KVIDKPEDEW	NIDKMLVAAN	MSRAQLMRRF	KSQVGLSPHA	FVNHIRLQKG
251	ALLLKPPEDS	VLEAVLSVGF	QSETHFGKAF	KROYHVSFGQ	YRKEGGQK*

m160.seq

1	ATGGACATTC	TGGACAAACT	GGTCGATTTC	GCCCAATTGA	CGGGCAGTGT
51	GGATGTGCAG	TGCCTTTTGG	GCGGACAATG	GTCGGTACGG	CATGAACCT
101	TGCAACGCAGA	AGGATTGGTA	CACATTGTTA	GTCGCGGCAC	CGGCTATCTC
151	TGCATCGCAG	CGGAAACTTC	CGCCGCTCCG	GTCAGTACAG	GGGATATTGT
201	ATTTTTCCCG	CGCGGCTTGG	GTCATGTGTT	GAGCCACGAC	GGAATAATGCG
251	GAGAAAGTTT	ACAACCGGAT	ATGCGGCAGC	ACGGTGC GTT	TACGGTCAAG
301	CAGTGC GGCA	ACGGACAGGA	TATGAGCCTG	TTTTGCGCCC	GTTTCGGCTA
351	CGACACCCAC	GCCGATTGTA	TGAACGGGCT	GCCTGAAACC	GTTTTTCTGA
401	ACATTGCCCA	TCCGAGTTTA	CAGTATGTGG	TTTCAATGCT	GCAACTGTGA
451	AGCAAAAAAC	CTTTGACGGG	GACGGTTTCC	ATGGTCAACG	CATTGTCTGA

```
m160.pep
1 MDILDKLVDVF AQLTGSVDVQ CLLGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCNGNQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*
```

Homology with a predicted ORF from *N. gonorrhoeae*

		10	20	30	40	50	60
m160.pep		MDILDKLVDF	AQLTGSVDV	QCLLGGQWS	VRHETLQRE	GLVHI	VTSGSGYLCIDGETSPRP
g160		MDILDKLVDLA	QLTGSADV	QCLLGGQW	---	HETLQREGLV	HIVTAGSGYLCIDGETSPRP
		10	20	30	40	50	
		70	80	90	100	110	120
m160.pep		VSTGDIVFF	PRGLGHVLS	HSDGKCGES	LQPDMRQHGA	FTVKQCGNGQ	DMSLFCARFRYDTH
		:					
g160		VGTGDIVFF	PRGLGHVLS	HSDGKYGES	LQPDIRQNGT	FMVKQCGNGL	DMSLFCARFRYDTH
		60	70	80	90	100	110
		130	140	150	160	170	180
m160.pep		ADLMNGLPET	VFLNIAHPS	LQYVVSMLQ	LESKKPLTGT	VSMVNALSS	VLLVLILRAYLEQ
g160		ADLMNGLPET	VFLNIAHPS	LQYVVSMLQ	LESEKPLTGT	VSVVNALPS	VLLVLILRAYLEQ
		120	130	140	150	160	170
		190	200	210	220	230	240
m160.pep		DKDVELSGV	LKGWQDKRL	GHLIQKVID	KPEDEWNVD	KMVAAANMS	RAQLMRRFKSRVGLS
g160		DKDVELSGV	LKGWQDKRL	GHLIQKVID	KPEDEWNID	KMVAAANMS	RAQLMRRFKSQVGLS
		180	190	200	210	220	230
		250	260	270	280	290	300
m160.pep		PHAFVNHIR	LQKGALLK	KNPDSVLS	VALSVGFQ	SETHFGKAF	KRQYHVSPGQYRKEGGQ
g160		PHAFVNHIR	LQKGALLK	KTPDSVLE	VALSVGFQ	SETHFGKAF	KRQYHVSPGQYRKEGGQ
		240	250	260	270	280	290
m160.pep		KX					
g160		KX					

```

a160.seq
1  ATGGACATTC TGGACAACT GGTGCATTTC GCCCAATTGA CGGGCAGTGT
51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

```

101 TGCAACGCGA AGGATTGGTA CACATTGTGA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCGGCA ACGGACAGGA TATGAGCCTG TTTTGCGCCC GTTTCCTGTA
351 CGACACCCAC GCCGATTGTA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCCTGCTG GTGCTTATCC TGCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTGCG TTTTGTGGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAGA AGGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep  MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||||
a160       MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60

          70      80      90     100     110     120
m160.pep  VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||||
a160       VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          70      80      90     100     110     120

          130     140     150     160     170     180
m160.pep  ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTV SMNALSSVLL VLILRAYLEQ
          |||||
a160       ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTV SMNALSSVLL VLILRAYLEQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m160.pep  DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||||
a160       DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240

          250     260     270     280     290     300
m160.pep  PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||||
a160       PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          250     260     270     280     290     300

m160.pep  KX
          ||
a160      KX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG  CAAAAAAGA  CATTTTAGGA  TCGGGCTGGA  TGCTGGTGGC
51  GGCGGCCTGC  TTCACCGTTA  TGAACGTATT  GATTAAAGAG  GCATCGGCAA
101 AATTTGCCCT  CGGCAGCGGC  GAATTGGTCT  TTTGGCGCAT  GCTGTTTTCA
151 ACCGTTACGC  TCGGTGCTGC  CGCCGTATTG  CGGCGGACA  CCTCCGCAC
201 GCCCCATTGG  AAAAACCAC  TAAACCGCAG  TATGGTCGGG  ACGGGGGCGA
251 TGCTGCTGCT  GTTTTACGCG  GTAACGCATC  TGCCTTTGAC  AACCGGCGTT
301 ACCCTGAGTT  ACACCTCGTC  GATTTTtttg  GCGGTATTTT  CCTTCCTGAT
351 TTTGAAAGAA  CGGATTTCCG  TTTACACGCA  GGCGGTGCTG  CTCCTTGGTT
401 TTGCCGGCGT  GGTATTGCTG  CTTAATCCCT  CGTCCGCAG  CGGTCAGGAA
451 CCGGCGGCAC  TCGCCGGGCT  GGCGGGCGGC  GCGATGTCCG  GCTGGGCGTA
501 TTTGAAAGTG  CGCGAACTGT  CTTTGGCGGG  CGAACCCGGC  TGGCGCGTCG
551 TGTTTTACCT  TTCCGCAACC  GGCGTGCGCA  TGTGCTCggt  ttgggcgacg
601 Ctgaccggct  ggCACaccct  GTCCTTTcca  tcggcagttt  ATCtgtCGGG
651 CATCGGCGTG  tccgcgCtgA  TTGCCCAaCT  GtcgatgAcg  cGCGcctaca
701 aaGTCGGCGA  CAAATTCACG  GTTGCCCTCG  tttcctaTat  gaccgtcGTC
751 TTTTCCGCC  TGTCTGCCGC  ATTTTCTg  ggcaagagc  ttttctggCA
801 GGAAATACTC  GGTATGTGCA  TCATTATcct  CAGCGGCATT  TTGAGCAGCA
851 TCCGCCCAT  TGCCTTCAA  CAGCGGCTGC  AAGCCCTCTT  CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG  SGWMLVAAAC  FTVMNVLIKE  ASAKFALGSG  ELVFWRMLFS
51  TVTLGAAAVL  RRDTRTPHW  KNHLNRSMVG  TGAMLLLFYA  VTHLPLTTGV
101 TLSYTSSIFL  AVFSFLILKE  RISVYTOAVL  LLGFAGVVLL  LNPSFRSGQE
151 PAALAGLAGG  AMSGWAYLKV  RELSLAGEPG  WRVVFYLSAT  GVAMSSVWAT
201 LTGWHTLSFP  SAVYLSGIGV  SALIAQLSMT  RAYKVGDKFT  VASLSYMTVV
251 FSALSAFFL  GEELFWQEIL  GMCIIILSGI  LSSIRPIAFK  QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG  CAAAAAAGA  CATTTTAGGA  TCGGGCTGGA  TGCTGGTGGC
51  GGCGGCCTGC  TTTACCATTA  TGAACGTATT  GATTAAAGAG  GCATCGGCAA
101 AATTTGCCCT  CGGCAGCGGC  GAATTGGTCT  TTTGGCGCAT  GCTGTTTTCA
151 ACCGTTGCGC  TCGGGGCTGC  CGCCGTATTG  CGTCGGGACA  mCTTCCGCAC
201 GCCCCATTGG  AAAAACCAC  TAAACCGCAG  TATGGTCGGG  ACGGGGGCGA
251 TGCTGCTGCT  GTTTTACGCG  GTAACGCATC  TGCCTTTGGC  CACTGGCGTT
301 ACCCTGAGTT  ACACCTCGTC  GATTTTttTG  GCGGTATTTT  CCTTCCTGAT
351 TTTGAAAGAA  CGGATTTCCG  TTTACACGCA  GGCGGTGCTG  CTCCTTGGTT
401 TTGCCGGCGT  GGTATTGCTG  CTTAATCCCT  CGTCCGCAG  CGGTCAGGAA
451 ACGGCGGCAC  TCGCCGGGCT  GGCGGGCGGC  GCGATGTCCG  GCTGGGCGTA
501 TTTGAAAGTG  CGCGAACTGT  CTTTGGCGGG  CGAACCCGGC  TGGCGCGTCG
551 TGTTTTACCT  TTCCGTGACA  GGTGTGGCGA  TGTGTCGGT  TTGGGCGACG
601 CTGACCGGCT  GGCACACCCT  GTCCTTTCCA  TCGGCAGTTT  ATCTGTCGTG
651 CATCGGCGTG  TCCGCGTGA  TTGCCCAACT  GTCGATGACG  CGCGCCTACA
701 AAGTCGGCGA  CAAATTCACG  GTTGCCCTCG  TTTCTATAT  GACCGTCGTT
751 TTTTCCGCTC  TGTCTGCCGC  ATTTTCTG  GGCGAAGAGC  TTTTCTGGCA
801 GGAAATACTC  GGTATGTGCA  TCATCATCCT  CAGCGGTATT  TTGAGCAGCA
851 TCCGCCAC  TGCCTTCAA  CAGCGGCTGC  AATCCCTGTT  CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG  SGWMLVAAAC  FTIMNVLIKE  ASAKFALGSG  ELVFWRMLFS
51  TVALGAAAVL  RRDTRTPHW  KNHLNRSMVG  TGAMLLLFYA  VTHLPLATGV
101 TLSYTSSIFL  AVFSFLILKE  RISVYTOAVL  LLGFAGVVLL  LNPSFRSGQE

```

458

```

151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSCIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	: : : :					
g161	MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLSTVTLGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKHNLRSMVGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
	: : : : :					
g161	RRDTFRTPHWKHNLRSMVGTGAMLLLFYAVTHLPLTTGVTLSYTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFAVGVLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	: : : :					
g161	RISVYTQAVLLLGFAVGVLLNPSFRSGQEPAAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSCIGVSALIAQLSMTRAYKVGDKFT					
	: : : : :					
g161	WRVVFYLSATGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	: : : :					
g161	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
	250	260	270	280	290	300
m161.pep	X					
	I					
g161	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

```

a161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGCC
51  GGCGGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATGGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCACT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTACGCG GTAACGCATC TGCCTTGGC CACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGGTGCTG CTCCTTGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACC CGC TGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCATCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTGT
651 CATCGGCGTG TCCGCGCTGA TTGCCAACT GTCGATGACG CGCGCTACA
701 AAGTCGGCGA CAAATTCAG GTTGCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTCTCTG GCCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA

```

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMFLS
51 TVALGAAAVL RRDTFRTPHW KNHLNRSMSG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSICIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	10	20	30	40	50	60
m161.pep	RRDXFRTPHWKNHLNRSMSGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSMSGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
m161.pep	RISVYTQAVLLLGFGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGFGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTTAACGTT TTCCATTTTt
151 ctgGGTTTt tgctGATACT CTCGGTCAGC GGTTTGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGCC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC


```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCCTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACACT CTCGGAATTC
851 TGGTGCGCCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTGTGTTTA TCGC GCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTGCGGGTT TTGCTCATCC CCGGCCGTGT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAACCTCT GCCGACTCCG GGATTATATG
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGCGCGTTAT GTGGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGC GGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGC GGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCCG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAAC TG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

```

g163.pep
1 MVILTTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51 LGFLLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLF AAGM GVGLMFFGVVA
101 EPLMHYFS DI TVGAPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFGVQV LIIAAVMSLA VVSAISGVGK GVKVLSENLN
251 GLAFLLLFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQGEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

```

m163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTTGTT TGTGTTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGTTTTTATG TTTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CTTGGTCCGG GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

```

```

m163.pep
1  MVILTTLFFV  CVLVVLVLTV  PDQVQMWLDR  AKEVIFTEFS  WFYVLTFISIF
51  LGFLILSVS  SLGNIRLGRQ  EDVPEFGFLS  WLAMLFAAGM  GVGLMFFGVVA
101 EPLMHYFSDI  TAGTPEHRQD  QALLHTVFHW  GVHAWSVYGT  IALALAYFGF
151 RYKLPLALRS  CFYPLLKEKI  SGRFGDAIDI  MALLATVFEG  ITTLGFGASQ
201 LGAGLQEMGW  IAENSFSVQV  LIIAAVMSLA  VVSAISGVGK  GVKVLSELNL
251 GLAFLLLFFV  LAAGPTVYLL  SAFGDNIGNY  LGNLVRLSFK  TYAYEREHKP
301 WFESVTVLYW  AWCWSWAPFV  GLFIARISKG  RTIREFVFGV  LLIPGLFGVL
351 WFTVFGNTAI  WLNDGVAGGM  LEKMTSSPET  LLKFFNYNLP  LPELTSIVSL
401 LVISLFFVTS  ADSGIYVLNN  ITS RDKGLSA  PRQWAVMWGV  LMSAVAVLLM
451 RSGGLGNLQS  MTLIVSLPFA  LLMLIMCFSL  WKGLSADKKY  FETRVNPTSV
501 FWTGGKWKER  LVQIMSQTQE  QDILKFLKQT  ASPAMHELQR  ELSEEYGLSV
551 RVDKMFHRDE  PAIEFVIRKE  TMRDFMYGIK  SVGQDVSDQL  INDGKLPHIR
601 HQTTYKPYAY  FFDGRVGYDV  QYMNKDELIA  DILKNYERYL  MLLDDVGQEL
651 MAHEQVELAE  *

```

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163	98.6% identity in 660 aa overlap					
	10	20	30	40	50	60
m163.pep	MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS					
g163	MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m163.pep	SLGNIRLGRDEDVPEFGFLSWLAMLF AAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ					
	:					
g163	GLGNIRLGRDEDVPEFGFLSWLAMLF AAGMGVGLMFFGVAEPLMHYFSDITVGAP EHRQQ					
	70	80	90	100	110	120
	130	140	150	160	170	180

462

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWAENSFSVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSLKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQLKFLKQTASPAMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQLKFLKHTASPAMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGTTATTTT TGACGACTTT GTTTTTTG TGTTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGTCTTGGCT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTTTAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTTATG
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGAT
1451 TGAGTGCGBA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTGAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCCGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

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This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

a163.pep

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1  MVILTTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFISIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGV
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKQ RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITSROKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQDEL
651 MAHEQVELAE *

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m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFISIFLGFLILSVS
          |||||
a163      MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFISIFLGFLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ

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464

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|||||
a163      SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
              70      80      90      100      110      120

              130      140      150      160      170      180
m163.pep  QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
              |||||
a163      QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
              130      140      150      160      170      180

              190      200      210      220      230      240
m163.pep  MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
              |||||
a163      MALLATFFGIITTLGFGASQLGAGLQEIWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
              190      200      210      220      230      240

              250      260      270      280      290      300
m163.pep  GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              |||||
a163      GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              250      260      270      280      290      300

              310      320      330      340      350      360
m163.pep  WFESWTVLYWAWWCWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
              |||||
a163      WFESWTVLYWAWWCWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
              310      320      330      340      350      360

              370      380      390      400      410      420
m163.pep  WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              |||||
a163      WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              370      380      390      400      410      420

              430      440      450      460      470      480
m163.pep  ITS RDKGLSAPRWQAVMWGVLM SAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
              |||||
a163      ITS RDKGLSAPRWQAVMWGVLM SAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
              430      440      450      460      470      480

              490      500      510      520      530      540
m163.pep  WKGLSADKKYFETRVNPTS VFWTGGKWKERLVQIM SQTQE QDILKFLKQTAS PAMHELQR
              |||||
a163      WKGLSADKKYFETRVNPTS VFWTGGKWKERLVQIM SQTQE QDILKFLKHTAS PAMHELQR
              490      500      510      520      530      540

              550      560      570      580      590      600
m163.pep  ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
              |||||
a163      ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
              550      560      570      580      590      600

              610      620      630      640      650      660
m163.pep  HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLM LDDVQGELMAHEQVELAE
              |||||
a163      HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLM LDDVQGELMAHEQVELAE
              610      620      630      640      650      660

m163.pep  X
          |
a163      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
  1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
 51  CAAGGCGCGC TTCCTGTTTC CCTCGGCCCG CCTGTCAAAA GAATTGGCGG
101  GCCTGAAGGC GCAAACGCCC GTCGAAAAAA TCATTTGGAC GGACAAAAGC
151  CGGCCGGCCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201  CCGCTTCCCC GAAAAACCCG ACTTGGGCCG CCAACCCCGG ATAAATGATT
251  TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301  CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351  CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTcctg ccgatgTTCC
401  ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451  TCGATTATTT TGGTCAAAtc cgttttCCcC ttttccaacg TTTTGAAACA
501  GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551  CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTCAGATG GTTCAACCGC
601  ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651  CGATTTTAAA GCCAAGTTCC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701  TGAGCGAAGC CTCGCCCCGC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751  GCGCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801  TGAAGAATTG GTCGAAGTGC CGCGCGCGA AGTGGGCGAA CTGATCGTCA
851  GGGGCGGTTT GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901  GAAACCATCG TCAACGGCTG GTTGAAAACG GGCATTTCG TTACCATAGA
951  CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GCGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTGCG
1151 GCGAGGACGA aatccgccc caccTGCGTA CCGTGCTGGC AAATTTCAAA
1201 ATCCCCAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
  1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
 51  RPAGETAEGD AFFENVRRFP EKPD LG RQPR INDLAHIIT SGT TGH PKGA
101  LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151  SIILVKSVP FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201  IRLFISGGAP LAEQTILDFK AKFPRAKLLE GYGLSEASPV VAVNTPERQK
251  ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301  ETIVNGWLKT GDFVTIDEDG FIFIVDRKKD LIISKGQNVY PREIEEEIHK
351  LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRVTLANFK
401  IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
  1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
 51  CAAAAACGGA AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101  ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151  ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201  AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTCGCCG
251  TACCGATGAA CACATTTTTG AAAACAGCG AATACGCGTA TATCCTGAAC
301  GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351  GCGGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAATCATT TGGACGGACA
401  AAAGCCGTCC GACCGCGGAA ACGCGGAAG GCGATGCCTT TTTTGAAGAC
451  GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501  TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551  GCGCGCTAAT CAGTTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601  CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651  GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701  CGTGTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTC CAACGTTTTG
751  AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TACCCGCGAT
801  TTACACCGCG ATGAGCAAGG CGAAAATCCC TTGGTATTTC AGATGGTTCA
851  ACCGCATTCT CCTGTTTATC AGCGCGGCG CGCCTTTGGC GGAACAAACC
901  ATCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA

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466

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951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGCCAAAGCC
1051 GTCGATGAAG AATTGGTCGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTGGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACCTCGA TGCCGTCGAA GCCGCCGCGC TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNQ NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKRD R FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNV L
251 KQTLKRA TV FLGVPAIYTA MSKAKIPWYF RWFNRIRLF I SGGAPLAEQT
301 ILDFKAKFP R AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVP R GEVGELIVRG GSVMRGYLMN PAATDETIVN GWLKTGDFVT
401 IDEGDFIFIV DRKKDLISK GQNVYPREIE EEIYKLDAVE AAIVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
501 TGKVLKRVLK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

          60      70      80      90      100      110
m164.pep  GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g164      MNTFLKNSEYAYILNDCKARFLFASAGLSK
          10      20      30

          120      130      140      150      160      170
m164.pep  ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g164      ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT
          40      50      60      70      80      90

          180      190      200      210      220      230
m164.pep  SGTGHPKGALISYANL FANLNGIERIFKISKRD RFIVFLPMFHSFTLTAMVLLPIYMAC
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g164      SGTGHPKGALISYANL FANLNGIERIFKISKRD RFIVFLPMFHSFTLTAMVLLPIYMAC
          100      110      120      130      140      150

          240      250      260      270      280      290
m164.pep  SIILVKSVPFSPNV LKQTLKRA TVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAP
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g164      SIILVKSVPFSPNV LKQALLKRA TVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAP
          160      170      180      190      200      210

          300      310      320      330      340      350
m164.pep  LAEQTILDFKAKFPRAK LLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEEL
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g164      LAEQTILDFKAKFPRAK LLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEEL
          220      230      240      250      260      270

          360      370      380      390      400      410

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a164.seq
1 ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CGCCTGCCG
51 CAAAAACGGC AACGGCAGCG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT AACGACAGAA GCCGAAGCCG TTGCGCGGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTTG AAAACACAGC AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGTTCCT GTTCGCTCG CGCGGCTGT CAAAAGAATT
351 GCGGGCTTG AAGGCCAAA CGCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCGCT TCCCCGAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTCGCTAAT CAGCTACGCC AACCTGTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGCTC AAATCCGTTT TCCCCTTTTC CAACGTTTTG
751 AAACAGGCAC TGCTCAAAGC CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA GCAAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGG AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCGA AGTCCGCGCG GCGGAAGTGG CGCAATCGAT
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTATCGTCT GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAAG GGTCAAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACCTCGA TGCCGTCGAA GCCGCGCGCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGCAAGG TATTGAAACG GGTGTTGAAG GACAGTTTTG ACGGAATCAA
1551 ATGA

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a164.pep
  1  MNRTYANFYE MLTAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
 51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101  DCKARFLFAS AGLSKELAGL KAQTPVEKII VTGQSRPDGE MAEGDAFFED
151  VRRFPEKPDG GRQPRINDLA HIIYTSGTTG HPKGALISYA NLFANLNGIE
201  RIFFKSKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251  KQALLKRATV FLGVPaiYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301  ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351  VDEELVEVPR GEVGELIVRG GSVMRGYLNM PAATDETIVN GWLKTGVDFVT
401  IDEDGFIFIV DRKKDLII SKQNVYPREIE EEIYKLDAVE AAAVIGVKDR
451  YADEEIVAFV OLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
```


468

501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

	10	20	30	40	50	60
m164.pep	MNRTYANFYEMLAACRKNGNGTAVFDGKEKTAYRALKQEAEEVAAYLQNIGVKFGDTVA					
	:					
a164	MNRTYANFYEMLTAAACRKNGNGTAVFDGKEKTAYRALKQEAEEVAAYLQNIGVKFGDTVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m164.pep	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	:					
a164	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m164.pep	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETTG					
	:					
a164	KAQTPVEKIIWTDKSRPDGEMAEAGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETTG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m164.pep	HPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
	:					
a164	HPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m164.pep	KSVFPFSNVLKQTLKRATVFLGVPAYITAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
	:					
a164	KSVFPFSNVLKQALLKRATVFLGVPAYITAMSKTKIPWYFRWFNRIRLFISGGAPLAEQT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m164.pep	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSVGIPLPGLEAKAVDEELVEVPR					
	:					
a164	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSVGIPLPGLEVAVDEELVEVPR					
	310	320	330	340	350	360
	370	380	390	400	410	420
m164.pep	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
	:					
a164	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m164.pep	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
	:					
a164	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
	430	440	450	460	470	480
	490	500	510			
m164.pep	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
	:					
a164	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq

1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC

469

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51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCGCCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGATTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCCTCTT CCTCGGCGCG GGCGCGCGCG CACTGACCCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAAC TTCC TCAAGCAAGG CTCGTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CcTGCTGGgc gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSQR FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GLPVSGLFFR NSNPETAEQH NAKVYQASV GAPPMVPHL
301 DTRNVDGKRH LMFPGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GGCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGTGCGCAAT GGGATTATCG ATCCGCGCGC CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGATTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GGCGGCGGCG CGCTGACCCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAAC TTCC TCAAGCAAGG CTCGTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQR FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF

```

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201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLCAGWA
351 NMPLTK...

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
g165	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEAGTDVDF					
g165	HCRYLQKRYDVFKTQKLFENMEFSTDRNKISDWAPLIMRGRDENQPVAANYSAEAGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165.pep	GRLTRQMVKYLOGKGVKTEFNHVEDIKRESGDGAWVLKTADTRNPDGQLTLRTRFLFLGA					
g165	GRLTRQMVKYLOGKGVKTEFNHVEDIKRESGDGAWVLKTADTRNPDWQLTLRTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSPVPHL					
g165	GGGALTLLQKSGIPEGKGYGGPLVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSPVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	
m165.pep	DTRNVDGKRHLMFPGYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK					
g165	DTRNVDGKRHLMFPGYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
g165	ELRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

```

a165.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC

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471

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601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCC GCCCTTACGC
951 AGGCTTCCGT TCCAATTCC TCAAGCAAGG CTCATTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACGCGA
1451 AAGTGTGGA TATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```

a165.pep
  1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSAWN
 51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQR FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAA N YSAEGTDVDF GRLTRQMKY LQGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFRR NSNPETAQH NAKVYGQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTEERF ASLLEYYPEA NPDDWELITA GQRVQIIKGD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165/a165 99.7% identity in 356 aa overlap

```

              10      20      30      40      50      60
m165.pep    MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSAWNAGTGHSALC
              |||
a165        MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSAWNAGTGHSALC
              10      20      30      40      50      60

              70      80      90     100     110     120
m165.pep    ELNYAPLGANGIIDPARALNIAEQFHVSQRQFWATLVAEGKLEDNSFINAVPHMSLVMNED
              |||
a165        ELNYAPLGANGIIDPARALNIAEQFHVSQRQFWATLVAEGKLEDNSFINAVPHMSLVMNED
              70      80      90     100     110     120

              130     140     150     160     170     180
m165.pep    HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAA N YSAEGTDVDF
              |||
a165        HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAA N YSAEGTDVDF
              130     140     150     160     170     180

              190     200     210     220     230     240
m165.pep    GRLTRQMKY LQGKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLTLRTRFLFLGA
              |||
a165        GRLTRQMKY LQGKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190     200     210     220     230     240

              250     260     270     280     290     300
m165.pep    GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSPVPHL
              |||
a165        GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSPVPHL
              250     260     270     280     290     300

```

q165-1.seq

1	ATGGCTGAAG	CGACAGACGT	TGTCTTGGTG	GGCGGCGGCA	TTATGAGCGC
51	GACTTTGGGC	GTTTGTCTCA	AAGAATCTCGA	ACCGTCTTGG	GAATCATCCC
101	TGATTGAACG	CTTGGAAgat	gTGGCGTTGG	AATCGCTCAA	cGCGTGGAAc
151	AACGcCGgca	CGGGGCATTc	cgGCGTGTgc	GAATTGAACt	ATgcgccGCT
201	GGGtgcggaac	ggcgctcatCA	ATCCGGCGCg	cgCCTGAAt	ATTGCGGCAAc
251	AGTTTCAATGT	CATCGGCCAG	TTTGGGCGga	cgctggTCGC	GGAGGCGCAAG
301	TTTGAAGAACA	ATTCCTTCAT	CAATGCGGCG	CCGATATATG	CTTTGGTGAT
351	GAACGAAGAC	CACTGCCGTT	ACCTGCAAAA	ACGCTATGAT	GTGTTTAAAA
401	CGCAGAAACT	TTTTGAAATt	ATGGAATTTT	CCGCGATCG	GAACAAAAAT
451	TCCGATTGGG	CtcgcCTGAT	TATGCGGGCG	CGGACGAA	ACCAACCCGT
501	CGCGGCCAAC	TATTCCGCCG	AAGGCACGGA	TGTCGATTTC	GGACGGCTGA
551	CGCGCCAGAT	GGTGAAATAT	TTGCAGGGCA	AGGGCGTAA	AACCGAGTTC
601	AACCGCCACG	TCAAGACAT	CAACCGCGAA	TCCGACGGCG	CGTGGGTGCT
651	CAAAACCGCC	GATACCCGCA	ACCGACACTG	GCAGCTCACC	CTCCGCACCC
701	GCTTCCTCTT	CCTCGGCCGg	GGCGCGGGCG	CAGTGAACCT	GCTGCAAAAA
751	TCCGGCATCC	CGGAAGGCA	AGGCTACGGC	CGCTTACCCT	TGTCGCGCCT
801	GTTCTTCCGC	AACAGCAACC	CGAAACCCG	CGAACAAAC	AACGCCAAG
851	TGTACGGGCA	GGCTTCCGTC	GGCGCGCCG	CGATGTCCGT	CCGCACTTCG
901	GACACACAG	ACGTAGACGG	CAACAGACAC	CTTATGTTCC	GTCCTTACGC
951	AGGTTTCCGT	TCCAACCTTC	TCAAGCAAGG	CGTGTATTAT	GATTTGCCGC
1001	TGTCATCCCA	TATGGACAAC	CTCTATCCTA	TGCTGCGCGC	CGGCTGGGCG
1051	AATATGCCCG	TGACCAATCA	CCTGTGCGGC	GAATTTCGTA	AAACCAAGA
1101	AGAACGCTtt	gCCTCCCTGC	TGgaataata	cccGaggcag	accCGACGAC
1151	tggtactcat	cacgcagync	acGCGTcata	tcattanata	tgactCgaaa
1201	ctgcgcgtgc	tgcagttgtta	cgagatgtgt	ccaCGCGtag	ctcgcctcgcg
1251	cattcttgga	cgctgcgcgcg	catcacgctn	tgcgctgcga	tccgctgatg
1301	acactcctcc	gGCGGcgccc	ctctttgaaa	gtgtctga	

g165-1.pep

1	1	MAEATDVVLV	GGGIMSATLG	VLLKELEPSW	EITLIERLED	VALESSNAWN
51		NAGTGHSA LC	ELNYPALGAD	GVINPARALN	IAEQFHVSRQ	FWATLVAEGK
101		LEDNSFINAV	PHMSYVMNED	HCRIYLQKRY	VFKTKQLFEN	MEFSTDNRNI
151		SDWAPLIMRG	RDENQPVAAN	YSAEGTDVDF	GRLTRQMVKY	LQKGKVKTEF
201		NRHVEDIKRE	SDGAWVLTKA	DTRNPDOQLT	LRTREFLFLG	GGGATLLQK
251		SGHPGEGKYG	GLPVSGLFFR	NSNPETAELN	NAKVYQASV	GAPFMSVPHL
301		DTRNVDGKRH	LMFGPYAGFR	SNFLKQGSFM	DLPLSIHMND	LYPLMLRGWA
351		NMPLTKYLLG	ELDKRKEERF	ASLLEYPRQ	TTRLVLITQX	TRHIIXYDSK
401		LRVLOLYEIV	PRDARSIRLE	RGASRXALI	SADDTAPSAP	VLESV*

m165-1.seq

1	ATGGCTGAAG	CGACAGACGT	TGTCTTGGTG	GGCGGCGGCA	TTATGAGCGC
51	GACTTTTGGG	GTTTTGCTCA	AAGAACTCGA	ACCGCTTTGG	GAATATACCC
101	TGATTGAAGC	CTTGGAAGAT	TGGCGCTTGG	AATCGTCAA	CGCGTGGAA
151	AACGCCGCGA	CGGGGACATC	CGCGCTGTGC	GAATTGAAC	ATGCGCCGTT
201	GGGTGCAAA	GGGATTATCG	ATCCGGCGCG	CGCCCTCAAT	ATTGCGCAAC
251	AGTTTCAATG	CAGCCGCTCAT	TTTGGGCGA	CGCTGGTCTG	GGAAGCGAAG
301	TTGGAAGACA	ATTCTTCCAT	CAATGCGCTG	CCGATATATG	CTTTGGTGAT
351	GAATGAAGAC	CATTGTCTTT	ATCTTCAAAA	ACGTATATGAC	GCCTTTAAAA
401	CCCAAAAACT	TTTTGAAAT	ATGGAATTTT	CCACCGATCG	GACAAAAATT
451	TCCGATTGGG	CTCCGCTGAT	GATGCGCGCG	CGGGACGAAA	ACCAACCCGT
501	CGCGCCCAAC	TACTCCGCGG	AAGGTACGGA	TGTCGATTTC	GGACGGCTGA
551	CGCGCCCAAT	GGTGAATAT	TTGACGGGGA	AGGGCGTAAA	AACCGAGTTC
601	AACCGCCACG	TCAAGACAT	CAAACGCGAA	TCCGACGGCG	CTGGGTGCTC
651	CAAAACCGCC	GATACCCGCA	ACCCGACGGG	CGAGCTACCC	CTCCGTACCC
701	GCTTCTCTTT	CCTCGGCGCG	GGCGGCGGCG	CGCTGACCCT	GCTGCAAAAA
751	TCCGGCATCC	CCGAAGGCGA	AGGCTACGGC	GGCTTCCCCG	TATGCCGCGCT
801	GTCTTTCGAC	AACAGCAACC	CCGAAACCGC	CGAACAAAC	ATGCCGCAAG

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851 TGTACGGGCA GGCTTCCGTC GGGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGAGCA AACCCCGACG
1151 ACTGGGAACT CATCACCACA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTTAA
```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

m165-1.pep

```
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKGD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*
```

m165-1/g165-1 89.7% identity in 428 aa overlap

m165-1.pep	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
g165-1	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
	10	20	30	40	50	60
m165-1.pep	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165-1	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
m165-1.pep	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDRDNQPVAAANYSAGTDVDF					
g165-1	HCRYLQKRYDVFKTQKLFENMEFSTDRNKISDWAPLIMRGDRDNQPVAAANYSAGTDVDF					
	130	140	150	160	170	180
m165-1.pep	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKYLQKGKVKTEFNHVEDIKRESGAWVLKTADTRNPDGQLTLRTRFLFLGA					
g165-1	GRLTRQMVKYLQKGKVKTEFNHVEDIKRESGAWVLKTADTRNPDWQLTLRTRFLFLGA					
	190	200	210	220	230	240
m165-1.pep	250	260	270	280	290	300
m165-1.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSPVPHL					
g165-1	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSPVPHL					
	250	260	270	280	290	300
m165-1.pep	310	320	330	340	350	360
m165-1.pep	DTRNVDGKRHLMFPGYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG					
g165-1	DTRNVDGKRHLMFPGYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
m165-1.pep	370	380	390	400	410	420
m165-1.pep	ELRKTKEERFASLLEYYPEANPDWELITAGQRVQIIKGDSEKGGVLQFGTEIVAHADGS					
g165-1	ELRKTKEERFASLLEYPR-QTRRLVLITQXTR-HIIXYDS-KLRVLQLYEIVPRDARS					
	370	380	390	400	410	
	430	440	450	460	470	480

```

m165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNNPERADEIIA
:           |||
g165-1      ILERRGASRXALISADDTAPSAPVLESVX
           420       430       440

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

```

a165-1.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAAC ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT GAGCGCCAG TTTTGGGCGA CGTTGGTGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATGTTCCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGAATTT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCTG
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGCGCG CGCTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCGGCCTT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACTTATG GATTTGCCGC
1001 TGTCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATAA CTGCTGGGCG GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCGGAGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGCGTGT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACGCGA
1451 AAGTGTGGA TATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

```

a165-1.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWTALVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFTDRNKI
151 SDWAPLMRGR RDNQPVAAAN YSAEGTDVDF GRLTRQMKY LQKGKVFTEF
201 NRHVEDIKRE SDGAVVLKTA DTRNPDGQLT LRTFLFLGA GGGALTLLQK
251 SGIEPEGKGYG GFFVSGLFFR NSNPETAQEH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGLM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLEYYPEA NPDDWELITA GQRVQIIKID
401 SEKGGLQFQF TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLEKEL VPGYGIKLNE NPERADEIIA YTAKVLDI*

```

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
m165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
	10	20	30	40	50	60
	70	80	90	100	110	120
a165-1.pep	ELNYAPLGANGIIDPARALN	IAEQFHVSQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
m165-1	ELNYAPLGANGIIDPARALN	IAEQFHVSQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
	70	80	90	100	110	120
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFTDRNKISDWAPLMRGR	DENQPVAAANYSAEGTDVDF			
m165-1	HCSYLQKRYDAFKTQKLFEN	MEFTDRNKISDWAPLMRGR	DENQPVAAANYSAEGTDVDF			
	130	140	150	160	170	180
	190	200	210	220	230	240

```
al65-1.pep  GRLTRQMVKYLOGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
|||||
m165-1      GRLTRQMVKYLOGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
al65-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYGOASVGAPPMSVPHL
|||||
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYGOASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
al65-1.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
|||||
m165-1      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
al65-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
|||||
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
al65-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
|||||
m165-1      LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
al65-1.pep  YTAKVLDIX
|||||
m165-1      YTAKVLDIX
```

al65-1/p33940

sp|P33940|YOJH_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION
>gi|1736851|gnl|PID|d1016718 (D90850) ORF ID:o372#5; similar to [SwissProt Accession Number
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical
to 490 residues of YOJH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct
identical to GB: ECOHU49_33
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
Score = 458 bits (1167), Expect = e-128
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```
Query: 3  EATDVVLVGGGIMSATLGVLKLEPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30 QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63 NYAPLGGANGIIDPARALNIAEQFHVSROFWATLVAEGKLED-NSFINAVPHMSLVMNEDH 121
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90 NYTPQNADGSISIEKAVAINAEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

Query: 122 CSYLQKRYDAFKTQKLFENMEFSTDNRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDFG 181
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150 VNFLRARYAALQQSSLFRGMRYSEDHAQIKWAPLVMGRDPQKVAATRTEIGTDVNYG 209

Query: 182 RLTRQMVKYLOGKG-VKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
+TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210 EITRQLIASLQKKSNSFLQSLSEVRALKRNDNTWTVTVADLKNGTAG-NIRAKFVFIGA 268

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYGOASVGAPPMSVPHL 300
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVVNHHLAKVYGKASVGAPPMSVPHI 328

Query: 301 DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329 DTRVLDGKRVLFGPFATFSTFKLKNGLSLDMSSTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389 QVMLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDAEKGGVLRGLGTEVVSDDQGT 448

Query: 421 XXXXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478
```


P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPIMLNLLLEKVFGRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508
 Query: 479 IAYTAKVLDI 488
 + YT++VL +
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq
 1 atggcgggcg cggaaataaa acgccccctc gctgtcgatt tccagcacat
 51 agcgtccggt ctgcacggcg gcatagccgc ttttgccctgc ctgatagggt
 101 tgcagggcg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc
 151 ggcgatatgg cccaccagtt tggcaaaciaa ggtatggcac acgccgtttt
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg
 251 acgacggcct ccaagtcggt gggatgcttt ccggtcagcc ggacggcggt
 301 ttgttccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt
 351 tggtttttgc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta
 401 ttgtcgatgt atttgacttt gaaaaccggg ttcggcgcg tttgtgcgcg
 451 attttgcggc tgttccgcgc tattttcggg tttgccgcag gcggcaagca
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
 551 tgatgggttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg
 601 aggttcggac ggcatgggt ttatttcaac gggcggatgc cgaccgcac
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgct ttttgcgcgc
 701 ctgcctgcaa aatctcttcg atttgcgaa gattagaggt caatgcgttg
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQVV GMLSGQPDGV
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDFD ENRFRRLCR
 151 ILRLFRRIFG FAAGGKQQA AOHGKRYFQH SALLMVSKCR LKCRLLKRRR
 201 RFRHWWYFN GRMPTASRTL SNNSRASLRA FCAPACKISS ICEGLEVNAL
 251 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq
 1 ATGGCGGCGG CGGAAATAAA ACGCCCCCTC GCTGTTCGATT TCCAGCACAT
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCTGC CTGATAGGGT
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC
 151 GGCGATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
 201 CTGCCCCACC TGCCGGACTG TCCTTATCAT CGGTTTCCAT ACATTTGCCG
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT
 351 TGGTTTTGCC TTCGCTGCTT TGTCCCAAT CCAAACGGC AATCGCCGTA
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTGTACCGC
 451 GTTTTGCGGC TGTACCGCCG TATTTWCGGA TTTGCCGCaC GGCaaArGCAG
 501 CAGGCAGCCG CCCAATACGG CAAAArAwGT wTTCAGCATT CCACaYTCCT
 551 GATGGTTTCA AAATGCCGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA
 651 ATAATTCGCG TGCTTCTTTA CGCGCTTTTC CCGCGCCTGC CTGCAAAATC
 701 TCTTCGATT GCGAAGGGTC GCGGTCAGC TCGTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRLYR
 151 VLRLYRRIXG FAATAQQQA AQYKXXXQH STXLMVSKCR LKGRRRRFRG
 201 HRVHFNGRMP TASGTLSNNS RASLRAFAAP ACKISSICEG SAVSSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 204 shows 82.0% identity over a 250 aa overlap with a predicted ORF (ORF 204.ng) from *N. gonorrhoeae*:

m204/g204

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIAASVLHGGIAAFACLIGLQGGMRNXVIRQFAAVFGDIAHQFGKQ					
g204	MAAAEIKRPLAVDFQHIAASVLHGGIAAFACLIGLQGGMRNQVISQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
g204	GMAHAVFRPARRRVLSVGFHTFADDGFQVVGMLSGQPDGVLFRQAFNRITDLFFAVVGFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m204.pep	FAALSQIQTGNRRRVIDIYDFENRFRALYRVLRLYRRIXGFAATAXQQAAQYKXXXQH					
g204	FATLSQSQTGNRRRIVDVDFENRFRALCRILRLFRIFGFAAGGKQAAAQHGKRYFQH					
	130	140	150	160	170	180
	190	200	210	220	230	
m204.pep	STXLMVSKCRLK----RGRRRFGRHRVHFNGRMPTASGTLNNRSRASLRAFAAPACKISS					
g204	SALLMVSKCRLKCRLKGRRRFGRHWVYFNGRMPTASRTLSNNRSRASLRAFCAPACKISS					
	190	200	210	220	230	240
	240					
m204.pep	ICEGSAVSSLX					
g204	ICEGLEVNAL					
		250				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

a204.seq	1	ATGGCGGCGG	CGGAAATAAA	ACGCCCCCTC	GCTGTCGATT	TCCAGCACAT
	51	AGCGTCCGTT	CTGCACGGCG	GCATAGCCGC	TTTTGCCTGC	CTGATAGGGT
	101	TGCAGGCGG	AATGCGAAAT	CAGGTAATCC	GTCAGTTTGC	CGCCGTCTTC
	151	GGCGATATTG	CCCACCACTT	TGGCAAACAA	GGTATGGCAC	ACGCCGTTTG
	201	CCGCCAGCC	CGAAGGCGCG	CCCTTTCCGT	CGGTTTCCAT	ACATTTGCCG
	251	ACGACGCTT	CCAAGTCGTT	GGGATGCTTG	CCGGTCAGCC	GGACGACGTT
	301	TTGTTCCGGC	AAGCCTTT..
	351
	401
	451
	501
	551AAGAG	GTTCCGACGG
	601	CATTGGGTTT	ATTTCAACGG	GCGGATACCG	ACCGCATCAC	GTACTTTGCC
	651	CAATAATTCG	CGTGCTTCTT	TACGCGCTTT	TTGCGCGCCT	GCCTGCAAAA
	701	TCTCTTCGAT	TTGCGAAGGG	TCGGCGGTCA	GCTCGTTGTA	G

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

a204.pep	1	MAAAEIKRPL	AVDFQHIA	SVLHGGIA	AFACLIGL	QGGMRN	QVIRQFA
	51	GDIAHQFGKQ	GMAHAVCR	PAARRALS	SVGFHTF	ADDGFQV	VGMLAGQ
	101	LFRQAF....
	151KRFR
	201	HWVYFNGRIP	TASRTL	PNNSRAS	LRAFCAP	ACKISS	ICEGSA
							SSSL*

m204/a204 54.5% identity in 246 aa overlap

```

      10      20      30      40      50      60
m204.pep  MAAAEIKRPFVDFQHIASVLHGGIAAFACLIQLGGMRNXVIRQFAAVFGDIAHQFGKQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a204      MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLGGMRNQVIRQFAAVFGDIAHQFGKQ
          10      20      30      40      50      60

      70      80      90      100     110     120
m204.pep  GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA
          |||||  | : | : ||||| |||||:|||| | :||| |||
a204      GMAHAVCRPARRRALSVMGFHTFADDGFQVVGMLAGQPDDVLFQRQAF-----
          70      80      90      100

      130     140     150     160     170     180
m204.pep  FAALSQIQGTGNRRIVDIYDFENRFRRALYRVLRLYRRIXGFAATAXQQAAAQYGKXXXQH
a204      -----

      190     200     210     220     230     240
m204.pep  STXLMVSKCRLKGRRRFGRHRVHFNRMPTASGTLNNSRASLRAFAAPACKISSICEG
          :|||| | :||||:|||| | ||||| ||||| ||||| |||||
a204      -----KRFGRHWVYFNGRIPTASRTLPNNSRASLRAFCAPACKISSICEG
          110     120     130     140     150

m204.pep  SAVSSLX
          |||||
a204      SAVSSLX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

```

g205.seq
1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgcttgccgc
51  ctgcggcaaa tccgaaaata cggcggaaca gccgcaaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaa atcatcgaca tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaagga cgcgccttcg ggctgggcgg aaaacggcgt
351 gtgccatacc ttgtttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaaaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgcctgcag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

```

g205.pep
1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNIA EDGGKLT DYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

```

m205.seq
1  ATGCTGAAWA CwTyTTTTCG CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tGCGCAAAT CCGwAAATAC GGCGGTACAG CCGCAAACG CCGGTACAAAG
101 CGCGCCGAAA CCGGTTTTC AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGA AGCCGTCAGC GGCAAATGTA
301 TGGAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTCGCAA ACTGGTGGC AATATCGCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTCGCATGC CGCCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

```
m205.pep
  1  MLXTXFAVLG GCLLXCRCGK SXNTAVQPQN AVQSAPKPVF KVIYIDNTAI
 51  AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101  METDDKDSPA GWAENGVCHT LFAKLVGNIA EDGGKLTDL VSHAALQPYQ
151  AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

```
m205/g205

      10      20      30      40      50      60
m205.pep  MLXTXFAVLGGCLLXCRCGKSXNTAVQPQNAVQSAPKPVFKVIYIDNTAIAGLDLGQSSE
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205       MLKIPFAVLGGCLLLAACGKSENTAEQPQNAASAPKPVFKVKYIDNTAIAGLALGQSSE
          10      20      30      40      50      60

      70      80      90     100     110     120
m205.pep  GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSPAGWAENGVCHT
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205       GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT
          70      80      90     100     110     120

      130     140     150     160     170     180
m205.pep  LFAKLVGNIAEDGGKLTLDYLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205       LFAKLVGNIAEDGGKLTLDYLISHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          130     140     150     160     170     180

m205.pep   YX
           |
g205       Y
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

```
a205.seq (partial)
  1  TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
 51  CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG
101  ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGGCGT GTGCCATACC
151  TTGTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACGTAC
201  GGATTACCTG ATTTGCGATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
251  GCGGCTATGC CGCCGTGCAG AACGGACGCT ATGTGCTGGA AATCGACAGC
301  GAGGGGGCGT TTTATTTCCG CCGCCGCCAT TATTGA
```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

```
a205.pep (partial)
  1  SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT
 51  LFAKLVGNIA EDGGKLTDL ISHSALQPYQ AGKSGYAAVQ NGRYVLEIDS
101  EGAFYFRRRH Y*
```

m205/a205 88.3% identity in 111 aa overlap

```
      50      60      70      80      90     100
m205.pep  KVIYIDNTAIAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC
          | | : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a205       SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC
          10      20      30

      110     120     130     140     150     160
m205.pep  METDDKDSPAGWAENGVCHTLFAKLVGNIAEDGGKLTLDYLVSHAALQPYQAGKSGYAAVQ
```

g205-1.seq (partial)

g205-1.pep (partial).

m205-1.seq..

m205-1.pep

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKSENTAEQPNAAQSAPKPVFKVKYIDNTAIAGLALGQSSE					
m205-1	MLKTSFAVLGGCLLLAACGKSENTAEQPNNAVQSAPKPVFKVKYIDNTAIAGLDLGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT					
m205-1	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDL EAVVGKCMETDDKDSAGWAENGVCHT					

481

```

              70      80      90      100      110      120
              130      140      150      160      170
g205-1.pep    LFAKLVGNI AEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAF
              |||||
m205-1        LFAKLVGNI AEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
              130      140      150      160      170      180
m205-1        YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
1  CCTCTTAAAG GCTTGCCGGA ACAAACGTC GTCCGGCTGA CCGGCAAGCA
51  TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
101 AGGGCGCGCC TTCGGGCTGG GCGGCAAACG GCGTGTGCCA TACCTTGTTT
151 GCCAAACTGG TGGGCAATAT CGCCGAAGAC GCGCGCAAAC TGACGGATTA
201 CCTGATTTCG CATTCCGCCG TGCAACCCTA TCAGGCAGGC AAAAGCGGCT
251 ATGCCGCCGT GCAGAACGGA CGCTATGTGC TGGAAATCGA CAGCGAGGGG
301 GCGTTTTATT TCCGCCGCCG CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
1  PLKGLPEQNV VRLTGKHPND LEAVVGKCM ETDGKGAPSGW AANGVCHTLF
51  AKLVGNIAED GGLTDYLI SLSALQPYQAG KSGYAAVQNG RYVLEIDSEG
101 AFYFRRRHY*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

              50      60      70      80      90      100
m205-1.pep    KYIDNTAIAGLDLGQSSEKGTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCM E
              |||||
a205-1        PLKGLPEQNVVRLTGKHPNDLEAVVGKCM E
              10      20      30
              110      120      130      140      150      160
m205-1.pep    TDDKDSPAGWAENG VCHTLFAKLVGNI AEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNG
              |||||
a205-1        TDGKGAPSGWAANG VCHTLFAKLVGNI AEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNG
              40      50      60      70      80      90
              170      180
m205-1.pep    RYVLEIDSEGAFYFRRRHYX
              |||||
a205-1        RYVLEIDSEGAFYFRRRHYX
              100      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
1  atgttttccc cgcacaaaac ccttttcctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct ccggcaaaaca ccgccaaccg aaacccaaac
101 agacagtcgc gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctccgactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcattccatg ccccggcagc
451 ggcaaaaacca tcaaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttgga gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```

m206.seq

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

m206 . pep . .

Computer analysis of this amino acid sequence gave the following results:

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/q206

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq

1	ATGTTTCCCC	CCGACAAAAC	CCTTTTCCTC	TGTCTCAGCG	CACTGCTCCT
51	CGCCTCATGC	GGCAGGACCT	CCGGCAAACA	CCGCCAACCG	AAACCCAAAC
101	AGACAGTCCG	GCAAATCCAA	GCCGTCCGCA	TCAGCCACAT	CGACCGCACA
151	CAAGGCTCGC	AGGAAGTACAT	GCTCCACAGC	CTCGGACTCA	TCGGCAGGCC
201	CTACAAATGG	GGCGGCGACA	GCACCGCAAC	CGGCTTCGAT	TGCAGCGGCA
251	TGATTCAATT	CGTTTACAAA	AACGCCCTCA	CGGCTAAGCT	GCCGCGCACC
301	GCCCGCGACA	TGGCGGCGGC	AAGCCGCAAA	ATCCCCGACA	GCCGCGTTAA
351	GGCCGGCGAC	CTCGTATTCT	TCACACCGG	CGGCGCACAC	CGTACTCAC
401	ACGTCGGACT	CTATATCGGC	AACGGCGAAT	TCATCCATGC	CCCCAGCAGC
451	GGCAAAACCA	TCAAACCCGA	AAACTCTTCC	ACACCGTTTT	ACGCCAAAAA
501	CTACCTCGGC	GCACATACTT	TCTTTACAGA	ATGA	

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPR TARDMAAASRKIPDSRXKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPR TARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLS TPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLS TPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
1  atgctgcggc atttaggaaa cgacttcgcc ttgggcgcggt tgtttttcga
51  tgctgcggtt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcgggttcag ataggttttg gcgaacatcg ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatcg
451 gtcgtcgccg tatttttctt tgatggtctg cagttcgggt gcggcgccac
501 gcattttcgc catcgaaagg taggaggcgt tgggtcaatg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gcccagcccc agttgccgat
601 aatgttgtgc agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgtcggc gatgtttgcg
701 ataacggatg tggtttgccg accggcatac aggttgaccg ccattttcgg
751 ttttgcccc cggttgggga tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
1  MLRHLGNDFL LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQHRQTAA QRVDLFLFEK LHHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEPE ERRCEPVYFT VFVCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDGSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
1  ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGgGCGTT GTTTTTTCAT
51  GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAGGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGGGT CGGTCGGCGG
201 CGGGTTTCTA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```



```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTCCGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGGTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGGAGAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTCGGGG TTTTGCGGAT GTATTGCGCC
951 TCGGATTTGC CGGATTGGC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
  1 MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
 51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDGDL DLQQRQAAA QRVDLVCVK LHHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDDGCGLR AGVEVDGFGF
251 FAPFWMAAKG TLTLVLYSL LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSP V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng) from *N. gonorrhoeae*:

```

m209/g209
      10      20      30      40      50      60
m209.pep MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR
g209      MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVENQTGREEEEHDGENQRHDFHHFR
      10      20      30      40      50      60
      70      80      90      100     110     120
m209.pep LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAAEVGNPTQPRCLAQFYGGEQCPIQSDG
g209      LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAAEVGNPAQPRCLAQFYGGEQCPVQADEG
      70      80      90      100     110     120
      130     140     150     160     170     180
m209.pep DLQQRQAAAQRVDLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
g209      DLQQRQQTAAQRVDLVEKLHHRLLLRHTVVAVFFFDGLQFGCGGTHFRHRTVGGVGQW
      130     140     150     160     170     180
      190     200     210     220     230     240
m209.pep IQYGFDDDGXNDNRPAPVADDVVQLVQEP EERGEPVYFAVVFGQLQVVG DVCDDGCGLR
g209      IQYGFDDDGQNDDCPAPVADNVVQLVQEP EERRCEPVYFTVVFQQLQVVG DVCNDGCGLR
      190     200     210     220     230     240
      250     260     270     280     290     299
m209.pep AGVEVDGFGGF-APFWMAAKGTLTLVLYSLRLMSMLHSPAAQTLCLPLGWRIQVDMK
g209      :|::|| | | | |
      250
      TGIQVDRHFRFWPPGWDG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
  1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

```

51  TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGTGATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTGCGCG
201 GCGGGTTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AAGCCAGCCA
301 AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGTCT GCGCCATACG
451 GTCGTCGCGG TATTTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601 CAGTTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCAGT
651 GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTGCGC GATGTTTGGC
701 ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGCTGTA
801 CAGCTTGTCT TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851 AAACGCTTTG TCCGCCTTTG GGTGGAGGA TCCAGGTGGA CATGAAGTGG
901 TGTTCAATCA TGCCGAGCCA GCCGGTCGGG GTTTTGCGGA TGTATTCGGC
951 CTCGGATTTG CCGGATTTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```

a209.pep
1  MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDGDL DLQQRQAAA QRVDFLVCVK LHHGLLLRHT
151 VVAVFLFDGL QFGRGGTHFR HRTVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQKPK EGGGEPVYFA VVFGQLQVVG DVCNDCGLW AGVEVDGGFG
251 FAPFWIAAKG TLTLVLYSLS LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*

```

m209/a209 95.6% identity in 341 aa overlap

```

m209.pep      10      20      30      40      50      60
MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYVPVQYQTGREEEEHDGENQRHDFHHFR
|||||
a209          10      20      30      40      50      60
MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR

m209.pep      70      80      90      100     110     120
LHRVGRRRVQISLGEHRCRHNDGDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG
|||||
a209          70      80      90      100     110     120
LHRVGRRRVQIGLGEHRCRHNDGDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG

m209.pep      130     140     150     160     170     180
DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
|||||
a209          130     140     150     160     170     180
DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGRGGTHFRHRTVRGVGQW

m209.pep      190     200     210     220     230     240
IQYGFDDDGXNDNRPAVADDVVQLVQEPEERGGEVYFAVVFGQLQVVGDVCDGCGLR
|||||
a209          190     200     210     220     230     240
IQYGFDDDGXNDNRPAVADDVVQLVQKPKEGGGEVYFAVVFGQLQVVGDVCDNCGCLW

m209.pep      250     260     270     280     290     300
AGVEVDGGFGFAPFWMAAKGTLTLVLYSLSLRLMSMLHSPAAQTLCLPLGWRIQVDMKW
|||||
a209          250     260     270     280     290     300
AGVEVDGGFGFAPFWIAAKGTLTLVLYSLSLRLMSIRQSPAAQTLCPPLGWRIQVDMKW

m209.pep      310     320     330     340
CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX

```

486

a209 |||||
 CSIMPSQPVGVLRLMYSASDLPDLASSKSEKLTFWKLPSGVX
 310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

g211.seq
 1 atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atggtgcggc
 51 ggtgggaaac ggggtcgata agtttggcg tggctgat aatcaggttg
 101 agtttttga aggaacctg attgtagtcg gcgcgtccgg gcgtgccgct
 151 gtaacggtag ccgtggcgca attcgagcgt gcgtttgttgc tcttcagcg
 201 agaagttacc ttctttggcg aagatgatgt tgcgcgccg gtttttgtcc
 251 tggtcgcgca ggaacaggtt ttcatgatg ccggaattcg tgtcaaaggt
 301 ttcgacgaaa taaacctgc cgttgcgctt gcccaagtta ttgaactcgc
 351 cggcttcac caaagacaat tctgtcttct gttcaaaat ttcggcatat
 401 tcgcggtgc gcagctctgc ccacggatc acccaaagct gcatgacggc
 451 aatcaggtg gcaaacggca cggcaaactg catgacgggg cgtatccact
 501 gtttcaacgc caatccgcag gatag

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

g211.pep
 1 MLRIAAANQL GGRNGAAVGN GVDKFGRGAD NQVEFLEGNL IVVGASGRAA
 51 VTVAVAQFER AFVVLQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGVKG
 101 FDEINPAVAL AQVIELAGFH QRQFLLLQLN FGIFAAAQLC PRYHPKLHDG
 151 NQDGKRHGKL HDGAYPLFQR QSAG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

m211.seq
 1 ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
 51 GGTGGGAAAC GGGGTGATG AGTTTGGCG TGGTGCTGAT AATCAGGTTG
 101 AGTTTTTGA AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
 151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTG TCGTTCAGCG
 201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTCGCCGCC GTTTTGTCC
 251 TGTTCCGCGCA GGAACAGGTT TTTCATGATG CCGGATTCGG TATCGAAGGT
 301 TTCGACAAAA TAAACCTGC CGTTGCGCTT GCCCAAAGT TTGAACCTGC
 351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
 401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
 451 AACCAAAACG GCAAACGGCA CGGCAAAGT CATCACCGGG CGTATCCATT
 501 GTTCAATGC CAATCCGCA GATAG

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

m211.pep
 1 MLRVAAANQL GGRNGTAVGN GVDEFGRGAD NQVEFLEGNL IVVGASGRAA
 51 VTVAVAQFER AFVVVQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGIEG
 101 FDKINPAVAL AQTVELACLH QRQFLLLQLD FSVFAAAXLC PRYHPKLHDG
 151 NQNGKRHGKL HHRAYPLFQC QSAG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

m211/g211

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	: : : : : : : : : :					
g211	MLRIAAANQLGGRNGAAVGNVDKFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH					

```
a211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTTGGA AGGAAACCTG ATTGTAGTCG GCGGTCGCGT GCGTGCCGTT
151 GTAACGGTAG CCGTGCGCA ATTTCGAGCGT GCGTTTGTGT TCGTTACAGCG
201 AGAAGTTACT TTCTTTGGCG AAGATGATGT TGTCCCGGCC GTTTTTGTCC
251 TGTTCCGCGCA GGAACAGGTT TTTCATGATG CCGGATTCGG TATCGAAGGT
301 TTCGACAAAA TAAACCCTGC CGTTGCGCTT GCCCAAAC TGGAACCCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAACCGGCA CGGCAAAC TGATCACCGG CGTATCCATT
501 GTTTCAATGC CAATCCGCAG GATAG
```

a211.pep

1	MLRVAAANQL	GGRNGTAVGN	GVDEFGRGAD	NQVEFLEGNL	<u>IVVGASGRAA</u>
51	VTVAVAQFER	AFVVVQREV	FFGEDDVVAA	VFVLFAQEQV	FHDAGFGIEG
101	FDKINPAVAL	AQTVEPACFL	QRQFLLLQD	<u>FSVFAAA*LC</u>	PRYHPKLHDG
151	NONGKRHGK	LHRRAYPLFOC	QSAG*		

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGN	GVDEFGRGADNQVEFLEGNL	LIVVGASGRAAVTVAVAQFER			
a211	MLRVAAANQLGGRNGTAVGN	GVDEFGRGADNQVEFLEGNL	LIVVGASGRAAVTVAVAQFER			
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVAAV	FVLFAQEQVFHDAGFGIEGF	DKINPAVALAQTVELACLH			
a211	AFVVVQREVTFFGEDDVAAV	FVLFAQEQVFHDAGFGIEGF	DKINPAVALAQTVEPACLH			
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFS	VFAAAXLCPRYH	PKLHDGNQNGK	RHGKLGHHRAY	PLFQCQSAGX	
a211	QRQFLLLLQDFS	VFAAAXLCPRYH	PKLHDGNQNGK	RHGKLGHHRAY	PLFQCQSAGX	
	130	140	150	160	170	

```

g212.seq (partial)
  1  atggacaatc tcgtatggga cggcattccc gacatccgca cactcgacca
 51  aaccatccgc aaacacgcac acccgctcaa cctgattgtc tgccctcccc
101  ataatcagat tcccgatattt caaacgcgac aagatgcttc ggactcgga
151  tgccgtctga agcaccgttt ggatcaggca acccagtgcc tccagttcga
201  cagcatcaac ctcatcgaac acatcctgcc cgatgtccgc ttctgggttc
251  ttcccccttc acgcacccgc cgctgcacg aacacttcca ccacatttcc
301  ttgacagacc aagccatccc gcaaaccgaa agcaagtccg acaaaccctg
351  gtttgactt ccacaaacat ccgaacggaa aaaaccggaa cacgtcctcg

```

```

401 tcatcggtgc aggcattgcc ggcgcacga ccgcccacgc cttagcatca
451 cacggcattt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctcggaacaca tcctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcacctctct cagccatccg ctgatcgaac tatatgaaaa cacaacgtta
901 accggcattt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcatctactg caccggcgcg cacagcccct
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacgggcc tcacaccgtc caccctgtt tccgaacaac tgcgttgcgc
1101 cgtttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgcactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgcca agcattggca caccttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKPKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVWLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNROALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCTCCCCG
101 ATAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCCTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGTCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAACCCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GGCGCGGCAA CCGCCCACGC CTTAGCATCA
451 CACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAAGTTTTC CTTGCCGGCT ACGGCTACAC CAAACGCTTG
601 CTCGGACACA TCCTGCCCCG ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTCTGTC
851 GCACCTCTCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCTTTC
901 ACCGACATTT CCCACGACGG GGAAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCGCA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCCTTGCCT
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCACG
1301 CCGCCATACG CTGCGACAGC CCGGACCACC TTCCCCTAGT CGGCGCACTC
1351 GGCGACATTG CCGCCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAATAACCGC ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GGACTCGCCA CCGCCCCCAT CTGCGCCGCC

```

1501 GmCAwTGCAG CCCAAATCst AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 1551 gCGCCACGCC cTACACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE
 51 CRLKHRLDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS
 101 WQTEAIPQTE SKPDKPWFAL PQTSEKQKPE HILVIGAGIS GAATAHALAS
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LH CYGASFIP NSSHTGWNEA
 401 EEASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCDS PDHPLVLGAL
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng) from *N. gonorrhoeae*:

m212/g212

m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLIIICLPDNQIPDFQTAQDASDAECRLKHRLDQA
g212	MDNLVWDGIPDIRTLDQTIRKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRKHRLDQA
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPDKPWFAL
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRRLHEHFHHISWQTEAIPQTESKSDKPWFAL
m212.pep	PQTSEKQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS
g212	PQTSEKQKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPYLPETNL AALPLRQIRGQTGLTPSTPF
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAEEASNRQALAHLPALSES

490

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      |||||
g212  SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSNTGWNEAEEASNRQALAHLPALAESL
      370      380      390      400      410      420

      430      440      450      460      470      480
m212.pep FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN
      |
g212      F

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 737>:

```

a212.seq
1  ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51  AACCATCCGC AAACACGCAC ACCCGCTCAA CCTGATTGTC TGCCTCCCCG
101 ATAATCAGAT TCCCAATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ACCCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTGATTGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCGC CGCCTGCACG AACACTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGTAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGAGC GGGCATATCC GGCGCGGCAA CCGCCCACGC CTTAGCATCA
451 TACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAAAC CGAACTGCTG CTTGCCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACATA TCCTGCCGGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACGCA GGCAGAAGCC
751 GAAAAAATCG CCGGCATCCC TCTGAACACG CCCTACGCCG AACCATTATG
801 CGGACTGTTT TGGCAGTACG GCGTATGGCT CAATCCTCCC ACATTCTGTC
851 GCGCCCTCCT CAGCCATCCG CTCATTGGAC TACACGAAGA CACACCGTTA
901 ACCGACATTT CCCACGACGG GGAAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCCGA AACCACCTC GCCACCTGC CCCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TCGGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCACG
1301 CCGCCATACG CTGCGACAGC CCCGACCACC TTCCCCTAGT CGGCGCACTC
1351 GCGGACATTG CCGCTATGCA ACAAACCTAC GCCAAACTCG CGCTGGACAA
1401 AAATATATCG ATCGATGCCC CCTGCCCGTA CCTGCCCAAT GCCTACGCCA
1451 ACACCGCCCA CGGCACACGC GGGCTTGCCA CCGCCCCCAT CTGCGCCGCC
1501 GCCGTTGCAG CCGAAATCCT AGGCTTGCCC CATCCCCTCT CAAAACGCCT
1551 GCGCCACGCC CTACACCCCA ACCGCGCCAT CATCCGCGCC ATCGTCAGAA
1601 GGAAGGATCT AACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 738; ORF 212.a>:

```

a212.pep
1  MDNLAWNGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPNF QTAQDASDAE
51  CRLKHRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKPDKPWFAL PQTSEKQKPE HILVIGAGIS GAATAHALAS
151 YGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
201 LGHILPESET WGGNGIHLN YSRTEQQRNH ELGLQKHHNH LYRSITQAEA
251 EKIAGIPLNT PYAEPLCGLF WQYGVWLNPP TFVRALLSHP LIGLHEDTPL
301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL ATLPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
401 EEASNRQALA HLNPALESLS FAANPNPQKH QGHAAIRCDSP DHLPLVGAL
451 GDIAAMQQTY AKLALDKNYR IDAPCPYLPN AYANTAHGTR GLATAPICAA
501 AVAAEILGLP HPLSKRLRHA LHPNRAIIRA IVRRKDLTP*

```

m212/a212 93.7% identity in 539 aa overlap

```

      10      20      30      40      50      60
m212.pep MDNLVWDGIPDIRTLQDAIRKHAPPLNLIICLPDNQIPDFQTAQDASDAECRLKHRLDQA
      |||||:|||||:|||||:|||||:|||||:|||||
a212      MDNLAWNGIPDIRTLQDQIRKHAHPLNLIVCLPDNQIPNFQTAQDASDAECRLKHRLDQA

```

491

	10	20	30	40	50	60
m212 . pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212 . pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212 . pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212 . pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212 . pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212 . pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212 . pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212 . pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214 . seq
1  atgatacaaa agatatgtaa gctattttgtt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagcgtc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggg aaagggcgcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gtttcagcca aacgttggac gggggcaaag ggacggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgctgttc
351 tgaccggcaa tgccaaaagt cagcgcgcg ggcaggttgc cgaaggtgcg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214 . pep


```

1  MIQKICKLV LIVIFATSPA FALQSDSRP IQIEADQGS DQANQRTTFS
51  GNVIIRQGT NISASCVNVT RGRQRRRIE GGRFARPLQ NVGRGQRDGA
101 RSGKQRYLFL RRKHCRSDRQ CQSAARRRRC RRCGHYLQHQ NRSLYHQHQH
151 EIGCEIRFQN RQGQRRHPAF KHTKNRITPM PSETETQFRR HLPTEPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGGCGCG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLV LIAFFSASPA FALQSDSRP IQIEADQGS DQANQSTTFS
51  GNVIIRQGT NISAAARVNVT RGRQRRRIE GGRFASPLQ DIGRRQRHGA
101 RTGKQRCLEI CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQHQH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

```

m214/g214
      10      20      30      40      50      60
m214.pep  MIQKICKLVLI AFFSASP A FALQSDSRPIQ IEADQGS LDQANQSTTFSG NVVIRQGT
          |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g214       MIQKICKLV LIVIFATSPA FALQSDSRPIQ IEADQGS LDQANQRTTFSGNV IIRQGT
          10      20      30      40      50      60

      70      80      90     100     110     120
m214.pep  NISAAARVNVT RGRQRRRIE GGRFASPLQ PDIGRRQRHGARTG KQRCLEI CRQHRSLNRX
          |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g214       NISASCVNVT RGRQRRRIE GGRFARPLQ PNVGRGQRD GARS GKQRYLFL RRKHCRSDRQ
          70      80      90     100     110     120

      130     140     150
m214.pep  CQSTARRRCRRRC GDYIQHQ NRSLYHQ RQH KI
          |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g214       CQSAARRRRC RCGHYLQH QNRSLYHQ RQHEIGCEIRFQ NRQGQRRHPAFKHTKNRITPM
          130     140     150     160     170     180

g214       PSETETQFRRHLPTEPRRDY
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGGC.GGC AAAGGCGGCG AATCCGTGAG GCGGAAGGTT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC GGCGGCAAAG GCACGGTGCG
301 CGGACAGGCA AACAACGTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```

493

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGACGCG CATTTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
  1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
 51 GNVVIRQGT L NISAA RVNVT RGXQRRRIE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRCLF I CRQHRSLNR* CQSTARRRRC RRCGDYIQH Q NRSLYHQ RQH
151 KIRRKIRFQ I RQGQRRYP AF EYAKIRIIP M PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m214.pep	MIQKICKLFVLIAFFSASP AFALQSDSRQPIQIEADQGS LDQANQSTTFS GNVVIRQGT L					
a214	MIQKICKLFVLIAFFSASP AFALQSDSRQPIQIEADQGS LDQANQSTTFS GNVVIRQGT L					
	10	20	30	40	50	60
	70	80	90	100	110	120
m214.pep	NISAA RVNVT RGRQRRRIE GGRFASPLQ PDIGRRQRH GARTGKQRCLFICRQHRSLNRX					
a214	NISAA RVNVT RGRQRRRIE GGRFASPLQ PDIGRRQRH GARTGKQRCLFICRQHRSLNRX					
	70	80	90	100	110	120
	130	140	150			
m214.pep	CQSTARRRRCRRRCGDYIQHQNRSLYHQ RQH KI					
a214	CQSTARRRRCRRRCGDYIQHQNRSLYHQ RQH KIRRKIRFQIRQGQRRYP AF EYAKIRIIP M					
	130	140	150	160	170	180
a214	PSETXTWFG RHLPTEILKRYLX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTTCGAAC
 51 TTCTCCCGCT TTTGCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGTAC CACATTTAGC
151 GGCAATGTCA TCATCAGACA GGTACGCTC AACATTTCCG CCTCGCGCGT
201 CAACGTCACA CGCGCGGCGA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCCGTCCG CTTACGCCAA ACGTTGGACG GGGGCAAAGG GACGGTGCGC
301 GGTCAAGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CCGCAGCACG
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
  1 MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQSTTFS
 51 GNVVIRQGT L NISAS RVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
101 GQANNVTYSS AGSTVVL TN AKVQRGGDVA EGAVITYNTK TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
 51 GTCCCGCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT

```

494

```

201 CAATGTTACA CGCGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTACGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGCGC CAAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51 GNVVIRQGT L NISAARVNV T RGGKGGESV R AEGSPVRF S Q TLDGGKGTVR
101 GQANNVAY S S AGSTVVL T GN AKVQRGGD V A EGAVITYN T K TEVYTISGS T
151 KSGAKSASK S GRVSVVIQ P S STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

	10	20	30	40	50	60
m214-1.pep	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGS	L DQANQSTTFS	GNVVIRQGT L
g214-1	MIQKICKLFV	LIVIFATSP	FALQSDSRRP	IQIEADQGS	L DQANQSTTFS	GNVIRQGT L
	70	80	90	100	110	120
m214-1.pep	NISAARVNV	TRGGKGGES	VR AEGSPVRF	S Q TLDGGKGT	VR GQANNVAY	SSAGSTVVL T GN
g214-1	NISASRVNV	TRGGKGGES	VR AEGSPVRF	S Q TLDGGKGT	VR GQANNVY	SSAGSTVVL T GN
	130	140	150	160	170	
m214-1.pep	AKVQRGGD	VAEGAVITYN	TKTEVYTIS	GSTKSGAKS	ASKS GRVSVVIQ	PSSTQKSEX
g214-1	AKVQRGGD	VAEGAVITYN	TKTEVYTING	STKSGAKS	ASKT GRVSVVIQ	PSSTQKTEX

g214-1/p38685

sp|P38685|YHBN_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_ol85 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

Query: 19 PAFALQSDSRQPIQIEADQGS L DQANQSTTFS GNVVIRQGT L NISAARVNVTR--GGKGG 76
PAFA+ D+ QPI IE+DQ SLD TF+GNV++ QGT+ I+A +V VTR G +G
Sbjct: 24 PAFAVTGD TDQPIHIESDQQSLDMQGNVVTF TGNVIVTQGT IKINADKVVVTRPGGEQ GK 83

Query: 77 ES VRAEGSPVRF S Q TLDGGKGT VR GQANNVAY SSAGSTVVL T GN AKVQRGGD VA EGAVIT 136
E + G P F Q D GK V G A + + Y A VVLTGNA +Q+ +G IT
Sbjct: 84 EVIDGYGK PATFYQM DNGK -PVEGHASQ MHYELAKDFV VLTGNAYLQQVDS NIKGDKIT 142

Query: 137 YNKT E 142
Y K +
Sbjct: 143 YLVKEQ 148

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

```

1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTCCG CCGCCCGCGT
201 CAATGTTACA CGCGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTACGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGCGC CAAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

```

51 GNVVIRQGTI NISAARVNVT RGGKGGESVR AEGSPVRFSSQ TLDGGKGTVR
 101 GQANNVAYSS AGSTVVLGTN AKVQRGGDVA EGAVITYNTK TEVYTISGST
 151 KSGAKSASKS GRVSVVIQPS STQKSE*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQICKLFLVLI	AFFSASP	FALQSDSR	QPIQIEAD	QGSGLDQ	ANQSTTF
m214-1	MIQICKLFLVLI	AFFSASP	FALQSDSR	QPIQIEAD	QGSGLDQ	ANQSTTF
	10	20	30	40	50	60
	70	80	90	100	110	120
a214-1.pep	NISAARVNVT	RGGKGGES	VRAEGSP	VRFSQTL	DGGKGT	VRGQANN
m214-1	NISAARVNVT	RGGKGGES	VRAEGSP	VRFSQTL	DGGKGT	VRGQANN
	70	80	90	100	110	120
	130	140	150	160	170	
a214-1.pep	AKVQRGGD	VAEGAVIT	YNTKTEV	YTISGST	KSGAKS	ASKSGRV
m214-1	AKVQRGGD	VAEGAVIT	YNTKTEV	YTISGST	KSGAKS	ASKSGRV
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq

```

1  atgaaagtaa gatggcggta cggaattgcg ttccattga tattggcggg
51  tgcttggggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
101 tcgaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
151 ttggacggaa ggcggtttga cgaacagggg tacttgaaag aacatttgag
201 cgcgaaaggt gcgaaacagt ttccgaaaa cagcgacatc cattttgatt
251 cgccgcattc cgtgttcttc caagaaggca ggctgttgta cgaagtcggc
301 agcgatgaag ccgtttacca taccgaaaac aaacagggtc tttttaaaaa
351 caacgtttgt ctgacaaaaa ccgccgacgg caggcggcag gcgggtaaa
401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaacc
451 gatacgctg tcagtttcca atatggcgcg tcgcacgggc aggcgggcgg
501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
551 aagccgcgat ttatgataca aaagatatgt aa

```

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep

```

1  MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
51  LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPLVFF QEGRLLYEVG
101 SDEAVYHTEN KQVLFKNNVV LTKTADGRRQ AGKVETEKHL VDTESQYAQT
151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAYDT KDM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)

```

1  ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
51  CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG CGCGAAGGGC
151 GCGAAACAGT TTCCGAAAG CAGCGACATC CATTTTGATT CGCCGCATCT
201 CGTGTCTTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG
251 CCGTTTACCA TACCGAAAAC AAACAGGTTT TTTTAAAAA CAACGTTGTG
301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG
401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG CATGACTTAC
451 GACCACAwwA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT
501 TTATGATACA AAAGATATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)

```

1  ..SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG
51  AKQFPENSDI HFDSPLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNNVV
101 LTKTADGKRQ AGKVEAEKLH VDTESQYAQT DTPVSFQYGA SHGQAGGMTY

```

151 DHXTGMLNFS SKVKATIYDT KDM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40
m215.pep		SLSAWLGR	ISEVEIEE	VRLNPDEP	QYTMDSLDGRRFDEQG
g215	MKVRWRYGIAFPLILAVALG	SLSAWLGR	ISEVEIEE	VRLNPDEP	QYTMDSLDGRRFDEQG
	10 20 30 40 50 60				
	50 60 70 80 90 100				
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQ	EGRLLYE	VGSD
g215	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQ	EGRLLYE	VGSD
	70 80 90 100 110 120				
	110 120 130 140 150 160				
m215.pep	LTKTADGKRQAGK	VEAEKLV	HD	TESQYAQ	TDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
g215	LTKTADGRRQAGK	VETEKLV	HD	TESQYAQ	TDTPVSFQYGASHGQAGGMTYNHKTGMLNFS
	130 140 150 160 170 180				
	170				
m215.pep	SKVKATIYDTKDMX				
g215	SKVKAAYDTKDM				
	190				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq

1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCCATTGA	TATTGGCGGT
51	TGCCTTGGGC	AGCCTGTCGG	CATGGTTGGG	ACGCATCAGC	GAAGTCGAGA
101	TTGAAGAAGT	CAGGCTCAAT	CCCGACGAAC	CGCAATACAC	AATGGACGGA
151	TTGGATGGCA	GGCGGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTTGAG
201	TTCGAAGGGC	GCGAAACAGT	TTCCCGAAAAG	CAGCGACATT	CATTTGACT
251	CACCGCATCT	CGTGTCTTTC	CAAGAAGGCA	GGTTGTTGTA	CGAAGTCGGC
301	AGCGATGAAG	CCGTTTACCA	TACCGAAAAC	AAACAGGTTT	TTTTTAAAAA
351	CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAAACGGCAG	GCGGGTAAAG
401	TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCCAACC
451	GATACGCCTG	TCAGTTTCCA	ATATGGTGCA	TCGCACGGTC	AGGCGGGCGG
501	CATGACTTAC	GACCACAAAA	CAGGCATGTT	GAACCTCTCA	TCTAAAGTGA
551	AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pep

1	MKVRWRYGIA	FPLILAVALG	SLSAWLGRIS	EVEIEEVRLN	PDEPQYTM
51	LDGRRFDEQG	YLKEHLSSKG	AKQFPSSDI	HFDSPHLVFF	QEGRLLYEVG
101	SDEAVYHTEN	KQVLFKNNVV	LTKTADGKRQ	AGKVEAEKLH	VDTESQYAQT
151	DTPVSFQYGA	SHGQAGGMTY	DHKTGMLNFS	SKVKATIYDT	KDM*

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40
m215.pep		SLSAWLGR	ISEVEIEE	VRLNPDEP	QYTMDSLDGRRFDEQG
a215	MKVRWRYGIAFPLILAVALG	SLSAWLGR	ISEVEIEE	VRLNPDEP	QYTMDSLDGRRFDEQG
	10 20 30 40 50 60				
	50 60 70 80 90 100				
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQ	EGRLLYE	VGSD

```

|||||:|||||
a215      YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
              70          80          90          100          110          120

              110          120          130          140          150          160
m215.pep  LTKTADGKRQAGKVEAEKLVHVDTESQYAQTDPVSFQYGASHGQAGGMTYDHXTGMLNFS
              |||||||
a215      LTKTADGKRQAGKVEAEKLVHVDTESQYAQTDPVSFQYGASHGQAGGMTYDHKTGMLNFS
              130          140          150          160          170          180

              170
m215.pep  SKVKATIIYDTKDMX
              |||||||
a215      SKVKATIIYDTKDMX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcgagctc ggtaccacgc gacgaaatca ccgccatcat
51  ccccgccactc aaacgcaaaag acattaccct cgtctgcac accgcccgcc
101 ccgattcaac catggcgcgc catgccgata tccacatcac cgcacgggt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttgccggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcggc
301 aaacgcctgc ttttgccgct tgccgacatt atgcacaaag gcggcgccct
351 gcccgcctgc cgactcggca cgccttgaa aggagccatc gtcagcatga
401 gcgagaaaag tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKDITLVC I TARPDSTMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVVLL RARAFTPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGA I VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT *
51  GCACGCCGAA GCGGAAGGCT TGC GCGAAAT TGCAGCGGAA TTGsACAAAA
101 ACTTCGTCCT TCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGCGACGC CTGCGTTTTT CGTCCACCCCT GCGGAAGCGG
251 CACACGgCGA TTTGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTCG TCctGCTGCG CgcACGCGCG TTCACGCCCG
551 ACGATTTTCG CTTGAGCCAT CCTGCCGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCTGCG CTGCCGTCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALLHCKGRVV

```

Homology with a predicted ORF from *N. gonorrhoeae*

m216/g216

	70	80	90	100	110	120
m216.pep	TMASTGTPAFFVHPAEAAHGDLGMIVDXDVVVAISNSGESDEIAAIIIPALKRKDITLVCI					
				::: :	:::	:::
g216	MISISSSVSPSEITAIIPALKRKDITLVCI					
				10	20	30
	130	140	150	160	170	180
m216.pep	TARPDMSTARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVLLRARAFTPPDDF					
	::: :					
g216	TARPDMSTARHADIHITASVSQEACPLGLAPTTSTTAVMALGDALAVLLRARAFTPPDDF					
	40	50	60	70	80	90
	190	200	210	220	230	240
m216.pep	ALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGRL					
	:::					
g216	ALIHAPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKGAIVSMSEKGLGMWAGTDGQRLS					
	100	110	120	130	140	150

a216.seq

1	ATGGCGATGG	CAGGAAACGA	AAAAATATCTT	GATTGGGCAC	GCGAAGTGT
51	GCACACCGAA	GCGGAAGGCT	TGCGCGAAAT	TGCGGCGGAT	TTGGACGAAA
101	ACTTCGCCCT	TGCGGCGGAG	GC GTTGTTC	ACTGCAAAGG	CAGGGTCGTT
151	ATCACGGGCA	TGGGCAAGTC	GGGACATATC	GGGCGCAAAA	TGGCGGCAAA
201	CATGGCTTCG	ACCGGCACGC	CGCGGTTTTT	GGTCCACCCCT	GGCGAAGCGG
251	CACACGGCGA	TTTGGGCATG	ATTGTGGACA	ACGACGTGGT	CGTCGCGATT
301	TCCAATTCCG	GTGAAAGCGA	CGAAATCGCC	GCCATCATCC	CCGCGCTCAA
351	ACGCAAAGAT	ATCACGCTTG	TCTGCATCAC	CGCCCCGCCC	GATTTCAACCA
401	TGGCGCGCCA	TGCCGACATC	CACATCACGG	CGTCGGTTTT	CAAGAAAGCC
451	TGCCCGCTGG	GGCTTGCCCC	GACCACGAGC	ACCACCGCCG	TTATGGCTTT
501	GGGCGATGCG	TTGGCGGTTG	TCCTGCTGCG	CGCCCGCGCG	TTACGCCCCG
551	ACGACTTCGC	CTTGAGCCAC	CCTGCGGGCA	GCCTCGGCAA	ACGCCCTACTT
601	TTGCGCGTTG	CCGACATTAT	GCACAAAGGC	GGCGGCCTGC	CTGCCGTCCG
651	ACTCGGCACG	CCCTTGAAAG	AAGCCATCGT	CAGATGAGT	GAAAAGGGG
701	TGGGCAATGT	GGCGGTAAAC	GACGGGCAAG	GCCGTCTGAA	AGGCGTATTC
751	ACCGACGGCG	ATTTGCGCCG	CCTGTTTCAA	GAATGCGACA	ATTTTACCGG
801	TCTTTTCGATA	GACGAAAGTCA	TGCATACGCA	TCCTAAACC	ATCTCCGCCG
851	AACGCTCTCG	CACCGAAGCC	CTGAAAGTCA	TGCAGGCAAA	CCATGTGAAC
901	GGGCTTTCGG	TTACCGATGC	AGATGGCGTG	CTGATCGGCG	CGCTGAATAT
951	GCACGACCTT	TTGGCGGCGC	GGATTGTATA	G	

a216.pcp

1	MAMAGNEKYL	DWAREVLHTE	AEGLREIAAD	LDEFNFAAAD	ALLHCKGRVV
51	ITGMGKSGHI	GRKMAATMAS	TGTPAFFVHP	AEAAHGDLGM	IVDNDDVVAI
101	SNSGESEIEA	AIIPALKRKD	ITLVCITARP	DSTMARHADI	HITASVSKEA
151	CPLGLAPTTS	TTAVMALGDA	LAVVLLRARP	ETPDDFALSH	PAGSLGKRLL
201	LRVADIMHKG	GGLPFAVLRT	PLKEATVSMS	EKGLGMLAVT	DQGGRLLKGVF
251	TDGDLRLRFQ	ECDNFTGLSI	DEVMTHTPKT	ISAERLATEA	LKVMQANHVN

301 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENGKYLDWAREVLHAEAEGLREIAAEELXKNFVLAADALLHCKGRVVITGMVKSGHI					
	: : : :					
a216	MAMAGNEKYLDWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVVITGMGKSGHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIIPALKRKD					
	: : : :					
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDNDVVVAISNSGESDEIAAIIIPALKRKD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
	: : : :					
a216	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
	: : : :					
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRCLKGVFTDGDRLRLFQECNFTGLSIDEVMHHPKTISAERLATEALKVMQANHVN					
	: : : :					
a216	DGQGRCLKGVFTDGDRLRLFQECNFTGLSIDEVMHHPKTISAERLATEALKVMQANHVN					
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADGVLIGALNMHDLAARIVX					
	: : :					
a216	GLLVTDADGVLIGALNMHDLAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggatg acggtttggt gcggcaactg tccgaaaaac ccagccaaag
51  tgcctctctt ctgccatttg acccattcgt tttcgagggt ttggactgcc
101 ttttggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgagg ttgccgccat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggcaa aacgtccgaa catggcgggt
251 tgattcacgt cggcatacca cgcgctgaca tcctgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgcgcgcga tttctccgtc caatccccaa
401 tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcag aaacggcgca acacgggcgc ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg cttccagca agtcggacac gactccaac
551 gcataaaaaa acgggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgataa gggttcgata ttcggggtta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGKKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAFAQQVGH ALQRIKKRLP AADFHVRNGI

```


500

201 RQCLRAGLRL SEHGFKRRI GFDIRG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

```

1  ATGGCGGATG  ACGGTGTGCG  GCGGCAACTG  TCCGGAAAAT  TGCGCCAATT
51  CGGTTTCCGC  CTCCATTG  ACCCATTCGT  TTTCAAGGTT  TTGGACTGAC
101 TTTTGGTCAT  CGGCTTCAGC  TTGGAACAAT  GTTTCAGCA  AATCCCGGCA
151 ACGCGCCACC  CATTGCGCGA  CCGTTGCGGG  CTGCCGCCAT  ATCCGTACAA
201 TATCCGTGAG  GGTTCGAGG  AAGGCGGCAA  AACGTCCGAA  CATGGCGGTT
251 TGATTACAGT  CGGCATACCA  CGCGCTGACA  TCCTGCCACA  TCGGATTGCC
301 GCCTTTGGGC  AGCATCCAGC  CCAATATCAT  GCGTTCTACC  GCCTGCTTCC
351 AGGTGAACAG  CTGATCCGTG  CCGCCGCGCA  TTTCTCCGTC  CAAACCCAG
401 TGGACGTTCA  AATCGGCAAC  CATGTCGTGC  AAAAGCGGTA  AATCGTCCTC
451 AGTCAGTCCG  AAACGGCGCA  ACACGGGCGC  GGTTCCTAAA  AGCACAAGCA
501 CTTTATCGAC  TTCAAATCGG  CTTTCCAACA  AGTCGAACAG  GCATGACAAA
551 GCATGAAACA  GCGGTTGGCG  GCGGCTGATT  TTCACGTCTG  ACACGGAATA
601 CGGCAATGCC  TGCGCACCgG  GctGCGCCTG  TCCGAACACG  GCTTCGATAA
651 AAGGCGTATA  GGATTGATA  TTCGGGGTTA  A

```

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVRRL  SGKLRQFGFR  LPFDPFVFKV  LDXLLVIGFS  LEQCFKQIPA
51  TRHPFADRCG  LPPYPYNIRQ  GFEEGGKTSE  HGGLIHVGIP  RADILPHRIA
101 AFGQHPAQYH  AFYRLLPGEQ  LIRAAAHFSV  QTPVDVQIGN  HVVQKRXIVL
151 SQSETAQHGR  GFXKHKHFID  FKSAFQVEQ  AXQSMKQRLA  AADFHVXHGI
201 RQCLRTGLRL  SEHGFDKRR  GFDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVRRLSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHPPFADRCG					
	: :: : : :					
g217	MADDGLLRQLSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHPPFADRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVA AFGQHPAQYHTVCRLLPGKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVVQKRXIVLSQSETAQHGRGFXKHKHFIDFKSAFQQVEQ					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKRIVPGQSETAQHGRGFKREHFADFKTAFQQVGH					
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGI RQCLRTGLRLSEHGFDKRRIGFDIRGX					
	: : : :					
g217	ALQRIKKRLPAADFHVVRNGIRQCLRAGLRLSEHGFKRRI GFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

```

1  GTGGCGGATG  ACGGTGTGCA  GCGGCAACTG  TCCGGAAAAT  TGCGCCAATT
51  CGGTTTCCGC  CTGCCATTG  ACCCATTCGT  TTTCGAGGCT  TTGGACTGCC
101 TTTTGGTCAT  CGCCTTCGAC  TTGGAACAAT  GTTTCAGCA  AATCCCGGCA
151 ACGCGCCACC  CATTCGTCAA  CCGTCGCAGG  TTGCCGCCAT  ATCCGTACAA

```

501

```

201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTTCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGTGCG GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TGC GCGCCG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 768; ORF 217.a>:

```

a217.pep
1 VADDGVQRQL SGKLRQFGFR LPFDPFVFEEA LDCLLVIAFD LEQCQFKQIPA
51 TRHPFVNRRR LPPYPYNIRO GFEEGGKTSE QGGLVHVIGIP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KHKHFID FKSAFQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRAGLRL SEHGFDKRRRI GFDIRG*

```

m217/a217 90.3% identity in 226 aa overlap

	10	20	30	40	50	60
m217.pep	MADDGVRRQLSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCQFKQIPATRHFPADRCG					
a217	VADDGVQRQLSGKLRQFGFRLPFDPFVFEEALDCLLVIAFDLEQCQFKQIPATRHFPFVNRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIROGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
a217	LPPYPYNIROGFEEGGKTSEHGGLVHVIGIPRADPLPHRIA AFGQHPAQYHAFYRLLPGEQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVVQKRKXIVLSQSETAQHGRGFXKHKHFIDFKSAFQQVEQ					
a217	LIRAAAHFSVQTPADVQIGNHVVQKRQIVLSQSEMAQHGRGFXKHKHFIDFKSAFQQVEQ					
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIGFDIRGX					
a217	AXQSMKQRLSADFHIRNGIRQCLRAGLRLSEHGFDKRRIGFDIRGX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 769>:

```

g218.seq
1 atggttgccg tggatcctta tacggcaaaa gtggtcaaca ccatgccgcg
51 caatcagggt tggatcaca ctatggatga aatccacggc gatatgatgc
101 tcggtgcggc aggcgattat cttttgaaa cggcagcttc actgaccatt
151 attatggttg tcagcggcgt gtacctttgg tgggcgaaac agcgcggcat
201 taaagcgatg ctgctgccgc caaaaagcag ggcgcgttct tgggtggcggg
251 atctgcacgg cgcgtttgga acttggtgtg cgttgatttt actggtgttc
301 tgccgtgctg gtattgcttg ggcaggatatt tggggcggca aattcgtgca
351 ggcttggaat cagttcccgg ccggcaaatg ggtgtgcgaa ccgaacccc
401 tttcaatcgt gccgaccac gccgaggtat tgaatgacgg caagggttaag
451 gaagtgcctg ggattttgga gcttatgcct atgcctgtct cagggacgac
501 tgtgggtgaa aacggcatta accccaccga gcccaataac attggaaacc
551 gtcgaccgtt tcgcgcggga aatcggtttc aaagggcggt atcagttgaa
601 tttgccc aaa ggcgaggacg ggtatggac tttgtcgag gattctatga
651 gttatga

```

This corresponds to the amino acid sequence <SEQ ID 770; ORF 218.ng>:

```

g218.pep
1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```

51 IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGNRRPFRAG NRFQRALSVE
 201 FAQRRGRGMD FVAGFYEL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq
 1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC
 101 TCGGTGCGGC AGGCGATTAT CTTTGGAAA CGGCAGCTTC ACTGACCATT
 151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
 201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAr GGCGCGTTCT TGGTGGCGGA
 251 ATCTGCACGG CACGTTTGA ACTTGGGTGT CGTTGATTTT GCTGTTGTTC
 301 TGCTGTTCGG GTATTGCTTG GGCGGTATT TGGGCGGCA AGTTCGTACA
 351 GGCTTGAGT CAGTTCCCTG CCGGTAAATG GGGTGTCGAA CCGAACCCCG
 401 TTTCAGTCGT GCCGACCCAC GGCGAGGTAT TGAATGACGG CAAGGTTAAG
 451 GAAGTGCCGT GGGTTTGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
 501 yGtgGGCAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAAACCG
 551 TCGACCGCTT TGC GCGGnGA AATCGGTTT AAAGGGCGTT ATCAGTTGAA
 601 TTTGCCCAAA GCGAGGACG GCGTATGGAC TTTGTCGAG GATTCTATGA
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep
 1 MVAVDPYTAK VVSTMPRNQG WYYTMDEIHS DMMLGAAGDY LLETAASLTI
 51 IMVVSGLYLW WVKRRGIKAM LLPSKGXARS WWRNLHGTFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWILELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRALSVE
 201 FAQRRGRMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWWYYTMDEIHS DMMLGAAGDY LLETAASLTI IMVVSGLYLW					
	: : : : :					
g218	MVAVDPYTAKVVNTMPRNQGWWYHTMDEIHG DMMLGAAGDY LLETAASLTI IMVVSGLYLW					
	10	20	30	40	50	60
70	80	90	100	110	120	
m218.pep	WVKRRGIKAMLLPSKGXARSWWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
	: : : : :					
g218	WAKQRGIKAMLLPPKSRARSWWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
	: : : : : : :					
g218	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKEVPWILELMPMPVSGTTVGENGINPTEPNN					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFQRALSVEFAQRRGRMD FVAGFYEL					
	: :					
g218	IGNRRPFRAGNRFQRALSVEFAQRRGRMD FVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq

```

1   ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51  CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GGCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGGG ACTTGGGTGT CGTTGATTTT ACTGTTGTTT
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCAA CCGAACCTTG
401 TTTCACTCGT GCCGACCCAC GGCGAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAAACCG
551 TCGACCGTTT TGCGCGG.GA AATCGGTTTC AAAGGGCGTT ATCAGCTGAA
601 TTTGCCCAAA GGCGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1   MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51  IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRLSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMDEIHS	DMMLGAAGDYLLETAASLTIIMVVSGLYLW				
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS	DMMLGSTGDYLLLETAASLTIIMIISGLYLW				
	10	20	30	40	50	60
	70	80	90	100	110	120
m218.pep	WVKRRGIKAMLLPSKGXARSWWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
a218	WVKRRGIKAMLLPPKGRARSWWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
a218	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFQRLSVEFAQRRGRMDFVAGFYEL					
a218	LETVDRFARXNRFQRLSAEFAQRRGRMDFVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```
g219.seq
1   atgacggcaa ggtaaggaa gtgccgtgga ttttgagct tatgcctatg
51  cctgtctcag ggacgactgt gggtgaaaac ggcattaacc ccaccgagcc
101 caataacatt ggaaccgctc gaccgtttcg cgcggaat cggtttcaaa
151 gggcggtatc agttgaattt gcccaaaggc gaggacgggg tatggacttt
201 gtcgcaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccgttcgg caaatattat gcggcaagca ttgcgctgca
351 tatggggact ttgggctggg ggagcgtggt ggcaacgct gtgttctgcc
401 ttgcccgtgat ttttatcggc atcagcggct gcgtgatgtg gtggaacgc
451 cgtccgtccg gcgtggcggg cattgttcct ccggcgcaaa aaatcaaact
501 gcccgctctg tgggcgatgg cattgccgct gctgttgatt gcactgcttt
551 tcccgaccgc gctgcttgcc attgccgtga tttggctggt ggataccttg
601 ctgctgtcgc ggattcctgt gttgaggaaa tggtttaaat ga
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```
g219.pep
1   MTARLRKCRG FWSLCLCLSQ GRLWVKALT PPSPITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLAV VFCLAVIFIG ISGCVMWWR
151 RPSGVAGIVP PAQIKLPVW WAMALPLLLI ALLFPTALLA IAVIWLDDTL
201 LLSRIPVLRK WFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```
m219.seq
1   ATGACGGCAA GGTAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACyGt gGGCAAAGAC GGCATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTGC GCGGnGAAAT CGGTTTCAAA
151 GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCCTTT GCCGACCGCA
251 CGGTACATAT CGACCAGTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTT
301 GACGATTACA ACCCGTTTCG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT CTGGGCTGGT GGAGCGTGTT GGCGAACGTC TTGTTCTGCC
401 TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGGTTTGG TGGATGATGG CATTGCCGCT ATTGGCAATC GCACTGCTCT
551 TCCCACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 TCGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```
m219.pep
1   MTARLRKCRG FWSLRCLFQ GRXWAKTALT LTRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLAV LFCLAVIFIG ISGCVMWWR
151 RPTGAVGIVP PAQVKLPVW WMMALPLAI ALLFPTSLA IAVIWLDDTL
201 LLSRIPVLRK WFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

```
m219/g219
10      20      30      40      50      60
m219.pep MTARLRKCRGFWSLRCLCFQGRXWAKTALTLSRXHWKPS TALRGEIGFKGRYQLNLPKG
|||||
g219      MTARLRKCRGFWSLCLCLSQGRLWVKALTTPSPITLETVD RFAREIGFKGRYQLNLPKG
10      20      30      40      50      60

70      80      90      100     110     120
m219.pep EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG
|||||
g219      EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG
```

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPTGAVGIVPPAQKVKLPVWWMALPLLAI					
	: : : : :					
g219	LGWWSVLANVVFCLAVIFIGISGCVMWKRRPSGVAGIVPPAQKIKLPVWWMALPLLII					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFVKX					
	: : : :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWFK					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1   ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTCG GCGG.GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGCATAT CGACCACTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTT GGCGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGTCCG GCGCGGTGGG CATGGTTCCG CCGGCGCAAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1   MTARLRKCRG FWSRLCLFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG LGWWSVLANV LFCLAVIFIG ISGCVMWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*

```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSRLCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	: : : :					
a219	MTARLRKCRGFWSRLCLFQGRWLWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	: : : :					
a219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPTGAVGIVPPAQKVKLPVWWMALPLLAI					
	: : : :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPSGAVGMVPPAQKIKLPVWWMAMAVPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFVKX					
	: : :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFVKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
  1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
 51  gatgcggcga gccgtaaatc adatcgacgc tgacggattt gaaccctgcc
101  tcacggggcg catcgatgac ttctttgggt tcttcgtagc tttggatgcg
151  gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgctca
201  tgcggttgaa gccgagtcctg ccgagcatga ggacggtgtc gcggtgact
251  ttgcgcgggt cgatttcgat ggaatattcg ccggacggtg tcagttcgaa
301  atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351  aggtcggcgt gccgcccgcg aagtgcagtt gggcaagctg gtgccgtccg
401  ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451  ggtatcggcg cggtttttgt ctttggatgat gattttgttg cagccgcagt
501  agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcggg
551  ttgttttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
  1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
 51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101  MFADHAEDTF DLFVAQKGRR AAAEVQLGKL VPSVQMWSEQ FHFFFKIFDV
151  GIGAAFVFGD DFVAAAVVAD GVAERNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
  1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
 51  CGACGCTGAC GGATTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101  TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151  GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201  GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251  TATTGCGCCG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGCGGAAGAC
301  ACGTTCGATC TGTTCGTCGC TCAAAAAGGt GCGTGCCcCCG CCGAAGTGCA
351  GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCCATT
401  TCTTTTCAA GATATTGAT GTAGGCATCG GCGCGGCTTT TGTCTTTGGT
451  GATGATTTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501  TGTGAATGTA AAGGAAAGC GTTTGTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
  1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
 51  VEILNADAH VEAESAHEH GVAADFARVD FDGVFAGGDx LEMFAYHAED
101  TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHFFFKIFD VGIGAAFVFG
151  DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

```
m221/g221
      10      20      30      40      50
m221.pep      MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVE
g221          ||:||:|||| ||||| ||: |||||:|||| |||||
      10      20      30      40      50      60
m221.pep      ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDxLEMFAHYHAEDTFDLFVAQKGA-
g221          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      70      80      90     100     110
m221.pep      ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR
g221          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      70      80      90     100     110     120
      120     130     140     150     160     170
```

507

```

m221.pep      CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFFVGDDFVAAAVVADGVAERNVNVK
               |||||||
g221          AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFFVGDDFVAAAVVADGVAERNVNVK
               130      140      150      160      170      180

m221.pep      GKRFVX
               |||||
g221          GKRFVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

```

a221.seq
1  ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51 CGACGCTGAC GGATTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGGAAGAC
301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTTCTTTTT CAAGAAATTC GATGTAGGCA TCGGCGCGGC TTTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACG
501 GAATGTGAAT GTAAAGGGAA AGCGGTTTGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

```

a221.pep
1  MVVLMRLSLV RQAVNQIDAD GFEPFRFARRI DDFFGFFVTL DAVDRRLHFG
51 VEILNADAH AVEAESAEHED GVAADFARVD FDGVFAGGD* LEMFAYHAED
101 TFDLVVAQKG RRAAAEVQLG KLVPSVQMW S EQFHFFFKKF DVGIGAAFFV
151 GDDEFVAAAV ADGVAERNVN VKGKRFV*

```

m221/a221 95.5% identity in 177 aa overlap

```

               10      20      30      40      50      60
m221.pep      MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDDFFGFFVTLDAVDRRLHFGVEILNADAH
               |||||
a221          MVVLMRLSLVRQAVNQIDADGFEPFRFARRIDDDFFGFFVTLDAVDRRLHFGVEILNADAH
               10      20      30      40      50      60

               70      80      90      100     110     119
m221.pep      VEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-CPAEVQLG
               |||||||
a221          VEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLVVAQKGRRAAEVQLG
               70      80      90      100     110     120

               120     130     140     150     160     170
m221.pep      KLVPSVQMWSEQFHFFFKIFDVGIGAAFFVGDDFVAAAVVADGVAERNVNVKGKRFVX
               |||||||
a221          KLVPSVQMWSEQFHFFFKIFDVGIGAAFFVGDDFVAAAVVADGVAERNVNVKGKRFVX
               130     140     150     160     170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

```

g223.seq
1  atggaattca ggcaccaggt agtggttagtt ggtgtcgaac catttggtca
51 tttcgatggc gaattggtct ttgttgccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggct atcgaagccg aaacgggcg gaatcgcgc
151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcgtta ggagcagctt ggtgtttcca gtttttctcg
251 cgcaggtctt tggcaacgtc gagcagctct tgttctactga tctctttgcg
301 ccagtatttt tcttgggcga atttcaattc acggaaggcg ccgacacgcg
351 ggaagcctga

```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..


```
m223.seq
1  GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTTGGTCA
51  TTTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
101 TCCAAAGACA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCsCTAC
201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTTCCAG TTTTCTCGC
251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTGCsCG
301 CAGTATTTTT CTTGTGCGAA TTTCAATTCT CGGAAGGCGC CGACACGCGG
351 GAAGCCTGA
```

```
m223.pep
  1  VEFRHQVVVV  GVEPFGHFDS  ELVFVTARQL  EELFQRQVLA  VEA EAGGNRA
 51  GGD LQVEDVV  VESEIXY GNE  IGVGS D LVFP  VFLAQVFSNS  QQFL LADFFA
101  PVFF LCE FQF  AEGAD TRE A*
```

```
m223/g223
```

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDV					
g223	MEFRHQVVVVGVEPFGHFDGELVFVAARQLEELFQRQVLAIEAETGGNRARGYLQVEDVM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYGNEIGVGSIDLVPFVFLAQVFSNSQQFLLADFFAPVFFLCEFAQEGADTREAX					
g223	VESEITYSNVISVRSSLVFPFVFLAQVFNVEQLLFTDLFAPVFFLGFEQTTEGADTREAX					
	70	80	90	100	110	

a223.seq						
1	GTGGAATTCA	GGCACCAAGT	AGTGGTAGTT	GGTGTCGAAC	CATTTGGTCA	
51	TTTCGATAGC	GAATTGGTCT	TTGTTACCGC	CGCCAGTTG	GAAGAATTGT	
101	TCCAAAGATA	GGTTTTGGCT	GTCGAAGCCG	AAGCGGGCGG	GAATCGCGCC	
151	GGTGGCGACT	TGCAGGTCGA	GGATGTGGTC	GTAGAAAGTG	AAATCGCCTA	
201	CGGCAACGTA	ATCGGCGTTG	GCAGCGGCCT	GGTGTTTCCA	GTTTTTCTCG	
251	CGCAAGTCTT	TAGCAACAGC	CAGCAATTCT	TGCTCGCTGA	TTTCTTTGCG	
301	CCAGTATTTT	TCTTGTGCGA	ATTTCAATTC	GCGGAAGGCA	CCGACACGCG	
351	GGGAAGCCTGA					

a223.pep

1	VEFRHQVWVV	GVEPFGHFDS	ELVFVTARQL	EELFQR*VLA	VEAEAGGNRA
51	GGDLQVEDVV	VESEIAYGNV	<u>IGVGSLVFP</u>	<u>VFLAQVFSNS</u>	QQFLLADFFA
101	PVFFLCEFQF	AEGTDTREA*			

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGV	EPFGHFDSELV	FVTARQLEELF	QRQVLAVEAE	AAGGNRAGGD	LQVEDVV
a223	VEFRHQVVVVGV	EPFGHFDSELV	FVTARQLEELF	QRXVLAVEAE	AAGGNRAGGD	LQVEDVV
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYGNEIG	VGSGLVFPVFL	AQVFSNSQQFL	LADFFAPVFF	LCFQFAEGAD	TREAX
a223	VESEIAYGNVIG	VGSGLVFPVFL	AQVFSNSQQFL	LADFFAPVFF	LCFQFAEGDT	TREAX

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcgcgtccg cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag ttgtccgaag acgaacagcc cgttttaccc
151 gtcaaccgag ccccgcccg gcgggcgggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251 ccgcccggcg ggcgggcaat gccgacaaac tcacgcggcag cgcgatgcgg
301 cttttgggta ttgcctaccg ctacggcggc acatcggtgt ctaccggttt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgccgcg cacgtcggcg gaacaggcgc ggatgggcgc acccgttgcc
451 cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551 acgcgcgcgc cacggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcgccgcg cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKKNDSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1  ..TTTTCAAACC CGGCAGTTTG GCGGTTTTTG TGGCTGAwGT TTGCCGTCGG
51  CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTTACC CATCAACCGA
151 GCCCCGCCCC GCGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201 GGGGCTTAAC GAACAGCCCG TTTTACCCGT CAACCGAGTC CCCGCCCGGC
251 GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301 CAGCCCGTTT TACCCGTCAA CCGAGCCCC GCGCGCGGG CGGGCAATGC
351 CGACGAACTC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401 ACGCGGGCAC ATCGGTTTCT ACCGGTTTTG ACTGCAGCGG CTTTCATGCAG
451 CACATCTTCA AACGCGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501 ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATG CAGCCCGGAG
551 ATATGGTGTT TTTCCGACG CTCGGCGGCA GCCGCATTTC CCATGTCGGA
601 CTTTATATCG GCAACAACCG CTTTCATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701 TCGCCGCGG GGTCAAGAAA AACGACCCGT CCCGCTTCT GAACCTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1  ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101 QVLPVNRAP ARRAGNADEL IGNAMGLLGI AYRYGGTSVS TGFDCSGFMQ
151 HIFKRAMGIN LPRTSAEQAR MGTPVARSEL QPGDMVFFRT LGGSRIHVG
201 LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

```
m225/g225
10 20 30 40 50
m225.pep FSNPAVWAVLWLXFAVRPALADELTNLSSREQILRQFAEDEQVLPINRAPARRAG
:|||||:|||||:|||||:|||||:|||||:
g225 MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQVLPVNRAPARRAG
```

		10	20	30	40	50	60
m225.pep	60	70	80	90	100	110	
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA						
g225	NADELIG-----GAMGLNEQPVVRVNRAXARRAGNA						
					70	80	90
m225.pep	120	130	140	150	160	170	
	DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPR TSAEQARMGTPVAR						
g225	DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPR TSAEQARMGAPVAR						
	100	110	120	130	140	150	
m225.pep	180	190	200	210	220	230	
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR						
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR						
	160	170	180	190	200	210	
m225.pep	240	249					
	VKKN D P S R F L N X						
g225	VKKN D P S R F L N						
	220						

```

a225.seq
1  ATGGATTCTT  TTTTCAAACC  GGCAGTTTGG  GCGGTTTTGT  GGCTGATGTT
51  TGCCGTCCGC  CCCGCCCTTG  CCGACAGAGT  GACCAACCTG  CTCAGCAGCC
101 GCGAGCAGAT  TCTCAGACAG  TTTGCCGAAG  ACGAACAGCC  CGTTTTACCC
151 ATCAACCGAN  CCCCCGCCCG  GCGGGCGGGC  AATGCCGACG  AACTCATCGG
201 CAGCGGATG  GGGCTTAACG  AACAGCCCGT  TTTACCCGTG  AACCANTCC
251 CCGCCCGGCG  GGCGGGCAAT  GCCGACNAAC  TCATCGGCAA  CGCGATGGGG
301 CTTAACGAAC  AGCCGCTTTT  ACCGTCAAC  CGAGTCCCCG  CCGGCGGGG
351 GGGCAATGCC  GACGAATCA  TCGGCAACGC  GATGGGGCTT  AACGAACAGC
401 CCGTTTTACC  CGTCAACCGA  GCCCCCGCCC  GGCGGGCGGG  CAATGCCGAC
451 GAACCATCG  GCAACGCGAT  GGGACTTTTG  GGTATTGCCT  ACCGCTACGG
501 CGGCACATCG  ATTTCTACCG  GTTTTGACTG  CAGCGGGCTT  ATGCAGCACA
551 TCTTCAAACG  GCCTATGGGC  ATCAACCTGC  CGCGACGTC  GCGAGAACAG
601 GCGCGGATGG  GTACGCCGGT  TGCCCGAAGC  GAATTGCAGC  CCGGGGATAT
651 GGTGNTTTC  CGCACGCTCG  GCGGCAGCCG  CATTTCCCAT  GTCGGACTTT
701 ATATCGGCAA  CAACCGCTTC  ATCCACGCGC  CGCGCACGGG  GAAAATATC
751 GAAATCACCA  GCCTGAGCCA  CAAATATTGG  AGCGGCAAT  ACGCGTTCGC
801 CCGCCGGGTC  AAGAAAAACG  ACCGTCCCG  CTTTCTGAAC  TGA

```

```
a225.pep
1  MDSFFKPAVW  AVLWLMFAVR  PALADELTNL  LSSREQILRQ  FAEDEQPVLP
51  INRXPARRAG  NADELIGSAM  GLNEQPVLPV  NRXPARRAGN  ADXLIGNAMG
101 LNEQPVLPVN  RVPARRAGNA  DELIGNAMGL  NEQPVLPVNR  APARRAGNAD
151 ELIGNAMGLL  GIAYRYGGTS  ISTGFDCSGF  MQHIFKRAMG  INLPRTSAEQ
201 ARMGTPVARs  ELQPGDMVXF  RLTGLSGRSH  VGLYIGNNRF  IHAPRTGKNI
251 EITSLSHKYW  SKGYAFARRV  KKNDPSRFLN  *
```

```

      10      20      30      40      50
m225.pep  FSNPAVWAVLWLXFVVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
          | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a225      MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAAG
          10      20      30      40      50      60

      60      70      79      80
m225.pep  NADELIGSAMGLNEQPVLPVNR-----VPARRAGNA

```

511

```

a225      |||||
          NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
          70      80      90      100      110      120

m225.pep  90      100      110      120      130      140
          DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
          |||||

a225      130      140      150      160      170      180
          DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF

m225.pep  150      160      170      180      190      200
          MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
          |||||

a225      190      200      210      220      230      240
          MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF

m225.pep  210      220      230      240      249
          IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLNX
          |||||

a225      250      260      270      280
          IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1   atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag tttgccgaag acgaacagcc cgtttttacc
151 gtcaaccgag cccccgccg gcgggcgggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcttaacg aacagcccgt tgtaecgctc aaccgagccn
251 ccgcccggcg ggcgggcaat gccgacaaac tcatcggcag cgcgatgcgg
301 cttttgggta ttgectaccg ctacggcggc acatcggtgt ctaccggttt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgccgcg cagctcgggc gaacaggcgc ggatgggcgc acccgttgcc
451 cgaagcgaat tgcagcccgg ggatatgggt tttttccgca cgctcggcgg
501 cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551 acgcgcccgc cacggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcgccgcg cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pep

```

1   MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDQPVLP
51  VNRAAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FRTLGGSRIS SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKKNDFSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1   ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTGTG GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAG CCCCCGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCGGTC AACCGAGTCC
251 CCGCCCGGGC GCGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGCCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGACTT TTGGGTATTG
401 CCTACCGCTA CGCGGCACA TCGGTTTCTA CCGGTTTGA CTGAGCGGC
451 TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501 GTCCGCAGAA CAGGCACGGA TGGGTACGCC GGTGCCCCGA AGCGAATTGC
551 AGCCCGGAGA TATGGTGT TTCCGCACGC TCGGCGGCAG CCGCATTTCC
601 CATGTCGGAC TTTATATCGG CAACAACCGC TTCATCCAG CGCCGCGCAC
651 GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701 AATACGCGTT CGCCCGCCGG GTCAAGAAAA ACGACCCGTC CCGCTTTCTG
751 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQPVLPV NRVPARRAGN ADELIGNAMG
101 LNEQPVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL
251 N*

```

m225-1/g225-1 84.9% identity in 251 aa overlap

```

              10      20      30      40      50      60
m225-1.pep  MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
              |||
g225-1      MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
              10      20      30      40      50      60

              70      80      90      100     110     120
m225-1.pep  NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
              |||
g225-1      NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA
              70      80      90

              130     140     150     160     170     180
m225-1.pep  DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
              |||
g225-1      DKLIGSAMRLGLIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR
              100     110     120     130     140     150

              190     200     210     220     230     240
m225-1.pep  SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR
              |||
g225-1      SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR
              160     170     180     190     200     210

              250
m225-1.pep  VKKNDPSRFLNX
              |||
g225-1      VKKNDPSRFLNX
              220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCGCG CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCC CGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCG CCCGCGGGG
351 GGGCAATGCC GACGAAC TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCGCGCC GCGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTGA CTG CAGCGGCTT ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCGGTG TGCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARARR NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDDPSRFLN *

```

a225-1/m225-1 88.6% identity in 280 aa overlap

```

      10      20      30      40      50      60
a225-1.pep MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRXPARRAG
|||||
m225-1     MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
      10      20      30      40      50      60

      70      80      90     100     110     120
a225-1.pep NADELIGSAMGLNEQVLPVNRXPARRAGNADXLIGNAMGLNEQVLPVNRVPARRAGNA
|||||
m225-1     NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA
      70      80      90

      130     140     150     160     170     180
a225-1.pep DELIGNAMGLNEQVLPVNRAPARRAGNADELIGNAMGLLGIARYGGTSISTGFDCSGF
|||||
m225-1     DELIGNAMGLNEQVLPVNRAPARRAGNADELIGNAMGLLGIARYGGTSVSTGFDCSGF
      100     110     120     130     140     150

      190     200     210     220     230     240
a225-1.pep MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
|||||
m225-1     MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
      160     170     180     190     200     210

      250     260     270     280
a225-1.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLNX
|||||
m225-1     IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLNX
      220     230     240     250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGTAACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGcgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tccgcctcg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcca
451 tttctgttgc ctccgcctct cctgccgcgc ctcggcccgc atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt ctttctcct Ccgggcctcg cccctcccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1  MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
101 GSVTGIVTGM YFAAWLGPDT QFSFPPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPLLPR LGPHTLRRFT ILPKLRPFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGTAACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

m226 . pep

1	<u>MNEILRQPSV</u>	<u>LLFLTLAVYA</u>	<u>LAIIVRTRTG</u>	<u>NIFCNPVLVS</u>	<u>TIVLIAYLKI</u>
51	<u>LGIDYAVYHN</u>	<u>AAQFIDFWLK</u>	<u>PAVVVLAVPL</u>	<u>YQNRKIFNQ</u>	<u>WLPVIVSQA</u>
101	<u>GSVTGIVTGM</u>	<u>YFAKWGAER</u>	<u>EVVLSLASKS</u>	<u>VTNPPIAIEIT</u>	<u>RSIGGIPAIT</u>
151	<u>AATVYIAGLV</u>	<u>GQIAGYKMLK</u>	<u>NTVVMPSVG</u>	<u>MSLGTASHAM</u>	<u>GIAASLRSR</u>
201	<u>RMAAYAGLGL</u>	<u>TFENGVLTAI</u>	<u>APLLIPVLGF</u>	*	

Homology with a predicted ORF from *N. gonorrhoeae*

m226/q226

		10	20	30	40	50	60
m226.pep		MNEILRQPSVLLFLT	LAVYALAIIV	TRTRTGNIFCNP	VLVSTIVLIA	YALKILGIDY	AVYHN
		:					
g226		MSEILRQPSVLLFLT	LAVYALAIIV	TRTRTGNIFCNP	VLVSTIVLIA	YALKILGIDY	AVYHN
		10	20	30	40	50	60
		70	80	90	100	110	120
m226.pep		AAQFIDFWLKP	AVVVLAVPLYQ	NRRIKIFNQW	LPVIVSQLAG	SVTGIVTGM	YFAKWLGAER
g226		AAQFIDFRLKP	AVVVLAVPLYQ	NRRIKIFNQW	LPVIVSQLAG	SVTGIVTGM	YFAAWLGPDT
		70	80	90	100	110	120
		130	140	150	160	170	180
m226.pep		EVVLSLASKSV	TNP	IAIEITRSIG	GIPAITAAT	VI	IAGLVGQIAGYKMLKNTV
		:					
g226		QFSFPPRLQY	LLFTPSGIP	IHTLYARVLP	PPFLPPPLL	PRLGPHTLR	RFTILPKKLRPFK
		130	140	150	160	170	180

a226.seq

1	ATGAACGAAA	TCCTCAGGCA	GCCGAGCATC	CTGCTTTTCC	TCACGCTTGC
51	CGTGTACGCG	CTTGCGATTA	TCGTGCGCAC	GCGACGGGT	AATATCTTCT
101	GCAACCCCGT	ACTCGTCAGC	ACTATCGTGC	TGATTGCCTA	CCTGAAAATC
151	CTCGGTATCG	ATTATGCGGT	GTACCAACAC	GCCGCGCAGT	TTATCGATTT
201	CTGGCTCAAG	CCCGCGCTCG	TCGTGCTTGC	CGTGCGCTC	TACCAAAACC
251	GCCGTAATAA	CTTCAACCAA	TGGCTGCCCG	TCATCGTTTC	GCAGCTTGGC
301	GGCAGCGCTA	CGGGCATTGT	TACGGGGATG	TATTTTGCCA	AATGGCTGGG
351	CGCGGAACAT	GAGTCGTCG	TCTCGCTCGC	GTCCAAATCT	GTTACCAATC
401	CTATCGCCAC	CGAAATCACC	CGCTCATCGC	GCGGCAATTCC	CGCAATTACC
451	GCCGCCACCG	TCATCATTGC	CGGCCTGGTC	GGACAGATTG	CCGGTTACAA
501	AATGTTGAAA	AACACGGTCG	TTATGCCCTC	ATCTGTCGGA	ATGTCGCTCG
551	GCACGGCTTC	GCACGGGATG	GGCATTGCCG	CCTCGCTCGA	ACGCAGCCGC
601	CGCATGGCGC	CATACGCGGG	GCTGGGGCTG	ACGTTCAACG	CGGTACTGAC
651	CGCGCTGATT	CGCGCGTGC	TTATCCCCGT	TTTGGGATTT	TGA

a226.pep

1	<u>MNEILRQPSI</u>	<u>LLFLT LAVYA</u>	<u>LAIIVRTRTG</u>	<u>NIFCNPVLVS</u>	<u>TIVLIAYLKI</u>
51	<u>LGIDYAVVHN</u>	<u>AAQFIDFWLK</u>	<u>PAVVVLAVPL</u>	<u>YQNRKRIFNQ</u>	<u>WLPVIVSOLA</u>
101	<u>GSVTGIVTGM</u>	<u>YFAKWLGAE</u>	<u>EVVLSLASKS</u>	<u>VTNPIAIEIT</u>	<u>RSIGGIPAIT</u>
151	<u>AATVIIAGLV</u>	<u>QGIAGYKML</u>	<u>NTVMPSSVG</u>	<u>MSLGTASHAM</u>	<u>GIAASLERSR</u>
201	<u>RMAAYAGLGL</u>	<u>TFNGVLTAL</u>	<u>APLLIPLVGF</u>	*	

10 20 30 40 50 60

515

```

m226.pep      MNEILRQPSVLLFLT LAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
|||||:|||||
a226          MNEILRQPSILFLT LAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
              10      20      30      40      50      60

              70      80      90      100     110     120
m226.pep      AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
|||||
a226          AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
              70      80      90      100     110     120

              130     140     150     160     170     180
m226.pep      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
|||||
a226          EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
              130     140     150     160     170     180

              190     200     210     220     230
m226.pep      MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
|||||
a226          MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1   atgaacatca tccgcgcgct cctcatcatc ctcggctgcc tcgccgccgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccggc agcatcgtcg
101 gcatgggcgt gctgtttgcg cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttacga cgcgctgatg gcaaacctga cgctgttcct
201 cgtgccgcc tgcgtggcgg tcatcagcta tttgatttg attgccgacg
251 attggtttc gatactggtt tccgcctcgg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1   MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLFA LLQAGWLKTS
51  WLQLTDALM ANLTFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1   ..ACGTCTTtGC TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTtG GATTtGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1   ..TSXLQQLTDA LMSNLTFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227
              10      20      30
m227.pep      TSXLQQLTDALMSNLTFLVPPCVAVISYL
              || |||||:|||||
g227          TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTFLVPPCVAVISYL
              20      30      40      50      60      70

              40      50      60

```


516

```

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
               |||||||||||||||||||||||||||||||||||
g227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
               80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
  1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
 51  CGAAACCGCC GTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101  GCATGGGCGT ACTGTTTGGC CTTTTCAGG CGGGTTGGGT CAAAACGTCT
151  TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201  CGTGCCGCCC TGGCTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251  ATTGTTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301  CTGGTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATTA TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
  1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLFA LLQAGWVKTS
 51  WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101  LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep      TSXLQQLTDALMSNLTFLVPPCVAVISYL
               || |||||||||||:|||||||||||||
a227          TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTFLVPPCVAVISYL
               20      30      40      50      60      70

m227.pep      40      50      60
               DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
               |||||||||||||||||||||||||||||||||||
a227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
               80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
  1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
 51  TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101  CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151  GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201  AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251  CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301  AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
  1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51  VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101  KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
  1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
 51  TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101  CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151  GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201  AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251  CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301  AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

```

a228.pep
  1 MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

m228/a228 100.0% identity in 107 aa overlap

```

m228.pep      10      20      30      40      50      60
MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD
|||||
a228          10      20      30      40      50      60
MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD

m228.pep      70      80      90     100
AAADAKASAE EAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX
|||||
a228          70      80      90     100
AAADAKASAE EAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

```

g229.seq
  1 atggctgccg tatcgggcgg cggtgcggtc ttctgataa tgcttcacaca
 51 tattgccgc gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag
101 aaatcgcat tgaagccgcc ggcgaaattg tatcggtgc cgccaagag
151 gttttgccg acaaacggca cggtgccgaa cgagcgcgtt accgaacggt
201 ttgatggcc gaacgacagg cgcaggttct gttcgtgaa atctttgtta
251 tcccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgccc
301 gcccgcattg atttcgcgcg acacgcccga gccgtagcgc aaaccgtgtg
351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat
401 tcaatcgttt ttctggacga agcgttggtt atagcggatt aacaaaaatc
451 aggacaaggc ggcgggccgc aggcagtacg gatggtacgg aaccggttcg
501 cccggtgctt ggacgcctta gggaaccggt ccctttgagc cggggcgggg
551 caacccgtag cggtttttgt tcatccgcca tattgtgttg a

```

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

```

g229.pep
  1 MAAVSGGGAV FLIMLPHIAR VQRPPAFAQ ASGEIGIEAA GEIVSAAAE
 51 VLPDKRHGAE RARYRTVLMR ERQAQVLAEE IFVIPIMHAA ADAAVEEMMP
101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFFGR SVVYSGLTKI
151 RTRRRRAAGST DGTEPVRPVL GRLREPFLS RGGATRTGFC SSAILC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

```

m229.seq (partial)
  1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC
201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCGCGA CACGCCTAAG
251 CCCTAGCGCA AACC GTGTC CTTTTCGCGC AGGCTGTCGG CGGTTTTCGT
301 CCAGCTTCTG CCCGCAAATT CAATCGTTTT TTCGGACGAA GCGTTGTTTA
351 TAGCGGATTA ACAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
401 AATAGTACGG AACCGATTCA CTTGGTGCTT CAGCACcTTA GAGAATCGTT
451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

```

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

```

m229.pep (partial)
  1 ..AQALGEIGIE AADEIVSAAA XEVLLDKRHD AERARYRTVF IAERQAQALF
 51 AEIFVIPIMH AAAADA AVEE MMPARIDFAR HAXALAQTVC LLRQAVGGFR
101 PASARKFNRF FGRSVVYSL TKIRTRQRSA DSTNSTEPIH LVLQHLRESR
151 SLFCSSAILC *

```

Computer analysis of this amino acid sequence gave the following results:

m229/g209

```

m229.pep                                10          20          30
                                         AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                         ||| ||||| ||||| ||||| ||| ||| |||
g229      MAAVSGGGAVFLIMLPHIARVQRQPPAFAQASGEIGIEAAGEIVSAAAEVLDPDKRHGAE
              10          20          30          40          50          60

              40          50          60          70          80          90
m229.pep    RARYRTVFIAERQAQALFAEIFVIPIMHAAAADAAVEEMMPARIDFARHAXALAQTVCLL
              ||||| :|:||||| :|:||||| ||||| ||||| ||||| ||||| :|:|||||
g229      RARYRTLMAERQAQQLFAEIFVIPIMHAAA-DAVEEMMPARIDFARHAQAVAQTVCLL
              70          80          90          100         110

              100         110         120         130         140
m229.pep    RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRE----
              ||||| ||||| ||||| ||||| ||||| ||||| :|:||| :|:||| :|:|||
g229      RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRRAAGSTDGTETPVRPVLGRLEPFPL
120          130          140          150          160          170

              150          160
m229.pep    -----SRSLFCSSAILCX
              :|:||||| |
g229      SRGGATRTGFCSSAILC
180          190
```

a229.seq (partial)

1	ATGGCTGTCTG	TATCGGGCGG	CGGTGCGGTC	TTCCTGATAA	CGCTTCCACA
51	TATTGCCAC	GTTCAGCGTC	AGCCGCCA..	GTTGCGTCAA	GGTCGGGAG
101	AAATCGGCAT	TGAAGCCGCC	GACGAAATTG	TATCGGCTGC	CGCCTAAGAG
151	GTTTTGTCTG	ATAAACGGCA	CGATGCCGAA	TGAGCGCGTT	ACTGAACGGT
201	TTTATAGCC	GAGCGACAGG	CGCAGGCTCT	GTTCGCTGAA	ATCTTTGTTA
251	TCCATAAGT	GACGCGCC	GCCGCTGATG	TCTCCGTAGA	GGAAATGATG
301	CCCGCCCGCA	TTGATTTCGC	GCGACACGCC	CAAGCCGTAG	CGCAAACCGT
351	GTGCCTTTTG	CGGCAGGCTG	TCGGCGGTTT	TCGTCCAGCT	TCGCGCTGCA
401	AATTCAATCG	TTTTTTCGGA	CGAAGCGTTT	TTTATAGCGG	ATTAACAAAA
451	ATCAGGACAA	GGCGACGAAG	CCGACAGTAG	ACAGATAGTA	CGGAACCGAT
501	TCATCTGGTG	CTTCAGCACC	TTAGAGAATC	GTCTCTTTGA	GCTAACGGCGA
551	GGCAACGCCG	TACTGGTTTT	TGTTTCATCCA	CTATA	

a229.pep (partial)

1	MAVVS	GGGAV	FLITLPHIAH	VQRQPPXFAQ	ASGEIGIEAA	DEIVSAAA*E
51	VLLDKR	HDAE	*ARY*TVFIA	ERQAQALFAE	IFVILIVHAA	AADVSVEEMM
101	PARIDFAR	HA	QAVAQTVCLL	RQAVGGFRPA	SACKFNRRFFG	RSVVYSGLTK
151	IRTRRRSADS		TDSTEPIHLV	LQHLRESSL*	AKARQRRRTGF	CSSTI

[illegible]

519

	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
a229	AKARQRRTGFCSTI					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

g230.seq

```

1   atgtttccatt ccatcgaaaa atacagaaca cccgcccaag tcttattagg
51  cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gtttcccatc
101 cgggcgccga ctacatcgtc caagtgggcg acgaaaaaat cagcgagcac
151 tcaatcaaca acgccatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtcacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtgtg
401 tcgaagaaat ccgcgatcag ttgccttgc agaatttggg aagcctcgtc
451 caaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcaggct
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcacgcacca agtcaaagcg tctgaagccg atttgcagaa atttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tggaatatgt
651 cgcccttgaa ctgaaggatt ttgcagacaa gcagaccgtc agtgaacagg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaag gcggttgccg acttcaacaa ggcaaaagaa aagctgggcg
851 acgatgcgtt caatcatccc tcctcgcttg ccgaagccgc caaaaacagc
901 ggtttgaaag tggaaaccca agaaaacttg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaaa acctaataca tgccgtattc agcgacgacg
1001 tattgaagaa aaaacacaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggtcg tccgcgccaa agaagtccgc gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatgcgg tgcgtcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

g230.pep

```

1   MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQAKLMGI SVSSEIQKM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSE DQFVEEIRDQ FALQNLVSLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAUF SDDVLKKKHN SEVLINSET
351 AWWVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

m230.seq (partial)

```

1   ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCc .GACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTGCTTGC AGAATTGGT AAACCTCGTC

```

520

```

451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGCA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGg
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGC.GT cAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT.. ...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
  1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
 51 SINNAIQNEQ ADGGGPPSPDA VFQSLQRAY LKQGAQLMGI SVSSEIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKPYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELMKKK AVADFNKAKE KLGDDAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VF SDDVLKKKHN SEVL TINSET
351 AWVVRakeVR EEKTLPFaea KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

```

m230/g230
      10      20      30      40      50      60
m230.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ
g230      MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ
      10      20      30      40      50      60

      70      80      90     100     110     120
m230.pep ADGGGPPSPDAVFQSLQRAYLKQGAQLMGISVSSEIKQIIVDDPNFHDANGKFDHALLN
g230      ADGGSPWRDAVFQSLQRAYLKQGAQLMGISVSSEIKQMIVDDPNFHDANGKFSHALLS
      70      80      90     100     110     120

      130     140     150     160     170     180
m230.pep RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
g230      QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
      130     140     150     160     170     180

      190     200     210     220     230     240
m230.pep PDEFIAQVKVSEADLQKPYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
g230      PDEFIAQVKASEADLQKPYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
      190     200     210     220     230     240

      250     260     270     280     290     300
m230.pep ERVARLPANEAKPSFEQEKA AVENELMKKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS
g230      ERVARLPAHEAKPSFEQEKA AVENELMKKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
      250     260     270     280     290     300

```

521

	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPF AEAKDAVRQAYIRTEAAKL					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGTCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGA CACTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCAAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCGG ACTTCAATAA GGCAAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCCCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 CCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51  SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGAQLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRKEVR EEKTLPF AEA KDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGSPDAVFQSLQRAYLKQGAQLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
a230	ADGGGSPDAVFQSLQRAYLKQGAQLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

522

```

m230.pep  RYLSQRHMSSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAAEQILRLTQVNRTIRSHTFN
a230      RYLSQRHMSSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAAEQILRLTQVNRTIRSHTFN
           130      140      150      160      170      180

           190      200      210      220      230      240
m230.pep  PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE
a230      PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE
           190      200      210      220      230      240

           250      260      270      280      290      300
m230.pep  ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGD DAVNHPSSLAEAAKNS
a230      ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGD DAFNHPSSLAEAAKNS
           250      260      270      280      290      300

           310      320      330      340      350      360
m230.pep  GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRakeVR
a230      GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRakeVR
           310      320      330      340      350      360

           370      380
m230.pep  EEKTLPPFAEAKDAVRQAYIRTEAAKL
a230      EEKTLPPFAEAKDAVRQAYIRTEAAKL
           370      380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCCGCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACCTTTG TCGGCTTCGG CGTCAGCACG GTTTCCTATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGGG GTGTTCCAAT CCCTGCTGCA ACGCGCTTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCTGAA GACCACTTGT
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAGCCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAAGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGG GCGGTCAAAT TGGAAATATG
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGGCTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGA AAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TGGAAACCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCGGGC ATGCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TCGGTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACCTTG CGAAAACAAG GCAAAAAGAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCAG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCTATG TCAGACTGAC CGGTCTGCGC
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCTCCGG AGGATATTGC
1401 CGCACAGCTT CCTCCTGCGA AACAGGCTTT GGCACAACAG CAGTCTGCCA
1451 ATACTTTCGA CTTGCTGATC CGCTATTTC ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAALMGI SVSSEAIKQM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMS DQFVEEIRDQ FALQNLVSLV

```

```

151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TPPEDIAAQL PPAKQALAQO QSANTFDLLI RYFNGKIKQT
501 KGAQSVDNQD GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCGTATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 GCGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTGCCTTGC AGAATTGTTT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCAGACCA TCCGTTCGCA CACTTTC AAC CCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACGGG
701 AAGTGAAAAA TGCATTGTA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCGCAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCCGAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTGC TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAAACAAG GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCGAGCAAGG CAGTCCATGC CGCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAAGT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGACACAGCT CCGCTTGCAA AACAGGCTTT GGCGCAACAG CAGTCTGCCA
1451 ATACTTTTCA CTTGTTGATA CGTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTGCA CAACGGCGAC GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGA KLMI SVSSEIKQI
101 IVDNPNFHD NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR EEKLPFAEA KDAVRQAYIR TEAAKLAENK AKDVLTQLNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAQO QSANTFDLLI RYFNGKIKQT
501 KGAQSVDNQD GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

	10	20	30	40	50	60
m230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230-1	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230-1.pep	ADGGGPSRDAVFQSLQRAYLKQGA KLMI SVSSEIKQI IVDNPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQGA KLMI SVSSEIKQIMVDNPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230-1.pep	RYLSQRHMESEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					
g230-1	RYLSQRHMESEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					
	130	140	150	160	170	180
m230-1.pep	RYLSQRHMESEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					
g230-1	RYLSQRHMESEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN					

a230-1.seq

1	ATGTTCCATT	CCATCGAAAA	ATACGAAACG	CCCGCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TFAACCTTCG	TCGGCTTCGG	GGTCAGCACG	GTATCCCATC
101	CGGGTGCCGA	CTACATCGTC	CAAGTGGGCG	ACGAAAAAAT	CAGCGACCAC
151	TCCATCAACA	AGCCCATACA	GACGAAACAG	CGCGACGGCG	GCGGCCCTTC
201	GCGCGACGCG	GTGTTCCAAT	CCCTGCTACA	ACGCGCCTAC	CTGAAACAGG
251	GCGCGAAGCT	GATGGGCATT	TCGGTTTCTT	CCGAACAAT	TCAGCAGATT
301	ATCGTGGACG	ATCCCAATT	CCACGACGCA	ACCGACAAAT	CAGCCACGCG
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGTCA	TATGTCTGAA	GACCAGTTTG
401	TCGAAGAAAT	CCGCGATGAC	TTTGCCCTGC	AGAATTTGGT	AAACCTCGTC
451	CAAAACGGCG	TATTTGGTCG	CGACGCGCAG	GCGGAACAGC	TGATCAGGCT
501	GACGCAAGTC	AACCGCACCA	TCGGTTTCGA	CACTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	TCTGAAGCCG	ATTTGCAGAA	GTTTATATAAC
601	GCAAAACAAA	AGAATCACTT	GCTTCCCAAA	CGCGTCAAA	TGGAATATGT
651	CGCCTTGAAT	TGAAAGACT	TGCGACAGA	ACAGACCGTC	AGCGAAACAG
701	AAGTGAAAAA	TGCGTTTGAA	GAGCGCGTGG	CGCGTTTGCC	GGCAAATGAA
751	GCCTAAACCTT	CTTTTCGACA	GGAAAAAGCC	GCCGTCGAAA	ACGAATTGAA
801	AATGAAAAAG	GCGGTTGCCG	ACTTCAATAA	GGCAAAAGAA	AAGCTGGGCG
851	ATGACGCGTT	CACCAATCCT	TCTCCTGCTG	CCGAAGCCGC	CAAAACACAGC
901	GGTTTGAAGG	TCGAAACCCA	AGAAATCTGG	CTGCGCAGGC	AGGATGCGCA
951	AATGTCCGGT	ATGCCCGAAA	ACCTGATCAA	TGCGGTATTC	AGCGCAGCAG
1001	TATTGAAGAA	AAAACACAA	TCCGAAGTGC	TGACCATCAA	CAGCGAAACC
1051	GCGTGGGTCG	TCCGCGCCAA	AGAAGTCCGC	GAAGAGAAAA	CCCTGCCGTT
1101	TGCCGGAAGC	AAGACGCGGG	TACGTCAGGC	TTATATCCGT	ACCGAAGCCG
1151	CCTAACTTGC	CGAAAAAGCG	GCAAAAGACG	TGCTTACCCA	ACTGCAAGGCG
1201	GGCAAGGCTG	TTGACGTGAA	ATGGTCGGAA	GTGTCCGTTT	TGGGCGCACA
1251	GCAGGCAAGG	CAGTCCATCG	CGCCCGAGGC	TTATGCGGAA	CTGCTGAAAG
1301	CAAAACCGGC	AACCGCAACA	CCCGCTTACG	TCAGGCTGAT	CGGTTCTGCCG
1351	GCACCCGTGA	TTGTCGAAGT	ACAGGCTGTA	ACCCGCGCGG	ATGATATCGC
1401	CGCACAAGCT	CCGCTTTGCA	AACAGGCTTT	GCGGCAAAAG	CAGTCTGCCA
1451	ATACCTTTGA	CTGTTTGATA	CGTTATTTCA	ACGGCAAAAT	CAAACAGACC
1501	AAAGGAGCGC	AATCGGTCGA	CAACGCGCAG	GGTCAGTAA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAKLMGI SVSSEIQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRKEVR EEKTLPFAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWSE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNGD GQ*
```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
m230-1	10	20	30	40	50	60
a230-1.pep	70	80	90	100	110	120
m230-1	70	80	90	100	110	120
a230-1.pep	130	140	150	160	170	180
m230-1	130	140	150	160	170	180
a230-1.pep	190	200	210	220	230	240
m230-1	190	200	210	220	230	240
a230-1.pep	250	260	270	280	290	300
m230-1	250	260	270	280	290	300
a230-1.pep	310	320	330	340	350	360
m230-1	310	320	330	340	350	360
a230-1.pep	370	380	390	400	410	420
m230-1	370	380	390	400	410	420
a230-1.pep	430	440	450	460	470	480
m230-1	430	440	450	460	470	480
a230-1.pep	490	500	510			
m230-1	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

```

g231.seq
  1  atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
 51  gccgccgttg caaaataatc cgccatttta ccgtaaaaac cgccgcctga
101  acttttttat cgcggcagac ggcggttgcg cgtctccgca aaaatgcagg
151  gcgcgcgggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtcttt
201  accaaatgcc caaccattcg cccacggaat ccatccaatc cttattgccc
251  ccgccgctcc tgcctgcccg gcggtacgcc cacggcgctt gcggattttt
301  agctttccac aatcctttgc gttccctttc cgcctgaatt tgagcgtcgg
351  catagtcggc aaaaatccgc ttatcctgct gttcttttagc ataactttta
401  taatgccacg ccgcccgcgc ctgcacctgc atcaggttca aatcggtttt
451  gccggcggat acctgcgcca cttcgcgtg atagcggctg gtttcaaaca
501  cacgtacact gactttccta ccctccgcgc ccgcgcgcag gttgtcgcgc
551  gaacgtgtac cgtaagcctg tttcatctcc ggtgcgtcga tatacgccat
601  ccgaatttta tgttcgcgcg cgtcgcgcgc gatgacgtga agggatcgcg
651  cgtcatagac tttggacacc gtgcctgtgt agctgtggcc ggatttcgcc
701  gatgcccgtc ggcgaaacggg cgcgtcgaaa cccacgtccc ctgcagtgcc
751  gagtacgtcg agtacggcaa ccgccgtccg caccgcctca ctgtcatatc
801  ccgtataacc caacgcgccc aaaagcgaca gggcgacggg aagccatttc
851  atgatttttt taatctgcat atttttcaaa tgccgatgcc gtctgaacat
901  ctctga

```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

```

g231.pep
  1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51  ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101  SFQSFAPFP RLNLVGVIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151  AGGYLRHFAL IAVGFKHTYT DFPTLRRRAQ VVARTCTVSL FHLRCVDIRH
201  PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFRRCPSANG RVETHVPCSA
251  EYVEYGNRRP HRLTVISRIT QRAQKRQGDG KPFHDFNLH IFQMMPMSEH
301  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

```

m231.seq (partial)
  1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAAC
 51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101  ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151  GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGGTGTCTTT
201  ACCAAATGCC CAACCATTCG GC....

```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

```

m231.pep (partial)
  1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51  ARGFQTAFV QGRAVSLPNA QPFG....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

```

m231/g231
      10      20      30      40      50      60
m231.pep  MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
g231      MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
      10      20      30      40      50      60

      70
m231.pep  QGRAVSLPNAQPFG
g231      QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPRLNLVGVIG
      70      80      90     100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

527

a231.seq (partial)

```

1   ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTGTGGAACA
501 CGCGGACGCT GACTTTCCTG CCTTCCGCCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGTCGGC GCGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1   MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51  ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRC SAAG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFG					
a231	QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1   ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAGGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTCGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaGtACaAt gagtttcgtA ccctccGCCG ccgcgcgCAG GTTGtcgcGC
551 GAACgtGTAC CGTAagcgtg TTtcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTtTa tGTttcgcgc cgtcgcCgtc gATGACGTGA AGGGtatcGC
651 CgtcATAGAC TTTGGACACC Gtgcctgcgt AGctGTGGCC GGATttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1   MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```

101 SFPOSFAFPF RLNLVGVIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
 151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSF FHLRCVDIRH
 201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGGTTGCG CGTCTCCGCA AAAATGCAGG
 151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
 201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCC
 251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTT
 301 AGCTTTCCAC AATCCTTTC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
 351 CATAATCGGC AAAATCGGCC TTATCCTGCT GTTCTTAGC ATAACTTTA
 401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTT
 451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTATCGAACA
 501 CGCGCACGCT GACTTTCCTG CCTTCGCGCG CCGCGCGCAG GTTGTGCGGC
 551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGCTCGA TATACGCCAT
 601 CCGGATTTTG TGTTCGCGC CGTCGCGGTC GATAACGTGA AGGGTGTGCG
 651 CGCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
 701 GATGCTCGGC GCGGGCGGG GCGGTCGGAA CCCGCTCCC CTGCCGCGCC
 751 GAGTACGTCG AGTACGGCAA CCGCCGTCCG CACCGCTCG CTGCCGTACC
 801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC
 851 ATGATTTTTT TAATCTGCAT ATTTTCAA TGCCGATGCC GTCTGAACAT
 901 ATCGGAATCG GATTTAGAC GGCATCTTAA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

1 MSKRKSINRP YQKPAELPPL QNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
 101 SFPOSFAFPF RLNLVGVIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
 151 ADRNLRHFAL VAVGIEHAHA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
 201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRCSAAGG RVGTRVPCRA
 251 EYVEYGNRRP HRLAIVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
 301 IGIGFQTAS*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAHGIHPILIAAPACPAVRPRRLRIFSFPQSFAFFRLNLVGVIG					
m231-1	QSRVSLPNAQPFAHGIHPILIAAPACSAVRPRRLRIFSFPQSFAFFRLNLVSVGIIG					
	70	80	90	100	110	120
g231-1.pep	KIRLILFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADNRNLRHFALVAVGIEHAHADFPFRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSFHLRCVDIRHPNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRRCASAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAIVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGGTTGCG CGTCTCCGCA AAAATGCAGG

529

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCGGTC CTGCACCTGC ATCAGGTTC AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCTG GTGTCGAACA
501 CGCGGACGCT GACTTTCCTG CCTTCGCGC CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGGCGGG CCGTCTCGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCGG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTT
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV  QSRVSLPNA QPFAHGIHPI LIAPAACP AVRPRLRIF
101 SFPQSFAFPF RNLNSVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLNRHFAL VAVGVEHADA DFPFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a231-1.pep	QSRVSLPNAQPFAHGIHPILIAPAACPAPVRPRLRIFSFPQSFAFPFRLNSVGIIG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAACPASAVRPRLRIFSFPQSFAFPFRLNSVGIIG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a231-1.pep	KIRLILFFSITFIMPRRPVHLHLHQVQIGFADRNLRFHFAVAVGVEHADADFPFRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVHLHLHQVQIGFADRNLRFHFAVAVGIEHAHADFPFRRRAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
a231-1.pep	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRRCSAAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
	250	260	270	280	290	300
a231-1.pep	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300
	310					
a231-1.pep	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1  atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatacctgtt
51  tggtcagatt ttgggaacgg cggttgccgg cgcgccgct tatattgtcg
101 ggatactggt tttgctggtc gccgtcggag gaacggccgg cagcctgttt

```

530

```

151 atgccgtccg taccgcgcaa ggctgccgat acccaaatcg agtggaaatat
201 tgtccgtggt acaaaatccc tgctgcgtga aacggtgcgg cacaatccccg
251 tttttaccgc cattatcggc atctcgtggt tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttggt ttccatcggg attgccgccg
401 gttcgggtact gtgtgccaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacggttg gtgcgttggg ttcgacggtt tgcggcctgg ttttgggtg
501 gctgacgcac ggacaccggt ttgaagggtt gaacggcatt ttttgggttt
551 tatcgcaagg atgggcatac cccgtgatgg cggatgatgac gctgatcggc
601 tttttcggcg gatttttctc cgttccgctc tatacctggc tgcaaacccg
651 cagcagcgag actttccgcg cccgcgccgt tgccgccaac aatatcggtt
701 acggcatctt tatggtttcc gccgccggtt tgagcgcggt attgctgttt
751 ttggttgaca gcattttccct gctgtatctg attgtcgctt tgggcaatat
801 tccgttggcg gtatttttga ttaagcgcg aaggcggtt ttaggcgcgg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

```

g232.pep
  1 MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
 51 MPSVPAKAAD TQIEWNIVRG TKSLRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGNLGI FWFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

```

m232.seq
  1 ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCG CCATCCTGTT
 51 CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTCGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCGCCAA GGCTGCCGAT ACACAAATTG AGTGGAATAT
201 TGTCCTGGC ACAAAATCCC TGCTGCGTGA AACGGTGCGG CACAAGCCCCG
251 TTTTACC GC CATTATCGGT ATTTCTGGT TTTGGTTTGT CGGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTT AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAkGG AACGCCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGT TGC GGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CGGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTCTC CGTTCGCTC TATACct(g)TG CAAACCGCCa
651 TAGCGAGaTT TCCGCGCCCg GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATG TTTCCGCTGC CGTTTGTAGC GCGGTGTTGC TGTTTTTGT
751 TGACAGCATT TCCTTGTGT ATCTGATTGT CGCTTTGGGC AATATTCCGT
801 TGTCGGTATT TTTGATTAAG CGCGAAAGGC GGTTTTTAGG CGCGCGGCCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

```

m232.pep
  1 MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
 51 MPSVPAKAAD TQIEWNIVRG TKSLRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGNLGI FXFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

```

m232/g232
      10      20      30      40      50      60
m232.pep  MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
          |||
g232      MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

531

	10	20	30	40	50	60
	70	80	90	100	110	120
m232.pep	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	130	140	150	160	170	180
m232.pep	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	190	200	210	220	230	
m232.pep	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAVAANNIVNGIFMVS					
	240	250	260	270	280	289
m232.pep	AAVLSAVLLFLFDSISLLYLIALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIALGNIPLAVFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232.seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAAGCC GCCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTCA
101 AAACCGCGCT GTTTGTGATG ATTGGGTTT ACGGTTTGGG GCAAAACGGC
151 TTCCTGCCTG CCGGACAGAT GTTGAAGTTC GCGCGTTGCG TGTATTATTT
201 GCCGTATTTT CTGTTTTCCT CGCTGTCGGG GCAGTTGGGT AACAAATTCG
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAAT GATCATTATG
301 GCGGTGGCGG CATACGGGTT TTATATCCGG TCTGCCCCGC TGCTTTTGGC
351 GTGTCTGTTT TGCATGGGCG CGCAATCGAC GCTGTTCCGG CCGCTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGGTAC GTTTGTCGCC ATCCTGTTTC GTGAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATTGTCGGG ATACTGGTTT
551 TGCTGCTCGC CGTAGGAGGC ACGGTCGGCA GCCTGTTTAT GCCGTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAATTGAG TGGAATATTG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CGGTGC GGCA CAAGCCCGTT TTTACCGCCA
701 TTATCGGTAT TTCGTGGTTT TGGTTTGTTC GCGCGGTTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTT CCATCGGTAT TGCCGCCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGGAA CGGCTGAGGT TGGCTTGGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTTG CCGCTTGGTT TTGGTGTGGC TGACGACCGG
951 ACACCGTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGCAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTTCGGCGGA
1051 TTTTCTCCG TTCCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCCGTTG CCGCCAACAA TATCGTTAAC GGTATTTTTA
1151 TGGTTTCCGC TGCCGTTTTG AGCGCGGTGT TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGT TGTATCTGAT TGTCGCTTTG GGCAATATTC CGTTGTCGGT
1251 ATTTTGTATT AAGCGGAAA GCGGTTTTT AGGCGCGGCG GCAATCAGGA
1301 AAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232.pep
1  MYAKKGGLGL VKSRRFAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAGQMLNL GALLFILPYF LFSSLSGQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLLACLF CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTVEA ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLFMPSV
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIIGISWF WEFVGAVYTTQ
251 LPTFTQIHLG GNDNVFNML ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```


532

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAAVL SAVLLFLFDS
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP*

m232/a232 95.9% identity in 290 aa overlap

m232.pep					10	20	30
					MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLCMGAQSTLFGPLKYAILPDYLD	DDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP					
	120	130	140	150	160	170	
m232.pep		40	50	60	70	80	90
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
		180	190	200	210	220	230
m232.pep		100	110	120	130	140	150
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSXERLMLAW					
a232		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSRERLRLAW					
		240	250	260	270	280	290
m232.pep		160	170	180	190	200	210
		VTVGALGLTVCGLVVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMVMTLIGFFGGFFSVPL					
a232		VTVGALGLTVCGLVVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMVMTLIGFFGGFFSVPL					
		300	310	320	330	340	350
m232.pep		220	230	240	250	260	
		YT-VQTAIARFRP- <u>AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS</u>					
a232		YTWLQTASSETFRARAVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
		360	370	380	390	400	410
m232.pep	270	280	289				
	VFLIKRERRFLGAAAIRKKPX						
a232	VFLIKRERRFLGAAAIRKKPX						
	420	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq
 .1 atgaaacgca aaaatatcgc gctgattccc gccgccggca tcgggggtgcg
 51 tttcgggtgcg gacaaaacca agcaatatgt cgaaatcgga agcaaaaccg
 101 ttttagaaca tgtacttggg atttttgaac ggcattgaggc cgtcgatttg
 151 accgtcgttg tcgtctcgcc cgaagacacg tttgccgata aggttcagac
 201 ggcatttcca cagggttcggg tgtggaaaaa cgggtggacag acccgcgccg
 251 aaactgtccg caacgggtgtg gcaaaactgt tggaaaccgg tttggcggcg
 301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgccgtc
 351 tgaagctctg gcgcggttga tagaacaggc gggcaacgcc gccgaaggcg
 401 ggattttggc agttcccgtt gccgatacgc tcaagcgcgc agaaagcggg
 451 caaatcagtg caactgtcga ccgttcgggg ctttggcagg cgcaaacgcc
 501 gcagcttttt caagcgggtt tgctgcaccg cgcattgggt gcggaaaact
 551 tgggcggcat taccgatgaa gcgtccgccg tggaaaaact ggggtgtgct
 601 ccgctactga tacaggcgca cgcgcgcaat ttgaaactga cgcagccgca
 651 ggacgcatac atcgtcaggc tgctgctcaa tgccgtctga

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep
 1 MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLEHVLG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
 101 ETDNILVHDA ARCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG

533

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR
 201 PLLIQGDARN LKLTQPDAY IVRLLLLNAV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC
 201 GGCATTTCCTA CAGGTTTCGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG
 401 GGATTTTGGC AATTCCCAT TCCGATACGC TCAAGTGCGC GGACGGTGGG
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFF QVRVWNGGQ TRAETVRNGV AKLLETGLAA
 101 ETDNILVHDA ARCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m233.pep	FADKVQTAFFQVRVWNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
g233	FADKVQTAFFQVRVWNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
	70	80	90	100	110	120
	130	140	150			
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESGQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC
 201 GGCATTTCCTA CAGGTTTCGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACGTCCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG
 401 GGATTTTGGC AATTCCCGTT TCCGATACGC TCAAGTGCGC GGACGGTGGG
 451 AACATTAGTG CAACCGTCTA GCGGACGAGC CTTTGCGAGG CGCAAAACGC
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAAAC
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC
 601 CCTTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAAACTGA CGCAGCCGCA
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

534

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51 TVVVVSPEDT FADKVQTAFF QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDVAV*
```

m233/a233 99.3% identity in 152 aa overlap

```

10      20      30      40      50      60
m233.pep  MKRKNIALIPAAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
          |||
a233      MKRKNIALIPAAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
          |||
          10      20      30      40      50      60

70      80      90      100     110     120
m233.pep  FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
          |||
a233      FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
          |||
          70      80      90      100     110     120

130     140     150
m233.pep  TRLIEQAGNAAEGGILAIPIADTLKCADGGNI
          |||
a233      TRLIEQAGNAAEGGILAIPIADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA
          |||
          130     140     150     160     170     180

a233      AENLDGITDEASAVEKLGIRPLLQGDARNLKLTQPQDAYIVRLLLDVAVX
          190     200     210     220     230
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgccgc catcgctttt gccgccgctg ccgtttcact
51 gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtgc
101 cctcctgcaa tacgcaatat cacggtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgctccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttccgg caaagcgag aacctgaaag gcgcagatta
351 tgctggtacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctatct
501 cacacagggc gcggggcgaat acgcactttc caaccgcaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPIISVG
51 TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRFNV LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGGTSY DATLNGKVL D
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
51 CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTTA GACTTGGCAA
101 TCCGCGAAGC .gtCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

535

m234.pep (partial)
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAI REAVNS LVQAVDNGAW
 51 QPNR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

m234/g234

				10	20	30
m234.pep				GAGEYALSNREI	IGFGGTSGY	DATLNGKVL
g234	LGRGKSQIAYAKVALNIVNVNTSEIVYSTQ	GAGEYALSNREI	IGFGGTSGY	DATLNGKVL		
	140	150	160	170	180	190

	40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX	
g234	DLAIREAVDNLVQAVDNGAWQSNRX	
	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)
 1 AACCGCACCT ATTTGAACGC ATTAAAACAG GAATCCGGCA TTTCCGGCAA
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTITGGGT
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)
 1 NRTYLNALKQ ESGISGKAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD
 101 ATLNGKVL DLAI REAVNSLV QAVDNGAWQP NR*

m234/a234 100.0% identity in 54 aa overlap

				10	20
30					
m234.pep				GAGEYALSNREI	IGFGGTSGY
a234	LGRGKSQIAYAKVALNIVNVNTSEIVYSAQ	GAGEYALSNREI	IGFGGTSGY	DATLNGKVL	
	50	60	70	80	90

	40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX	
a234	DLAIREAVNSLVQAVDNGAWQPNRX	
	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

536

```

1  atgaaacctt tgatttttagg gcttgccgcc gtgttggttc tgtctgcctg
51  ccaagttcga aaagctcccc acctcgacta cacgtcattc aaagaaagca
101 aaccggcttc aatttttggtg gttccgcccgc tgaacgagtc gcctgatgtc
151 aacggcactt gggggatgct ggcttcgacc gccgcgccga ttccgaagc
201 cggctattac gtctttcccg ccgcagtcgt ggaggaaacc ttcaaagaaa
251 acggcttgac caatgccgcc gatattcacg ccgtccggcc ggaaaaactg
301 catcaaattt tcggcaatga tgcggttttg tacattacgg ttaccgaata
351 cggcacttca tatcaaattt tagacagcgt gacgaccgta tccgccaaag
401 cacggctggt cgattcccg c aacgggaaaag agttgtggtc gggttcggcc
451 agcatccgcg aaggcagcaa caacagcaac agcggcctgt tgggggcttt
501 ggtcggcgca gtggtcaatc agattgccaa cagcctgacc gaccgcggtt
551 atcaggtttc caaaaccgcc gcatacaacc tactgtcgcc ctattcccgc
601 aacggtatct tgaaagggtc gagattcgtc gaagagcagc ccaaataa

```

This corresponds to the amino acid sequence <SEQ ID 870; ORF 235.ng>:

g235.pep

```

1  MKPLILGLAA VLALSACQVR KAPDLDTYSF KESKPASILV VPPLNESPDV
51  NGTWGMLAST AAPLSEAGYY VFPAAVVEET FKENGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVGA VVNQIANSLT DRGYQVSKTA AYNLLSPYSR
201 NGILKGPRFV EEQPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

```

1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTCTGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCCGGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGTTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC CAAAACCGCC GCATACAACC TGCTGTGCGC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTT GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235.pep

```

1  MKPLILGLAA VLALSACQVQ KAPDFDYSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYSFKESKPASILVVPPLNESPDVNGTWGVLAST					
g235	MKPLILGLAAVLALSACQVRKAPDLDTYSFKESKPASILVVPPLNESPDVNGTWGMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIAHAVRPEKLHQIFGNDAVL YITVTEYGTS					
g235	AAPLSEAGYYVFPAAVVEETFKENGLTNAADIAHAVRPEKLHQIFGNDAVL YITVTEYGTS					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           130      140      150      160      170      180

           190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
g235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1   ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTCTGACT CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACCGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1   MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
a235      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
           10      20      30      40      50      60

           70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
a235      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
           70      80      90      100     110     120

           130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           130     140     150     160     170     180

           190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1   ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51  CGGTTTCATA ACCTGCAACC GCGCCACAT  CGCGGGTGTA ATGCCAGCAG
101 CGTTCGCATT TTTCGCGTC  GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTCCGGCGC  GGTAATTTCG
251 GCTTCCGCCT  GCAAaggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTT
351 TCACCAgTTC GGCTTCGGCT TTTCGTTGA  TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TGGCGCGGGC GCGGCTGTGC
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGGAAAG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTGCAG  CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCACC ATATCCGCCT GTTGCACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAAcagG AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgcccgt gTAATCGGTG GATGCCGCCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTTCG TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATTT CGACATTTTG CGGCCGTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTATACGG TCGCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1   MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGGNGKFI
51  TDFHFCFRHQ QGKAQFFAQS IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLRAAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNV FHGEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAG
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1   ..TTGCACGGAC GAACCGACGG TTTTGTCCGC GCGCAAAGGC TCGATGGCGG
51  CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTTCACCACT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCKTCTTCGC CGCCGCCGwT GAYGTCCAC GCTTCTTCGC
201 CCGTGAAGCA CAAAATCGGT GCAATCAAGA GAACCAAAC GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTCA GGATGTCGAG GTAGAACGCA CCAAGTCTT
351 CCGAGCAGAA AGAAACaTG TCTTTTACGG CAAAGTGGAa kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG AACTCTTGC AGCTGACGTG CCAATACCAC
451 GGCGTAGCGG TCGATTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTG AGGATTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCGC CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCTTC GCGTCCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GGCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1   ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVPSME
51  EDAVXFAAAX DVPRFFAGEA QNRCNQENQT ACDVIQSLC AAACMAVCFG
101 GVEAVFQDVE VERTQVFRAE RNXFVYGKVE XITRIVIAQ TLLQLTCQYH
151 GVAVDFFHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQ
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236

				10	20	30	
m236 . pep				LHGRTDGFVGAQRLDGGGYRFAGFADCRPF			
				: : :			
g236	FRHQQGKAQFFAQSIQIAGHFFRRGNFGFRLQGR	TSFVGAQRLD	SGGYCFARFADCRPF				
	60	70	80	90	100	110	
m236 . pep		40	50	60	70	80	90
	FHQFGFGFFVDGREL	VPSMEEDAVXFAAAXD	VPRFFAGEAQNR	CNQENQTACD	VIQGS	SLC	
g236	FHQFGFGFFVDGREL	VPSMEEDAVFFAAADD	VPRFFAGEAQNR	CNQENQAARD	VVQGLR		
	120	130	140	150	160	170	
m236 . pep		100	110	120	130	140	150
	AAACMAVCFGGVEAV	FQDVEVERTQVFRA	ERNXVFYGVK	VEXITRIVIA	CQTLLQLT	CQYH	
g236	AAAGAAVFGGGVEAV	FQDVEVERAQVFRA	ERNNVFHGEVE	GIARIVTAC	QTLLQP	PRQYQ	
	180	190	200	210	220	230	
m236 . pep		160	170	180	190	200	210
	GVAVDFHHIRLLHG	IFNRIKVAQVGK	QKAQGIADTA	VAFGYAFED	FFGNRQFA	AVIGRCR	
g236	GVAVDFHHIRLLHG	IFNRIKVAQIGK	QEAQGIADAA	VAFGNAFED	FFGNRQFA	AVIGGCR	
	240	250	260	270	280	290	
m236 . pep		220	230	240	250	259	
	PQAQDVCAEFVINLL	RCDVADGFRHFFA	FAVDNETMGQ	QLFIRRATHX			
g236	PQAQDVRAEFVIDFL	RDDVADGFRHFA	AVLVNHETV	GQQLFIRCASHG			
	300	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```

a236 . seq
1   ATGGCGCGTT  TCGCCTTCTC  CGCCGACATT  CTCTGCACAG  CGTTTGCAGA
51  CGGTTTCATG  GCCTGCAACC  GCGCCACAT  CGCGGGTGTA  GTGCCAGCAG
101 CGTTCGCATT  TTTCACCATC  ACTGGCTTTA  GCGGCAACGG  CAAGTTCGCT
151 GCCTACTTTC  ACTTCTGCTT  TAGACACCAG  CAAAGCAAAG  CGCAATTCTT
201 CGCCCAAAGC  ATTCAGATAG  CCGGCCATTT  CTTCCGGCGC  GGTAATTTTCG
251 GCTTCGGCTT  GCAAGGACGA  ACCGACGGTT  TTGTCGGCGC  GCAAAGGCTC
301 GATGGCGGCG  GTTACCGCTT  CGCGGGCTTC  GCGGATTGCC  GTCCATTTTT
351 TCACCAGTTC  GGCTTCGGCT  TTTTCGTTGA  TGGTCGGGAA  CTCGTGCCAA
401 GTATGGA AAA  GCACGCTGTC  TTCTGCGCCG  CCGCGATGA  TGTCCACGCG
451 TTCTTCGCGG  GTGAAGCACA  AAATCGGTGC  AATCAAGAGA  ACCAGGCTGC
501 GCGTGATGTG  GTACAGGGCG  GTTTGCGCGC  TCGGCGGGC  GCGGCTGTGC
551 GCTTTGGTGG  TATAGAGGCG  GTCTTTCAGG  ATATCGAGGT  AGAACGCGCC
601 CAAGTCTTCC  GAGCAGAAAAG  AAACCATTTT  TTTCACGGCA  AAGTGGAAAG
651 CATAACGCGG  ATAAAAATCA  CCGGCAACGC  GTTCTTGCAG  CCGCCTTGCC
701 AACACCAAGG  CATAGCGGTC  GATTTCCACC  ATATCCGCCT  GTTGCACGGC
751 ATCTTCAATA  GGATTGAAGT  CGCTCAAGTT  GGCAAACAAA  AAGCTCAAGG
801 TATTGCGGAT  ACGGCGGTAG  CTTTCGGTTA  CGCGCTTGAG  GATTTCTTTG
851 GAAATCGCCA  ATTCGCCGCT  GTAATCGGTG  GATGCCGCCC  ACAGGCGCAG
901 GATGTCGCGC  CCGAACTCGT  TATACACTTC  TTGCGGCGCG  ACGACGTTGC
951 CGATGGATTT  CGACATTTTG  CGCCCGTTTT  GATCCACCAC  GAAACCATGG
1001 GTCAGCAGCT  GTTTGTACGG  CGCGCGACCC  ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

```

a236 . pep
1   MARFAFSADI  LCTAFADGFM  ACNRAHIAGV  VPAAFAFFTI  TGFSGNGKFA
51  AYFHF CFRHQ  QSKAQFFAQS  IQIAGHFFRR  GNFGFGLQGR  TDGFVGAQRL
101 DGGGYRFAGF  ADCRPFFHQF  GFGFFVDGRE  LVPSMEKHAV  FCAAADDVPR
151 FFAGEAQNRC  NQENQAARDV  VQGLLRAAAG  AAVGFGGIEA  VFQDIEVERA
201 QVFRAERNHF  FHGKVEGTR  IKITGNAFLQ  PPCQHQGIIV  DFHHIRLLHG
251 IFNRIEVAQV  GKQKAQGIAD  TAVAFGYALE  DFFGNRQFAA  VIGGCRPQAA
301 DVRAELVIHF  LRRDDVADGF  RHFAPVLIHH  ETMQQLFVR  RATH*

```



```

m236.pep          LHGRTDGFVGAQRLDGGGYRFAGFADCRPF      30
                   |:|||||
a236              FRHQQSKAQFFAQSIQIAGHFFRRGNFGFLQGRTDGFVGAQRLDGGGYRFAGFADCRPF      110
                   60       70       80       90       100      110

m236.pep          FHQFGFGFFVDGRELVPMSMEEDAVXFAAAXDVPRFFAGEAQNRCNQENQTACDVIQGSLLC      90
                   |||||
a236              FHQFGFGFFVDGRELVPMSMEKHAVFCAAADDVPRFFAGEAQNRCNQENQAARDVVQGGGLR      170
                   120      130      140      150      160      170

m236.pep          AAACMAVCFGGVEAVFQDVEVERTQVFRAERNXVIFYGKVEXITRIVIIACQTLQLTQCQYH      150
                   ||| ||| :||| :||| :||| | :||| ||| | : ::|| ||::
a236              AAAGAAVGFGGIEAVFQDIEVERAQVFRAERNHFFHGKVEGITRIKITGNAELQPPCQHQQ      230
                   180      190      200      210      220      230

m236.pep          GVAVDHFHHIRLLHGIFNRIKVAQVGKQKAQGIADTAVAFGYAFEDFFGNRQFAAVIGRCR      150
                   |:|||||
a236              GIAVDHFHHIRLLHGIFNRIEVAQVGKQKAQGIADTAVAFGYALEDDFFGNRQFAAVIGGCR      290
                   240      250      260      270      280      290

m236.pep          PQAQDVCAEFVINLLRCNDVADGFRHFFAFVDNETMGQQLFIRRATHX      259
                   ||||| ||::||: ||||| : |||||
a236              PQAQDVRAELVIHFLLRDDVADGFRHFAPVLIHETMGQQLFVRATHX      340
                   300      310      320      330      340

```

g237.seq

1	atgcggggaca	agggttgccgg	taatatcgca	ctccccgcc	cacgaatat
51	cgattctaac	atcggcaagc	tgcggaaaaa	ctttaagcat	atcttgccgg
101	acaagctcgg	tcatacgcgc	aggattgtcg	ataaaatctg	tatccttacc
151	gccgaaaagc	agcctgcccgt	ccgcgtgacg	gcggtaataa	tccaaaatat
201	ggcggttgtc	gcatactgcc	atattgtgtc	ggataagccc	ttttgtgcgc
251	gcgccaagg	gttcggtggc	aataataaag	gtgctgacgg	caatcgcctt
301	gcgttccaaa	ggccggaata	tcgggttcaa	accgacataa	gtattgacgg
351	catagaccac	atttttacac	tcgacgctgc	cttcgggctg	gtaaaccagc
401	caaccgtttt	gatacggttc	gatgcgcgtc	atcggggatt	gctcgaaaa
451	ctgcgcgccg	gcttcggcag	cggcgctggc	aacacccaac	gtgtaattga
501	gcggtgaag	atgcccgag	aagggatcga	actgtgcgcc	ttggtacata
551	tcgctgtcaa	gctgctgttt	caactcggct	ttatcccaa	gttgataatg
601	actcgcaccg	taatgccgtt	gggcgtgttc	atgccactgc	tgcaactctt
651	ccaatgctcg	cggacggaag	gcaaccgtgg	cataaccgcg	ctgccaatcg
701	caatcgatgg	catgtttcgg	gacgcgttcg	tccaccagtt	cgaccgcctg
751	caaaactgt	tgccaaaacc	attgcgcctg	ctccaagccg	acctgttttt
801	caatttcccc	cataccgcag	cgctagtctc	tgataacctg	cccgccactc
851	ctgccggaag	cgcggaagcc	gatacgtgcg	gcttccaaaa	cgacggcttc
901	atgtccgtgt	tccgccagcg	gcaatgcggt	acacaaaccg	ctcaaaccgc
951	cgccgataat	gcagggttcg	gcttttcagc	ggcattggag	tttcggataa
1001	acagtatgcg	gattaaccga	actaaaataa	taagaaggca	gatattcttg
1051	aaaatcaggg	cgaatcattg	gttttgcttt	atcgggtata	tttcggacg
1101	gaatgatata	gactgtccgg	ccatatcgtc	caaacagaaa	atcggttga

q237.pep

1 MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51 AEKOPAVRAE AVIIQNMAVV AYCHIVADKP FCARAQFGG NNGKADGNRL

```

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN
151 LRAGFGSGAG NTQRVIERMK MPQGIELCA LVHIAVKLLF QLGFIPKLIM
201 TRTVMLPLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF
301 MSVFRQRCQG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRQIFL
351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq

```

1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TCGGAAAAA CTTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG TCATaCGTC AGGATTGTCG ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGTAATAA TCCAAAATAT
201 GGCGGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTTGC GCGC
251 GCCCCAAGG GTTCGGTCGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGTTCCAAA GGCCGGAATA TCGGTTCAA ACCTGCATAA GTATTGACAG
351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTCGGGCGT GTAAACCAGC
401 CAACCGTTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAT
451 CTGCGCACCG GCTTCGGCAG CGGCACGAGC GATGCCCCAA GTGTAAGTGA
501 GCGGATGCAG GTGTCCGGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG
601 ACTCGCACCG TAATGCCGTT GGGCGTGTTT ATGCCACTGC TGCAACTCTT
651 CCAATGCTG CGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA
701 CAATCGACGG CATGTTTTCG GACGCGTTCG TCCACCAGTT CGACCGCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
801 CAATTTCCCC CATACCGCAG nCGTAATCGC TGATAACCTG CCCGCCACTC
851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTCAGAC GGCATTGAAG TTtCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTCGCTTT ATCAGGTGTA TTTTCGGACG
1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAwACAGAAA ATCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep

```

1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGH TL RIVDKLVILT
51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNKGADSNRL
101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN
151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIPKLIM
201 TRTVMLPLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRRAET DTRGFQHNRF
301 MSLLRQGQCS AQTTQSAADD TGIGFQTALK FRINSMRINR TEIIRQIFL
351 KIRANHCVCF IRCIFGRNDT GCRAISSXQK IG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGH TL RIVDKLVILTAEKQSAVRAE					
	: : : : :					
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH TR RIVDKFVILTAEKQPAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMAVVAYCHIVTDKPF CARPQGFGRNNKGADSNRLAFQRPEYRVQTCISIDSIDH					
	: : : : : :					
g237	AVIIQNMAVVAYCHIVADKPF CARAQGF GGNKGADGNRLAFQRPEYRVQTDISIDGIDH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					

g237	I F T L D A A F G R V N Q P T V L I R F D A R H R G L L E N L R A G F G S G A N T Q R V I E R M K M P G Q G I E L C A	130	140	150	160	170	180
m237.pep	L V H I A V K L L F Q L G F I P K L I M T R T V M P L G V F M P L L Q L F P M L R T D G N R G I T A L P I T I D G M F A	190	200	210	220	230	240
g237	L V H I A V K L L F Q L G F I P K L I M T R T V M P L G V F M P L L Q L F P M L R T D G N R G I T A L P I A I D G M F A	190	200	210	220	230	240
m237.pep	D A F V H Q F D R L Q R L L P K P L R L L Q A D L F F N F P H T A X V I A D N L P A T P S R R A E T D T R G F Q H N R F	250	260	270	280	290	300
g237	D A F V H Q F D R L Q R L L P K P L R L L Q A D L F F N F P H T A G V V A D N L P A T P A G R A E A D T C G F Q N D G F	250	260	270	280	290	300
m237.pep	M S L L R Q G Q C S A Q T T Q S A A D D T G I G F Q T A L K F R I N S M R I N R T E I I R R Q I F L K I R A N H C V C F	310	320	330	340	350	360
g237	M S V F R Q R C G T Q T A Q T A A D N A G F G F Q T A L E F R I N S M R I N R T K I I R R Q I F L K I R A N H C V C F	310	320	330	340	350	360
m237.pep	I R C I F G R N D T G C R A I S S X Q K I G X	370	380				
g237	I G Y I F G R N D T D C R A I S S X Q K I G X	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 885>:

```
a237.seq
1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCC GCCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TGC GGAAAAA CTTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG TCATACGCGC GGGATTGTCTG ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAI
201 GACGTTTGTC GCATACTGCC ATATTGTTGC GGATAAGCCC TTTTGCACGC
251 GCGCCAAGG GTTCTGTGGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGCTCCAA GGCTTGAATA TCGGATTCAA ACCGGCATAA GTATTGACGG
351 CGTACACCAG ATTTTTCGAT TCGACGCTGC CTTCCGGGGT GTAAACCAGC
401 CAACCGTTTT GATAAGGTTT AATGCGTATC ATGGGAGAAT GCTCAAAAAT
451 CTTCTACCA GCTTCGGCAG CGGCGCGGGC GATGCCAAC GTGTAATTGA
501 GCGGATGGAG ATGCCCCGAC AAGGGATCGA ACTGTGCGCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGCTT CAGTTTCACTG TTATCCCAGA GTTGATAATG
601 AGTTGCACCG TAAATATTTT GGGCGTGCTC ATGCCATTGT TGAATTCTT
651 CCCAATGCTG CGAACGGATG GCAACCGTGG CATAACCGCG CTGCCAATCG
701 CAATCAATGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGCCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCCAAACCT ACCTGTTTTT
801 CAATTTCTCT CATACCGCAG GCGTAATCGC TGATAACCTG CCCGCGACTC
851 CGTCCCGACG CGCCGAAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCTTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CTCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATTA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCGGGTATA TTTTCGGACG
1101 GAATGATACA GGCTGTCGAG CCATATCGTC CAAACAGAAA ATCGGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 886; ORF 237.a>:

a237.pap

1	MRDKVGGNVA	LPAPRIFFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	<u>AVIIQIONMTVV</u>	AYCHIVADPK	FCTRAQGFCG	NNKGADSNRL
101	ALQRLERYIQ	TGISIDGVHQ	IFAFDAAFKG	YNQPTVLIRF	NAYHGRMLNK
151	LRTSFGSGAG	DAQRVIERME	MPQGGIELCA	LVHIAVKLLL	QFSVIPELIM
201	<u>SCTVIFLGLV</u>	<u>MPLLQFFPML</u>	RTDGNRGITA	LPIAINGMFA	DAFVHQFDRL
251	QRLLPKPLRL	LQTDLFFNFL	HTAGVIADNL	PATPSRAET	DTRGFQHNRF
301	MSLLRQGQCS	AQTTQSAADD	TGIGFQTALK	FRINSMRINR	TEIIRRQIFL
351	KIRANHCVCF	IGYIFGRNDT	GCRAISSKOK	IG*	

m237/a237 85.6% identity in 382 aa overlap

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEQSAVRAE					
a237	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEQSAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMVAVYCHIVTDKPFPCARPOGFGNNKGADSNRLAFQRPYRVQTCISIDSIDH					
a237	AVIIQNMVAVYCHIVADKPFCTRAQGFNGGADSNRLALQRLYRIQTGISIDGVHQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDAHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVLC					
a237	IFAFDAAFGRVNQPTVLIHFAYHGRMLKRLTSFGSGAGDAQRVIERMEMPQGIELCA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m237.pep	LVHIAVKLLFQLGFIPKLIMTRTMPLGVFMPLQLFPMRLTDGNRGITALPITIDGMFA					
a237	LVHIAVKLLQFSVIPELIMSCTVIFLGVLMPQLLQFFPMRLTDGNRGITALPIAINGMFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m237.pep	DAFVHQFDRLQRLPKPLRLLQADLFFNFPHATAXVIADNLPATPSRAETDTRGFQHNRF					
a237	DAFVHQFDRLQRLPKPLRLLQADLFFNFPHATAXVIADNLPATPSRAETDTRGFQHNRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m237.pep	MSLLRQGCQAQTTSAAADTGIGFQTALKFRINSMRINRTEIIRRIQIFLKIRANHCVC					
a237	MSLLRQGCQAQTTSAAADTGIGFQTALKFRINSMRINRTEIIRRIQIFLKIRANHCVC					
	310	320	330	340	350	360
	370	380				
m237.pep	IRCI FGRNDTGCRAISSXQKIGX					
a237	IGYIFGRNDTGCRAISSXQKIGX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctggtggcag cggcaatatc
51  gatgctgcat atccccatta gtcatgcgaa cggtttggat gcccgtttgc
101 gcatgatgat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctgcgcgagc tgtaaaaaat cgggttttgc ccgtccaaac
201 atttgatgca actgcggtcg gccccatact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtccgtt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggac tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tggtccgcaa gccctttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttccgg ttttctcagc
601 cgtgcgggat aagcaggaaa actgatatgg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cggcatcgtc caaggtgcgg
701 ttaatccttt ttaacgggtt tttcaagggt tagggattgg ggcaattaca
751 gacagtgcgg taagcccggc cacagataga gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcaca cttgccgccg

```

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851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgccttgcc gtagcagagg ccgcaggtac ggtttggcgc ggtaaaaaag
1001 tagaacttaa cccgaccaa tgggattggg ttaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaata taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

```

g238.pep
  1 MNLPIQKFMM LLAAAIISMLH IPISHANGLD ARLRDDMQAK HYEPGGKYHL
 51 FGNARGSVKN RVCVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTs TKTKINTVPQ APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWRa NRMDDIRGIV QGAVNPFLTG FQGVGIGAIT
251 DSAVSPVTDt AAQQTlQGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAAGTVWR GKKVELNPTK WDWVKNtGYK
351 KPAARHMQtV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYt IDSNEKRNKI KNHGLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

```

m238.seq
  1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
 51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAA GCACCTCTGA
351 TTCAGCGGC GGTGTAGACG GCGGTTTAC TGTTTACCAA CTTCATCGAA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCAGGAG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACCTCA ACAAAAACAA AGACTAATAT TGTCCCTCAA GCCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCCTATGG ATGATGTTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTTAGGAA AATTAAAGTCC GGAAGCACAA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCAG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TTAATAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTCACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAATTTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

```

m238.pep
  1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPGGKYHL
 51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```

```

151 DYPPPPGGARD IYSYVVKGTS TKTKTNIVPQ APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQQTLOGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGIN
301 AKQWADAHPN ITATAQTALS AAEAAGTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMOTL DGEMAGGNKP IKSLPNSAAE KRKQNFEEKFN SNWSSASFDS
401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY
451 LDSNGNAVKT GNLOGKQAKD YLQQQTHIRN LDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng) from *N. gonorrhoeae*:

m238/g238

	10	20	30	40	50	60
m238.pep	MNLPIQKFMMLFAAAI SLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAAI SMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
g238	RVCAVQTFDATAVGPILPITHERTGFEGVIGYETHFSGHGHEVHSPFDNHSDSKSTSDFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPPGGARDIYSYVVKGTSTKTKTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGYPEPQGARDIYSYHIKGTSTKTKINTVPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m238.pep	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDDVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPDKNWRANRMDDIRGIVQGAVNPFLTG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m238.pep	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQ LAAASLLQDS AFAVKDGIN					
g238	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQ LAAASLLQDS AFAVKDGIN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m238.pep	AKQWADAHPNITATAQTALSAAEAAGTVWRGKKVELNPTKWDVVKNTGYKKPAARHMOTL					
g238	ARQWADAHPNITATAQTALAVAEAGTVWRGKKVELNPTKWDVVKNTGYKKPAARHMOTV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m238.pep	DGEMAGGNKPKISLPNSAAEKRKQNFEEKFNSNWSSASFDSVHKTLPNAPGILSPDKVKT					
g238	DGEMAGGNRPPKSI-TSE GKANAATYPKLVNQLNEQNLNIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	
	430	440	450	460	470	480
m238.pep	RYTSLDGKITIIKDNENNYFRIHDNSRKQYLD SNGNAVKTGNLOGKQAKDYLQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTS GGWL SRDGTRQYRPPT EKKSQFATTGIQANFETY					
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

```
a238.seq (partial)
1  ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51  GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTTGA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAGCGGC GCGTAGACG GTGGTTTTAC CGTTTACCAA CTTCATCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGAT ATATACAGCT ACTATGTCAA
501 AGGAACCTCA ACAAAAACAA AGAGTAATAT TGTTCGCCGA GCCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGCGG TAAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAA TGGGATTGGG TAAAAAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTTG GATGGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA
```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

```
a238.pep (partial)
1  MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPGGKYHL
51  FGNARGSVKN RYAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQQTLOGIN HLGNLSPAQ LAAATALQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALE VAEAATTVWG GKKVELNPTK WDWVKNTRYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ
```

m238/a238 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPGGKYHL	FGNARGSVKK
a238	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPGGKYHL	FGNARGSVKN
	70	80	90	100	110	120
m238.pep	RYAVQTFDA	TAVSPVLPIT	HERTFEGVIG	YETHFSGHG	HEVHSPFDNH	DSKSTSDFSG
a238	RYAVQTFDA	TAVGPILPIT	HERTFEGVIG	YETHFSGHG	HEVHSPFDNH	DSKSTSDFSG
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQ	LHRTGSEIHP	PEDGYDGPQ	GSFYPPPGG	ARDIYSYYV	KGTSTKTKNIVPQ
a238	GVDGGFTVYQ	LHRTGSEIHP	PEDGYDGPQ	GSFYPPPGG	ARDIYSYYV	KGTSTKTKSNIVPR
	190	200	210	220	230	240
m238.pep	APFSDRWLKEN	AAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDVRGIV	QGAVNPFLMG
a238	APFSDRWLKEN	AAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDIRGIV	QGAVNPFLMG
	250	260	270	280	290	300
m238.pep	FQGVGIGAIT	DSAVSPVTD	TAAQQTLOGI	NLDGKLSPEA	QLAAASLLQD	SAFAVKDGINS

a238	FQGVGIGAITDSAVSPVTDTAQQTLQG INHLGNLSPEAQLAAATALQDSAFAVKDGINSL 250 260 270 280 290 300
m238.pep	AKQWADAHPNITATAQTALSAEAEAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL 310 320 330 340 350 360
a238	ARQWADAHPNITATAQTALAVEAEATTVWG GKKVELNPTKWDWVKNTGYKT PAVRTMHTL 310 320 330 340 350 360
m238.pep	DGEMAGGNKPIKSLP-NSAAEKRKQNFEKFNSNWSSASFDSVHKLTLPNAPGILSPDKVK 370 380 390 400 410 419
a238	DGEMAGGNRPPKSITSNSKASTSQ : : : : : :

```
g239.seq
1  atgtttccacc ataaaaggtat tgcccgaaac cggcggatgg aggttttgtt
51  tttctgccgc cgccctgatc gcttcgtgat tcgccaaacg cgcttgttgc
101 agcctcatth gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatcacia
201 cggaaaaaac ggaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacgtt tttctctgtt attattccgg tatcggaccg
301 gcagtcgcgt ccgccacacg caaaactgcg ctctcgcgcc tcgggttggc
351 ggcaatttcc gcttcacccg gctttaatgc cctggccacg attttcaggg
401 gcggtatcgg caaatccgct tctctgacct cgcccagct cggcaggggc
451 tcggtgttgc aatatthttt gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaacgccc gccctctttc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gtaataaaag
601 atgcggaatg cctggaaggt gcgcgtcgca ggatcctgcc ccgcgtcgcg
651 agtacggacg ttttgtgcca cgatctgcgc cagcttgcgg gttgtatcga
701 ttggactttc cgcccgttgc gcgacaatgg cgcgcacaa ctggcggcta
751 aaccgctctt caccataa
```

g239.pap

1	MFHHKGIARN	RRMEVLFFCR	RPDRFVIRQT	RLLQPHLRII	LLQGDFLFFR
51	LVQSCEVEPV	LVLLHHNGKS	GNAHRKQOKE	IRFVHCRSDV	FLCYYSGIGP
101	AVRSATRKTA	LLALGLAAIS	ASPGFNALPT	IFRGSGSKSA	SLTAAQLGRG
151	SCCEYFLTNC	FTMRSSNEWK	AMTAKRPPSF	RRHMTCGNTA	PTSSSSRLIK
201	MRIAWKVRVA	GSCPRSRVRT	<u>FCATICASLR</u>	<u>VVSIGLSARC</u>	ATMARTIWRL
251	NRSSP*				

```
m239.seq
1   ATGCTCCACC ATAAAGGTmy kGCCCCGAAAC CGGCKgATGG AGGTTTGTGT
51  TTTCTGCCCG CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCTT GTTTTTTCAG
151 CTTATCCAAA CGTGTGAAAT TGAGCCTGTA CTGGTTTTGC TGCATCCGCA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTGG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCGCGCC TCGGATTGGC
351 GGCAATTTCC GCCTACCGTG GCTTTAATGC CCTGCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCCGT TCCCTGaCCG CGCCGACGCG CGGCAGGGGG
451 GCGTGTGGCG AATATTTTTT GACAAACTGC TTCACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTTGTGCCA CGATCTGCGC CAGCTTGCGG GTTGTATCGA
701 TTGGACTTTC CGCCCGTTCG GCAACAATGG CGCGCGCAAT cCGGCGGCTa
751 AACCGCTCTT cACCATAA
```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

548

m239.pep

```

1  MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
51  LIQSCEIEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIRRL
251 NRSSP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

```

              10      20      30      40      50      60
m239.pep      MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRRI LLQGDFLFFRLIQSCEIEPV
              |:||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g239           MFHHKGIARNRRMEVLFFCRRPDRFVIRQTRLLQPHLRRI LLQGDFLFFRLVQSCEVEPV
              10      20      30      40      50      60

              70      80      90      100     110     120
m239.pep      LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTA LLALGLAAIS
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g239           LVLLHHNGKSGNAHRKQOKEIRFVHCRSDVFLCYYSIGIGPAVRSATRKTA LLALGLAAIS
              70      80      90      100     110     120

              130     140     150     160     170     180
m239.pep      ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g239           ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF
              130     140     150     160     170     180

              190     200     210     220     230     240
m239.pep      RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g239           RRHMTCGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC
              190     200     210     220     230     240

              250
m239.pep      ATMARAIRRLNRSSPX
              |||||:| |||||
g239           ATMARTIWRLNRSSPX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq

```

1  ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTTGTT
51  TTTCTGCCGC CGCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTCG
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCCGCG ATTTTCAGGG
401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCG CGGCAGGGGC
451 GCGTGTTGCG AATATTTTTT GACAAACTGC TTCACAATGC GGTCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGATTG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTGTGCCA CGATCTGCGC CAGCTTGCGG GTTGTATCGA
701 TTGGACTTTC CGCCGTTGC GCAACAATGG CGCGCGCAAT CTGGCGGCTA
751 AACCGCTCTT CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
1  MLHHKGIARN  RRMEVLFFCR  RPDrfvvrQT  RLLQPHLRII  LLQGDfLFFR
51  LIQSCEVEPV  LVLLHHNGKS  GNAHRKQOKE  IQFVHCHSDV  FLCDCSGIGP
101 AVRSATRKT  LALGLAAIS  ASPGFNALPA  IFRGSGKSA  SLTAAQRGRG
151 ACCEYFLTNC  FTMRSSNEWK  AMTAKRPPSF  RRHMTCGNTA  PTSSSSRLIK
201 MRIAWKVRVA  GSCPRSRVRT  FCATICASLR  VVSIIGLSARC  ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

```

10      20      30      40      50      60
m239.pep  MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRILLQGDfLFFRLIQSCEIEPV
a239      MLHHKGIARNRRMEVLFFCRRPDRFVVRQTRLLQPHLRILLQGDfLFFRLIQSCEVEPV
10      20      30      40      50      60

70      80      90      100     110     120
m239.pep  LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS
a239      LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS
70      80      90      100     110     120

130     140     150     160     170     180
m239.pep  ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF
a239      ASPGFNALPAIFRGSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF
130     140     150     160     170     180

190     200     210     220     230     240
m239.pep  RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVISIGLSARC
a239      RRHMTCGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVISIGLSARC
190     200     210     220     230     240

250
m239.pep  ATMARAIIRRLNRSSPX
a239      ATMARAIWRLNRSSPX
250
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
1  atgatagaag tcatacat ttcggcgcc gaaacgcgca gacagtttgc
51  ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
101 gggtaaacad gggtatcatc gcgcacggga gacggtccga ttttataagg
151 ctgcgtattc agccgttcgt tcaaactcgg tttgcccgca tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac caggttcgat catatcggtt
251 acggcacggg tgcccgctg ttcgctgtct gcccgccggg gtctgttggg
301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttcg gcttttgct gatggtattc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt gccctgccgg tcccgcacaa caacttcgcg gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttctt gacctttgcc
601 gtcaatatcg gtaaatccga tgacgtgtgc aaacaggttg cccatcgggg
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
1  MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
51  LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVAPL FAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRSGFCLMVF DRLVQLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFTFLTFA
```

201 VNIGKSDDVC QVAHRVMAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

```
m240.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGCTGTCC CGGCCGGGCC TGTGTTGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 ArACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 902; ORF 240>:

```
m240.pep
1  MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFTFLTFVAV
201 NIGKSDDVCK QVAHRVMAF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

```
m240/g240

      10      20      30      40      50      59
m240.pep  MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIA -AHGRRSDFIRLRIQPFVQIG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      MIEVIHFFGAETRRQFACADVGRFLHNAAH IQRGVNMGIIAHGRRSDFIRLRIQPFVQIG
          10      20      30      40      50      60

      60      70      80      90      100     110     119
m240.pep  FARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXH
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      FARIQCLRNHERFDCRTRFDHIGYGTVAPLFAVCPAGSVGIVGGRIGQGEDFPRAGIQNH
          70      80      90      100     110     120

      120     130     140     150     160     170     179
m240.pep  HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRCFIARGVQAVHNIALPVPQNFR
          130     140     150     160     170     180

      180     190     200     210     220
m240.pep  AVFAMQAVFKRKFTFLTFVAVNIGKSDDVCKQVAHRVMAFX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      AVFAIQAVFKRKFTFLTFVAVNIGKSDDVCKQVAHRVMAF
          190     200     210     220
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

```
a240.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
```

```

251 GCACGGTTGC GCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
  1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
 51 RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH					
a240	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQNDFRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQNDFRA					
	130	140	150	160	170	180
	190	200	210	220		
m240.pep	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
  1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
 51 TTGTGCCGAC GTTGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
  1 MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS

```

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDL IGCI AHAFNR SFKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

```

m241.seq (partial)
1  ..CGGCAATCAG TGGTGGTGAT GACCGTGC GG CCGTGGACA TGACCGTGTG
51  CGATTTCTCT ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351 CCTCTTCCAC CAAAGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA TTGTTGGCAT CATACTCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

```

m241.pep (partial)
1  ..RQSVVMTVR AVDMTVCDL IGCI AHAFNR SLKADFHACQ RMVAVHHRLA
51  VGNIGYTIDD NIAGFRIVGF KHHADDFNR EHARIFD TDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

```

m241/g241
m241.pep                                10      20      30
                                RQSVVMTVR AVDMTVCDL IGCI AHAFNR
                                |||
g241      QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR TVDMTVCDL IGCI AHAFNR
                                70      80      90      100     110     120

                                40      50      60      70      80      90
m241.pep      SLKADFHACQ RMVAVHHRLA VGNIGYTIDD NIAGFRIVGF KHHADDFNR EHARIFD TDQ
                                |||
g241      SFKADFHACQ RMVAVHHRLA VGNIGYTIDD NIAGFRIVRF KHHTDLDFNR ERARIFD TDQ
                                130     140     150     160     170     180

                                100     110     120     130     140     150
m241.pep      LRILLAERIV GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
                                |||
g241      LRIMLTERIV GRKRHFDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL
                                190     200     210     220     230     240

                                160     170
m241.pep      IMQRNHGIFH DSHICPFRNS RLITGAFX
                                |||
g241      IMQRNHGIFC NSHICPFRNS RLITGAFX
                                250     260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

```

a241.seq
1  ATGCCAACAC GTCCAAC TCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCGGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCCTT TTCAGACGGC

```

553

```

251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCTCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```

a241.pep
1  MPTRPTRA AK HTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRREN FHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCD FL IGCIHTFN R SLKADFHACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDNR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241/a241 96.0% identity in 177 aa overlap

```

m241.pep                                10      20      30
                                RQSVVMTVR AVDMTVCD FLIGCIAHAFNC
                                |||:|||||:|||||:|
a241      QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVMTVR TVDMTVCD FLIGCIAHTFNR
                                70      80      90      100     110     120

                                40      50      60      70      80      90
m241.pep      SLKADFHACQ RMVAVHRLT VGNIGYTIDD NIAGFRIVGF KHHADFDNR EHARIFNTDQ
                                |||:|||||:|||||:|
a241      SLKADFHACQ RMVAVHRLT VGNIGYTIDD NIAGFRIVGF KHHADFDNR EHARIFNTDQ
                                130     140     150     160     170     180

                                100     110     120     130     140     150
m241.pep      LRILLAERIV GRKRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
                                |||:|||||:|||||:|
a241      LRILLAERIV GRKRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
                                190     200     210     220     230     240

                                160     170
m241.pep      IMQRNHGIFH DSHICPFRNS RLITGAFX
                                |||:|||||:|||||:|
a241      IMQRNHGILH DSHICPFRNS RLITGAFX
                                250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

```

g241-1.seq
1  ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTC AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGTGTTT GCTGTCTGCC CGGCCGGGCC TGTTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACACAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCTCT TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTGCCCC ATCGGGTAAT
651 GGCCTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

g241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPPSC RQSVVVMTVR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACGTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAACCCCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCCGTGGACA TGACCGTGTG CGATTTCTCT ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CCGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPPSC RQSVVVMTVR
101 AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFDQDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFC
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSETEQLFRRHQIPPPSCRQSVVVMTVRAVDMTVCDLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSETEQLFRRHQIPPPSCRQSVVVMTVRTVDMTVCDLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVVHRLAVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFDQDQ					
g241	SFKADFHACQRMVAVVHRLAVGNIGYTIDDNIAGFRIVRFKHTDLDFNRERARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIAIGILTVQRLFHQRENAVVTAVQIRNRFFGFIQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACGTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

555

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CCGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CCGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1 MPTRPTRA AK HPTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51 ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDLF IGCIATFNH SLKADFHACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRA	ANPPTPPTWLQT	AYCPRPPYRP	PSVQTRTP	PREPASSTCAAKS	ANRRENSHNA
a241	MPTRPTRA	AKHPTPPTWLQT	AYCPRPPYRP	PSVQTHTPHE	PASSTCAAKS	ANRRENFHNA
	10	20	30	40	50	60
	70	80	90	100	110	120
m241-1.pep	QPTYLLHPSN	KMPSETEQTLFRRHQIPPSQ	RQSVVMTVR	AVDMTVCDLF	IGCIAHAFNC	
a241	QPTYLLHPSN	KMPSEMEQTLFRRHQIPPSQ	RQSVVMTVR	TVDMTVCDLF	IGCIAHTFNH	
	70	80	90	100	110	120
	130	140	150	160	170	180
m241-1.pep	SLKADFHACQ	RMVAVHHRLAVGNIGYTIDD	NIAGFRIVGFKHHADFDENR	EHARIFD	T	TDQ
a241	SLKADFHACQ	RMVAVHHRLTVGNIGYTIDD	NIAGFRIVGFKHHADFDENR	EHARIFN	T	TDQ
	130	140	150	160	170	180
	190	200	210	220	230	240
m241-1.pep	LRILLAERIV	GRQRHIDRIAGILTVQRLFH	QRENAVVTAVQIRNRRFFGFV	QKLIVGIIHL		
a241	LRILLAERIV	GRKRHIDRIAGILTVQRLFH	QRENAVVTAVQIRNRRFFGFV	QKLIVGIIHL		
	190	200	210	220	230	240
	250	260				
m241-1.pep	IMQRNHGIFH	DSHICPFRNSRLITGAFX				
a241	IMQRNHGILH	DSHICPFRNSRLITGAFX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1 atgatcgggc aactgttgt tttgttcgtg atcgagcact tcaagcaacg
51 cgctggcggg atcgccccga aagtcgctgc ccaatttgc gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccg cggatttcgc
201 tttcgctcgcg cacgccgcc aaggccatac ggacataatt ccgccccgtt
251 gctttggcga tggattcgcc caaagagggt ttgccacgc ccggagggcc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttgagcgg
351 cgaggatttc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcgggc tttggcgatg tctttgctga cgcgggattt
451 tttcttccac ggcagtcgga gcagggtgtc gatgtagttg cgtacgacgg

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556

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501 tggattcggc agacatcggc ggcattcattt tgagtttttt cagttcggac
551 aggcattttt ctccgctttc tttggtcata cccgcctttt tgatgcctgc
601 ctccaaggca tccagttcgc cgttttcgtc ttcttcgccc aattctttgt
651 gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc
701 atttggcgtt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgtc
751 gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801 cgggaatctc caaaatctgt tggcgttgcg ccagtttcaa ctgcaaattgc
851 gctgcgaccg tatcggttag

```

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

```

g242.pep
1 MIGELVVLFV IEHFKQRAGG IAPKVAAQFV DFVEQEQRVS YACFCHILQN
51 LAGHRADIGT AVPADFAFVA HAAQGHDTIF PPRCFGDGFA QRGFAHARRA
101 DQTQNRTEFEL VHTFLDGEVF QNPFFDFFQA VVVGIQHQSG FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRRHHEFF QFGQAFFFRF FGHTRLFDAC
201 LQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQQE FHPFADFGNL QNLLALRQFQ LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

```

m242.seq
1 ATGATCGGCA AACTTGTGT TTTGTTCTGGG ATCGAGCACT TCGAGCAACG
51 CGCTGGCGGG ATCGCCTCGG AAGTCGTTAC CCAATTGTGC GATTTCGTCTG
101 AGCAGGAACA AGGGGTTTTT CACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATAGAGCCGA TATAGGTGCG GCGGTGTCCC CTGATTTCGC
201 TTTCGTCTCG CACGCCGCC AAAGCCATGC GGACATATT CCGCCCCGT
251 GCTTTGGCGA TGGATTCGCC CAAAGAGGTT TTGCCACGC CCGGAGGCC
301 GACCAGGCAC AGAATCGGGC CTTTGAGTTT GTCCATACGT TTTTGGACGG
351 CGAGGTATTC CAAAATCCGT TCTTTGACTT TTTCCAGGCC GTAGTGGTCG
401 GCATCCAGCA CCAGTCCGGC TTTGGCGATG TCTTTGCTGA CGCGGGATTT
451 TTTCTTCCAC GGCAGCTCGA GCAAAGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTCCGC AGACATCGGT GGCATCATTT TGAGCTTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCGCTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTTCTTTGT
651 GTATCGCTTT AATCTGTTCG TTCAGATAAT ATTCGCGCTG GGATTTTTC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATTT
801 CGGGAATTTT CAAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

```

m242.pep
1 MIGKLVVLFV IEHFEQRAGG IASEVVTQFV DFVEQEQQVF HAGFCHILQN
51 LTGHRADIGA AVSPDFAFVA HAAQSHADIF PPRCFGDGFA QRGFAHARRA
101 DQAQNRAFEV VHTFLDGEVF QNPFFDFFQA VVVGIQHQSG FGDVFADAGF
151 FLPRQLEQSV DVVAYDGGFR RHRWHHELF QFGQAFFFRF FGHTRLFDIC
201 FQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQQE FHPFADFGNF QNLLALRQFQ LQMRCDRIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

```

m242/g24290.3% identity in 289 aa overlap
      10      20      30      40      50      60
m242.pep  MIGKLVVLFVIEHFEQRAGGIASEVVTQFVDFVEQEQQVFHAGFCHILQNLGHRADIGA
          |||:||||| |||:||||| :||:||||| |||: ||| |||||:|||||:
g242      MIGELVVLFVIEHFKQRAGGIAPKVAAQFVDFVEQEQRVSYACFCHILQNLGHRADIGT
          10      20      30      40      50      60

      70      80      90     100     110     120
m242.pep  AVSPDFAFVAHAAQSHADIFPPRCFGDGFAQRGFAHARRADQAQNRAFEVHTFLDGEVF
          || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g242      AVPADFAFVAHAAQGHDTIFPPRCFGDGFAQRGFAHARRADQTQNRTEFELVHTFLDGEVF
          70      80      90     100     110     120

```

a242.seq

1	ATGATCGGCG	AACTTGTGT	TTTGCTCGGG	ATCAAGCACT	TCGAGCAACG
51	CGCTGGCGGG	ATCGCCCCG	AAGTGCTAN	CCAATTGTG	GATTTCGTG
101	AGCAGGAACA	ATGGGTTTT	TACGCGGCT	TTTGCCATAT	CTGCAAAAT
151	CTTACCGGGC	ATGGAGCCGA	TATAGGTGCG	CGGTGTCCC	TGGTATTCGC
201	TTTCGTGCG	CACGCCGCC	AAAGCCATGC	GGACATATTT	CCGCCCCGTT
251	GCTTTGGCGA	TGGATTCGCC	CAAAGAGGTT	TTGCCACGC	CTGGAGGGCC
301	GACCAGGCAC	AGAATCGGG	CTTTGAGTT	GTCCATACGT	TTTTGGACGG
351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTTCCAGCGT	GTAGTGGTCG
401	GTATCCGACA	CCAATCCGGC	TTTGGCGATG	TCTTTGCTGA	CGCGGGATTT
451	TTTCTTCCAC	GGCAGTTCGA	GCAGGGTGTC	GATGTAAGTTG	CGTACGACGG
501	TGGATTCGGC	AGACATCGGC	GGCATCATTT	TGAGCTTTTT	CAGTTCGGAG
551	AGGCATTTTT	CTTCCGCTTC	TTTGGTCATA	CCCGCTTTTT	TGATATCTGC
601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTCGTC	TTCTTCGCCC	AGTCTTTGT
651	GTATCGCTTT	AATCTGTTCG	TTCAGATAAT	ATTTCGCGCTG	GGATTTTTCC
701	ATTTGGCGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
751	GAGTTCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATTT
801	CGGGAATTC	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAAATGC
851	GCTGCGACCG	TATCGGTTAG			

a242.pep

1	MIGELVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHAWRA
101	DQAQNRAFEF	VHTFLDGEVF	QNPFFDFQFA	VVVGTHQHSQ	FGDVADAGF
151	FLPRQFEQGV	DVVAYDGGGF	RHRRHVHFEL	QFGQAFFFRF	FGHTRLFDIC
201	FQGIQFAVVF	FFAQFVFYRF	NLFVQIIFAL	GGFHLAFDAS	AYAFFGLHNV
251	EFGFQLCOQE	FHPFADGNGF	QNLLALRFQF	LQMRCDRIG*	

	10	20	30	40	50	60
m242.pep	MIGKLVVLF	GLGIEHFE	QRAGGIAS	EVVTVQFV	DFVEQEQQ	GVFHFAGF
a242	MIGELVVLL	GLGIKHFE	QRAGGIAP	EVAXQFVD	DFVEQEQQ	VVVFYAGF
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAF	VAHAAQSH	ADIFPPRC	FGDGFAQR	GFHARRAD	QAQNRAFE
a242	AVSPDFAF	VAHAAQSH	ADIFPPRC	FGDGFAQR	GFHAWRAD	QAQNRAFE
	70	80	90	100	110	120
	130	140	150	160	170	180
m242.pep	QNPFFDF	FQAVVVG	IQHQSGF	GDVFADAG	FFLPRQLE	QSVDVVAY
	130	140	150	160	170	180

558

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a242      QNPFDFDFQAVVVGIQHQSGFGDVFADAGFFLPRQFEQGVVDVAYDGGFGRHRRHHFELF
           130      140      150      160      170      180
           190      200      210      220      230      240
m242.pep  QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNFVQIIIFALGFFHLAFDAS
           |||||
a242      QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNFVQIIIFALGFFHLAFDAS
           190      200      210      220      230      240
           250      260      270      280      290
m242.pep  AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNQNLALRQFQLQMRCDRIGX
           |||||
a242      AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNQNLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGcC cgAGTTaccg CCGATGCCCG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTTGTTC
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCCG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCCACACG GGGGCGAAyA GGTCTTCCTC
201 TTCTGCAAA CCCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTTC
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

```

m243/g243
           10      20      30      40      50      60
m243.pep  MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||
g243      MVIVWLPELPPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60
           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTTGTTC
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMPL SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSEFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMPLSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAAATIFSMPLSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX					
	: :					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSEFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcctg aagcccgcc gccgggttca gacggcattg ccgctttact
51  tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggag
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga tttgcgtggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcacgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acatttcac ggcaaaactc tgtccggcga acttggtgct
451 atcggaatt tctgctggt ggcggcgccg caggttttgc tcgtttgcc
501 aagcgcgcag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacggtttc caccgcctcc acattttcaa
651 ccgcttcttc actggtttgc tgctgtgctt gttcgctcat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgcc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LPCHRNHSRA
51  QHTVGQGITL LHHTNHGIGF LLTGHRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFORIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFLRFQL GNPRQLILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSGYYPISKIR
251 TFSRNFQORQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq

560

```

1  ATGCCGTCCTG AAGCCCGACA GGCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCTT CTTCATCACA CCCACCACGG
201 TATTCGGCTC CTGTTCGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACCTT TGTCGGCGCA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GGCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTTCT GCACACCGTC
601 CGCATTTTCT ACTGTTTTCG CGGTTTCCAC CGCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGACA
751 TTTTCAAGAA ACTTCAAKCA AAKCAGAGA ATTTCAAATT CATTTTCAAA
801 TCCCCTACCG AAAAAATAAT ATAGACGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 932; ORF 244>:

```

m244 . pep
1  MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPRLQILISR LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLLCLFAHI VSLKTNWKS SSYYPRKIRT
251 FSRNFXQXQR ISNSFSNPLP KKXYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

	10	20	30	40	50	60
m244 . pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLPCHRNHSRAQHTVGGQITL					
	10	20	30	40	50	60
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244 . pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVQLRFQL					
	130	140	150	160	170	180
m244 . pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVQLRFQL					
	130	140	150	160	170	180
m244 . pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244 . pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244 . pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
g244	KSGYYPKIRTFSRNFKQRQEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1   ATGCCGTCTG AAGCCCGACA GGCgggttca GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTTCATCAGC CCCACCACGG
201 TATTGGGTTC CTGTTCGCTT GCCACGCCTT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCCCTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCGGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GGCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTGC TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAAAACAAA TTGGAAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1   MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQH FH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFQLVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244.pep	IAALIQKRHFQIILDRQHFGKLLSGELVRIRNFLLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFGKLLSGELVRIRNFLLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	240	250	260	270		
m244.pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1   atgccgcctg aagcccgcc gccgggttca gacggcattg ccgctttact
```

562

```

51  tcgatcggtt  tatacgcaaa  acgcgcttca  ggaaataaat  cagattattc
101 cccagacgcc  ttcaggcttc  cttccgtgcc  accgtaacca  tagccgggcg
151 caacacacgg  tcggacaggg  tataaccctt  cttcatcaca  ccaaccacgg
201 tattgggttc  ctgctcactg  gccaccgect  gcategcctg  atggatattc
251 ggatcgagct  ttcgcccgc  tttaggattg  atttccttga  ttgctggtgc
301 atcaaacgcc  tttcgcaact  cattcaaagt  catctgcaca  cccattttca
351 gcgcatcgaa  attaccgctc  tgatccaaaa  gcgccatttc  cagataatcc
401 ttgaccggca  acatttccac  ggcaaaactc  tgtccggcga  acttgtgcgt
451 atcggcaatt  tcctgctggt  ggcgcgcgcg  caggttttgc  tcgtttgcc
501 aagcgcgcag  ttgttcgtct  ttcaactgcg  cttccagctc  ggcaatccgc
551 gcctgcaaat  cctcataagc  cggctcggcg  gcagcctgtt  cctgtacacc
601 gtccgcattt  cctactgtct  cgacgggttc  caccgctcc  acattttcaa
651 ccgcttcttc  actgttttgc  tgctgtgtct  gttcgtcat  atcgatcccc
701 tcaaaacaaa  ttggaaatca  aaatccggtt  attaccggag  caagataagg
751 acattttcaa  gaaacttcaa  gcaaaggcag  gaaatttcac  atccgcccgc
801 gaatacccta  ccgcaaaaac  catataaacg  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pep

```

1  MPPEARPAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LPCHRNHSRA
51  QHTVGGQITL  LHHTHHGIGF  LLTGHLRL  MDIRIELIAR  FRIDFLDLRG
101 IKRLLQLIQS  HLHTHFQRIE  ITALIQKRHF  QIILDRQHFH  GKLLSGELVR
151 IGNFLLVAAA  QVLLVCQSAQ  LFFVQLRFQL  GNPRQLILIS  RLGGSLFLYT
201 VRISYCLDGF  HRLHIFNRFF  TVLLCLFAH  IVSLKTNWKS  KSGYPSKIR
251 TFSRNFQKQ  EISHPPPNTL  PQPKYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

m244-1.seq

```

1  ATGCCGTCTG  AAGCCCGACA  GCGGGTTC  GACGGCATTG  CCGCTTTACT
51  TCATCGGTT  TATACGCAAA  ACGCGCTTCA  GGAAATAAAT  CAGATTATTC
101 CCCAGACGCC  TTCAGGCTTC  CTTCTGCGCC  ACCGTAACCA  TAGCCGGGCG
151 CAACACGCGG  TCGGACAGCG  TATAACCCTT  CTTATCACA  CCCACCACGG
201 TATTCGGCTC  CTGTTCGCTT  GCCACGCCT  GCATCGCCTG  ATGGATATTC
251 GGATCGAGCT  TATCGCCCGC  TTTAGGGTTG  ATTTCCCTGA  TTTGCGTAGC
301 ATCAATGCT  TTCTGCAACT  CGTTCAAAGT  CATCTGCACG  CCCATTTTCA
351 CCGCATCGAA  ATTGCGGCTC  TGATCCAAAA  GCGCCATTTC  CAGATAATCC
401 TTGACCGGCA  GCATTTCAC  GGCAAACCTC  TGTCCGGCGA  ACTTGTGCGT
451 ATCCGCAATT  TyCTGCTGGT  GGCGCGGCG  CAGGTTTTGC  TCGTTTGCCA
501 AAGCGCGCTG  CTCGTCTTTC  AACTGCGTTT  CCAGCTCGGC  AATCCGCGCC
551 TGCAATCCCT  CATAAGCCGG  CTCTGCGGCA  GCCTGTTCT  GCACACCGTC
601 CGCATTTCTT  ACTGTTTCGA  CGGTTTCCAC  GCCTCCACA  TTTTCAACCG
651 CTTCTTCACT  GTTTTGCTGC  TGTGCTGTT  CGCTCATATC  GTATCCCTTA
701 AAACAAATTG  GAAATCAAAA  TCCAGTTATT  ACCCGCGCAA  GATAAGGACA
751 TTTTCAAGAA  ACTTCAAKCA  AAKCAGAGA  ATTTCAAATT  CATTTTCAAA
801 TCCCTACCG  AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pep

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LLRHRNHSRA
51  QHAVGQRITL  LHHTHHGIRL  LFACHRLHRL  MDIRIELIAR  FRVDFDLRS
101 IKCFLQLVQS  HLHAHFQRIE  IAALIQKRHF  QIILDRQHFH  GKLLSGELVR
151 IRNFLLVAAA  QVLLVCQSAL  LVFQLRFQLG  NPRLQILIS  LCGSLFLHTV
201 RISYCFDGFH  RLHIFNRFFT  VLLCLFAHI  VSLKTNWKS  SSYYPKIR
251 FSRNFXQQR  ISNSFSNPLP  KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLPCHRNHSRAQHTVGGQITL					
	10	20	30	40	50	60
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
g244-1	LHHTHHGIGFLLTGHLRLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120

	130	140	150	160	170	180
m244-1.pep	IAALIQRHFQIILDRQHFHGKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFQL					
g244-1	ITALIQRHFQIILDRQHFHGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVFQLRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTLLCLFAHIVSLKTNWKS					
g244-1	GNPRLQILISRLGGSFLFLHTVRISYCLDGFHRLHIFNRFFTLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKKX					
g244-1	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```

1   ATGCCGCTCTG AAGCCCCGACA GGCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCTT CTTCATCAGC CCCACCACGG
201 TATTGGGTTT CTGTTTCGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTAGGATTG ATTCCTTGA TTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACTTC TGTCGGCGCA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GGCGGCGGCG CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TCAACTGCG CTTCACGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CTAAGTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAACAACAA TTGGAAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

```

1   MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTSPGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFKQRQ RISNSFSNPL PKK*

```

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTSPGFLLRHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTSPGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQRHFQIILDRQHFHGKLLSGELVRIRNFLLVAAAQVLLVCQSA-LLVFQLRFQL					
a244-1	IAALIQRHFQIILDRQHFHGKLLSGELVRIRNFLLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	230
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTLLCLFAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240


```
g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgccct tcgttttcga
51  ccagacacag cgtgcccggt tcggcaacgg cgaagtttac gccgctcaag
101 ccgacatcgg cagtgcctga aatatcgcgc agggctttgc gggcgaaatcc
151 ggtcagttgg tccacgtcgt ctgtaagcgg tgtgccgagg ttttggctgga
201 acagttcgct gacctgtctt ttggttttat ggattgcggg catcacgtata
251 tgggtcgggt tttcgcctgc catttggacg ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataatggttc agctcgattt
351 cttcgctgac catggatttg cctttgacca tcagcttgcc gtttttggct
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgccca
451 gtgtactttc acgcccact tagtcagggt ttcttccaac tgctccagca
501 qcqcaggtaa
```

g246.pep

1	<u>MYGRNGSTQA</u>	<u>AVAFVFDQTO</u>	<u>RARFGNGEVY</u>	<u>AAQADIGSAV</u>	NIAQGFAGES
51	GQLVHVVCKR	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFFAC	HLDDKLAQVA
101	FHRLNAFCFK	IMVQLDFFAD	HGFAFDHQLA	VFGCDDVVND	LAGFGRGRFP
151	VYFHAOLSOV	FFOLLOORG*			

```
m246.seq (partial)
  1  ATGCACGGGC GGTACGGTGG TACTCAAGCG ACCGTTgCTT CGTTTTCCAC
 51  CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCACTCAAAC
101  CGACATCGGC AGTGCTGTAA ATATCGCGCA GTGCTTTACG GGCGAAGCCG
151  GTCAGTTGGT CTACATCGTC TGTCAGCGGC GTACCGAGGT TTTGGTGGAA
201  CAGTTCGCTA ACCTGTTCTT TGGTTTTGTG GATAGCAGGC ATCACGATAT
251  GGGTCGGTTT TTCGCCTGCC ATTTGGACGA TGAACTCGCC CAAGTCGCTT
301  TCTACCGCTT TAATGcYttT TGCTTCAAGA TAATGrTTCA GCTCGATTTC
351  CTCGCTGACC ATCGAATTGC CTTTGACCAT CAGCTTGCCG TTTTGTGGCTG
401  TGATGATGTC GTGGATAATT TGGCAGGCTT CGGTGCGGGT TTCTGCCCG
```

m246.pep (partial)

1	MHGRYGGTQA	TVAFVFHQQT	RTCFSNGKVY	ATQTDIGSAV	NIAQCFTGEA
51	GQLVYIVCQR	RTEVLVEQFA	NLFFGFVDSR	HHDMDGRFFAC	HLDDDELAQVA
101	FYRENAFCFK	IMXOLDFLAD	HRFAEDHOLA	VFGCDVVVDN	LAGEGRGFCR...

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

m246/g246

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVFHQTRTCFSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
	: : : : : : : : :					
g246	MYGRNGSTQA AVAFVFDQTRARFGNGEVYAAQADIGSAVNIAQG FAGESGQLVHVVCCKR					
	10	20	30	40	50	60
m246 . pep	RTEVLVEQFANLFFGFVD SRHHDMGRFFACHLDDELAQVAFYRFNAFCFKIMXQLD FLAD					
	: : : : : : :					
g246	CAEVLVEQFADLFFGFMD CGHHDMGRFFACHLDDKLAQVAFHRLN AFCFKIMVQLD FFAD					
	70	80	90	100	110	120

565

	70	80	90	100	110	120
	130	140	150			
m246 . pep	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246 . seq (partial)

1	ATGCACGGGC	GGAACGGTGG	TACTCAAGCG	ACCGTTGCCT	TCGTTTCCA
51	CCAGACACAG	CGTACCTGTT	TCAGCAACGG	CGAAGTTCAC	GCCACTCAAA
101	CCGACATCGG	CAGTGCTGTA	AATATCGCGC	AGTGCTTTAC	GGGCGAAGCC
151	GGTCAGTTGG	TCTACGTCGT	CCGTTAACGG	TGTGCCGAGG	TTTGGTGGA
201	ACAGTTCGCT	AACCTGTTCT	TTGGTTTTAT	GGATTGCGGG	CATCACGATA
251	TGGGTCGGTT	TTTCACCTGC	CATTGGACG	ATGAACTCGC	CCAAAGTCGCT
301	TTCCACCGCT	TTAATGCCTT	TTGCTTCAAG	ATAATGGTTC	AGCTCGATTT
351	CCTCGCTGAC	CATCGATTTC	CCTTTGACCA	TCAGCTTGCC	GTTTTGGCT
401	GTGATGATGT	CGTGGATGAT	TTGCGAGGCT	TCGGCCGGTG	TTTCCGCCCA
451	GTGTACTTTT	ACGCCCAACT	TGGTCAGGTT	TTCTTCCAGC	TGCTCCAGCA
501	G				

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246 . pep (partial)

1	MHGRNGGTQA	TVAFVFHQTO	RTCFNNGEVH	ATQTDIGSAV	NIAQCFTGEA
51	GQLVYVVR*R	CAEVLVEQFA	NLFFGFMDCG	HHDMGRFFTC	HLDDELAQVA
101	FHRFNAFCFK	IMVQLDFLAD	HRFAFDHQLA	VFGCDDVVDD	FAGFGRCFRP
151	VYFYAQLGQV	FFQLLQQ			

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVFHQRTQRTCFNNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQRTQRTCFNNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246 . pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFTCCHLDDELAQVAFHRFNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246 . pep	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
a246	HRFAFDHQLAVFGCDDVVDVDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247 . seq

1	atgaaacgta	aaatgctaaa	cgtaccaaag	ggcggttatg	atggtatgaa
51	gggttttacc	attgttgaat	ttctggttgc	gggcctgctc	agtataattg
101	tcctgatagc	ggctgatcgc	agttacttta	catcccggaa	attaaatgat
151	gtggcaaacg	agcgtcttgc	cattcaacag	gatttgcgga	atgcggcaac
201	attaattgtc	cgcatgcaa	gaatggcggg	gagcttcggt	tgtttcaata
251	tgcccgagca	tactaaagac	gatattgttg	attcaagtaa	tcaaactcaa
301	tctaaccctg	caaaaaccgg	tgccaaacaa	gaaaatcccc	ttttttcctt
351	aaaaaggagc	ggcatggata	aacaactgat	tcccgttgct	gaatccatag
401	atattaaata	tccgggtttt	atccagcgcc	ttaacgcatt	ggttttccaa
451	tacggtatcg	atgatcttga	tgcgagtgc	gagactgttg	tagtcagcag
501	ctgttccaaa	atagcaaaac	cgggtaagaa	aatatctacc	ttgcaagaag
551	caaagagtgc	attacagatt	actaatgatg	ataaacaaaa	tggaaatc

566

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601 acccgctcaga aacatgtggt caatgcctat gcggtcggca ggtttggcaa
651 taatgaggaa agtttggtcc gcttccaatt ggatgataag ggcaagtggg
701 gtaatcctca gttgctcgtg aaaaagggtta aacgtatgga tgtgcggtat
751 atttatgttt ccggttggtcc tgaagatgaa gatgccggca aagaggaaaa
801 attcagatat acgaataaat tcgacaaatc caaaaatgct gttacgcctg
851 ccgggggtgga ggtttttattg gatagcggcc ttaatgccaa gattgccgct
901 tcttcagaca atagtattta tgcttaccgt atcaatgcga caatacgcgg
951 gggaaatgta tgcgcaaaca gaacactttg a

```

This corresponds to the amino acid sequence <SEQ ID 948; ORF 247.ng>:

g247.pep

```

1 MKRKMLNVPK GGYDGMKGFT IVEFLVAGLL SIIVLIAVVS SYFTSRKLND
51 VANERLAIQQ DLRNAATLIV RDARMAGSFG CFNMSEHTKD DIVDSSNQTO
101 SNLAKPGAKQ ENPLFSLKRS GMDKQLIPVA ESIDIKYPGF IQRLNALVFQ
151 YGIDDLNASA ETVVVSCK IAKPGKKIST LQEAKSALQI TNDDKQNGNI
201 TRQKHVVNAY AVGRFGNNEE SLFRFQLDDK GKWGNPQLLV KVKRMDVRY
251 IYVSGCPEDE DAGKEEFKRY TNKFDKSKNA VTPAGVEVLL DSGLNAKIAA
301 SSDNSIYAYR INATIRGGNV CANRTL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

m247.seq (partial)

```

1 ATsAGACGTA AAATGCTAAA CGTwsyArAA GGCAGTTATG ATGGTATGAA
51 AGGTTTTTACC ATTATTGAAT TTTTGGTTGC GGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCCGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAAACG AGCGTCTTGC CGCGCAACAG GATTTCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTCATAA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTACGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AAGTTGTTC CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGC...

```

This corresponds to the amino acid sequence <SEQ ID 950; ORF 247>:

m247.pep (partial)

```

1 XRRKMLNVXX GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPDQTQNN
101 SPFSLKRNGI DKLIPIAESS NINYQNFFQV GSALIFQYGI DDVNSTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEESLF RFQLDDKQKW GNPQL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/g247

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTIIEFLVAGLLSMIVLMAVGSSYFTSRKLND	AANERLAAQQ				
	: : : :	: : : :	: : : :	: : : :	: : : :	: : : :
g247	MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIAVSSYFTSRKLNDVANERLAIQQ					
	10	20	30	40	50	60
	70	80	90	100		
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI	-----	PDTTQQNSPFSLKR			
	: : : : : : : : : : : :	: : : :	: : : :	: : : :	: : : :	: : : :
g247	DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAKPGAKQENPLFSLKRS					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	GIDK-LIPIAESSNINYQNFFQVGSALIFQYGIDVNSTATTVVSSCAAISKPGKQIPT					
	: :	: : : :	: :	: :	: : : :	: : : :

g247 GMDKQLIPVAESIDIKYPGFIQRLNALVFQYGIDDLDAEAEVTVSSCSKIAPGKKIST
130 140 150 160 170 180

m247.ppep 170 180 190 200 210 220
LEDAKKELKIPDQDK EQNGNIARQRHVVNAYAVGRIAD-EESLFRFQLDDKGKWGNPQL
|::||: |:| ::|| |||||:|:||||| |:: ||||| |

g247 LQEAKSALQITNDDK-QNGNITRQKHVVNAYAVGRFGNN EESLFRFQLDDKGKWGNPQLL
190 200 210 220 230

g247 VKVKVRMDVRYIYVSGCPEDEDAGKEEFRTYNKFDSKNAVTTPAGVEVL DSGLNAKIA
240 250 260 270 280 290

```
a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCTC  AGTATGATTG
101 TCCTGATGGC  GTTCGGATCG  AGTTACTTCA  CATCCCGGAA  ATTAATGATG
151 GCGGCAAAACG  AGCGTCTTTC  CGCGCAACAG  GATTTGCGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  TGTTTCAATA
251 TGTCCGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAACT
301 CAACATGTCC  CTGTAAAACC  CGGTGCCAAA  CAAGAAAATC  CCCTTTTTTC
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCCTATTGC  TGAATCCACA  GATATTAAAT  ATCCGGGTTT  TGCCAGGCT
451 CGTCCGGCAT  TGATTTTCCA  ATACGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGACTGTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAAGAGTG  CATTACAGAT  TACTAATGAT
601 GATAAACAAA  ATGGAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TGCGGTCCGC  AGGATTGCCG  GTGAGGAAGG  TTTGTTCCGC  TTCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCCTCAGT  TGCTCGTGAA  AAAGATTAGA
751 CATATGAAAG  TGCGGTATAT  CTATGTTTCC  GACTGTCCTG  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAAAATAG  GGGTACATTG  GACAGCTCCA
851 CAAATGCTGT  TACGCCGCC  GGGGTGAGG  TTTTATTGAC  TANCGGTACT
901 GATACCAAGA  TTGCCGCTTC  TTCAGACAAT  CATATTTATG  CTTACCGTAT
951 CGATGCGACA  ATACGCGGGG  GAAATGTATG  CGCAAACAGA  ACACTTTGA
```

a247.pep

1	<u>MRRKMLNVPK</u>	<u>GNYDGMKGFT</u>	<u>IIeFLVAGML</u>	<u>SMIVLMAVGS</u>	<u>SYFTSRKLND</u>
51	<u>AAANERLSAQQ</u>	<u>DLRNAATLIV</u>	<u>RDARMAGGFG</u>	<u>CFNMSEHTKN</u>	<u>DIIVDPSKQT</u>
101	<u>QHVPVKEGAK</u>	<u>QENPLFSLEW</u>	<u>ANTNNTNNNT</u>	<u>AKLIPIAEST</u>	<u>DIKYPGFAQA</u>
151	<u>RPALIFQYGI</u>	<u>DDLDAEAETV</u>	<u>VVSSCSKIAK</u>	<u>PGKKISTLQE</u>	<u>AKSALQITND</u>
201	<u>DKQNGNITRQ</u>	<u>RHVVNAYAVG</u>	<u>RIAGEEGLFR</u>	<u>FQLDDKGKWG</u>	<u>NPQLLVKKIR</u>
251	<u>HMKVRYIYVS</u>	<u>DCPEDDDAGK</u>	<u>EEKFKYTGTG</u>	<u>DSSTNAVTPA</u>	<u>GVEVLLSXGT</u>
301	<u>DTKIAASDN</u>	<u>HIYAYRIDAT</u>	<u>IRGGNVCANR</u>	<u>TL*</u>	

```

                                10          20          30          40          50          60
m247.pep  XXXRMLNVXXGSYDGMKGFTIIIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAANERLAAQQ
           ||||| 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a247       MRRKMLNVPKGNVDGMKGFTIIIEFLVAGMLSMIVLMAVGSSYFTSRKLNDAANERLSAQQ
                                10          20          30          40          50          60

                                70          80          90          100
m247.pep  DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFSLK-
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a247       DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTQHVPVKPGAKQENPLFSLEW
                                70          80          90          100          110          120

                                110         120         130         140         150         160
m247.pep  -----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISK
           1: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a247       ANTNTNTNNATAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDASETVVVSSCSKIAK
                                130         140         150         160         170         180

```

		170	180	190	200	210	220
m247.pep		PGKQIPTLED	AKKELKIP	DQDKEQNG	NIARQRHV	VNAYAVGRI	AD EESLFR
			::	: :	:		:
a247		PGKKISTL	QEAKSALQ	ITNDDK-Q	NGNITRQR	HVVNAYAV	GRIAGEEGL
				190	200	210	220
						230	
m247.pep		GNPQL					
a247		GNPQLLV	KKIRHMK	VRYIYV	SDCPEDDD	AGKEEFK	YTGTFDS
		240	250	260	270	280	290
							SSTNAVTP
							PAGVEVLL
							SXG

```

g247-1.seq (partial) ..
1 CCCGGTGCCA AACAAAGAAA TCCCCTTTTT TCCTTAAAAA GGAGCGGCAT
51  GGATAAACAAT CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATCGGA GTGCTGAGAC TGTTGTAGTC AGCAGCTGTT CCAAAATAGC
201 AAAACCGCGT AAGAAATAT TACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATCGGTT CGGCAGGTTT GGCAATAATG AGGAAAGTTC
351 GTTCCGCTTC CAATTGGATG ATAAGGGCAA GTGGGGTAAT CCTCAGTTGC
401 TCGTGAAAAA GGTAAACGT ATGGATGTC GGTATATTTA TGTTCCGGT
451 TGTCTGAAG ATGAAGATGC CGGCAAAAG GAAAAATCCA GATATACGAA
501 TAAATTCGAC AAATCCAAAA ATGCTGTTAC TCGTCCGGG GTGGAGTTG
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGTCTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TGCGACAATA CGCGGGGGAA ATGATGCGC
651 AAACAGAAC CTTTGA

```

g247-1.pep (partial) ..

1	PGAKQENPLF	SLKRSQMDKQ	LIPVAESIDI	KYPGFIQRLN	ALVFQYQIDD
51	LDASAEITVV	SSCSKIATPG	KKISTLQEAK	SALQITNDDK	QNGNITRQKH
101	VVNAYAVGRF	GNNEESLFRF	QLDDKGKWN	PQLLVKKVKR	MDVRYIYVSG
151	CEPEDAGKE	EKFYRITNKF	KSKNVATPG	VEVLDDSLGN	AKIAASSDNS
201	IYAYRINATI	RGGNVCANRT	L*		

```
m247-1.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAGTTATG  ATGGTATGAA
51  AGGTTTTACC  ATTATTGAAT  TTTTGCTTGC  GGGCCTGCCT  AGTATGATTG
101 TCTGTATGCG  GGTCGGATCG  AGTTACTTCA  CATCCCGGAA  ATTAATATGAT
151 GCGGCAACAG  AGCGTCTTGC  CGCGCAACAG  GATTTCGGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATCGCA  GAATGGCAGG  CGGCTTCGGT  TGTTTCAATA
251 TGTCGAGCA  TCCTGCAACT  GATGTTATT  CCGATACGAC  GCAACAAAAT
301 TCTCCTTTT  CCTTAAAAAG  GAACGGTATA  GATAAACTTA  TTCCCATAGC
351 GGAATCTTCA  AATATCAATT  ATCAGAAATT  TTCCAGGTT  GGTAGCGCAT
401 TGATTTTTCA  ATACGGAATC  GATGATGTTA  ATGCAAGCAC  CGCGCATACC
451 GTCGTCAGCA  GCTGTGCCGC  AATATCGAAA  CCGGGCAAGC  AAATCCCTAC
501 TTTAGAAGAT  GCAAAAAAAG  AATTGAAGAT  TCCGGATCAG  GATAAGGAGC
551 AAAATGGCAA  TATAGCCGAT  CAAAGGCAT  TGGTCAATGC  CTATCGCGTG
601 CGCAGGATTG  CCGATGAGGA  AGGTTTGTT  CGCTTCCAAT  TGGATGATAA
651 GGGCAAGTGG  GGTAACTCTC  AGTTGCTCGT  GAAAAGAGTT  AGACATATGA
701 AAGTGCGGTA  TATCTATGTT  TCCGGCTGTC  CTAAAGATGA  CGATGCCGGC
751 AAGAGAGAAA  CATTCAATAA  TACGGATAAA  TTCCGACAGC  CCGAAAATGC
801 TGTTACGCCC  GCCGGGTGAG  AGGTTTATTT  GAGTAGCGGT  ACTGATACCA
851 AGATTGCCGC  TTCTTCAGAC  AATCATATTT  ATGCTTACCG  TATCGATGCG
901 ACAATACGCG  GGGGAATATG  ATGCGCAAA  AGAACACTTT  GA
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```
m247-1.ppep
1  MRKMLNVPK  GSYDGMKGFT  IIEFLVAGLL  SMIVLMAVGS  SYFTRSKLND
51  AANERLAAQO  DLRNAATLIV  RDARMAGGFG  CFNMSEHPAT  DVPIDTTQON
101 SPFSLKRNGI  DKLPIAESS  NINYQNFFQV  GSALIFYQGI  DDVNASTATT
151 VSSCAAISK  PGKQIPTLED  AKKELKIPDQ  DKEQNGNIAR  QRHVVNAYAV
201 GRIADDEGLF  RQLQDDKGKW  GNPQLLVKKV  RHMKVRYIYV  SGCPEDDDAG
251 KEETFKYTDK  FDSAQNAVTP  AGVEVLLSSG  TDTKIAASSD  NHIYAYRIDA
301 TIRGGNVCAN  RTL*
```

	70	80	90	100	110	120
m247-1.pep	NAATLIVRDARMAGGFGCFNMSEHPATDVI	PDTTQQNSPFLSRNGIDK-LIPIAESSNI	: :	:	:	:
g247-1				PGAKQENPLFSLKRSGMDKQLIPVAESIDI		
				10	20	30
	130	140	150	160	170	180
m247-1.pep	NYQNFFQVGSALIFQYIGIDDVNASTATTVVSSCAAI	SKPGKIPTLED	DAKKELKIPDQDK			
g247-1	: : :	: : : :	: : : : :	: : : : : :	: : :	: :
	KYPGFQIRLNALVFQYGIDDL	DAEAETVVVSSCKIAKPGKKISTLQEAKSALQITNDDK				
	40	50	60	70	80	90
	190	200	210	220	230	240
m247-1.pep	EQNGNIARQRHVVNAYAVGRIAD-EEGLFRFQLDDKGKWGNPQLLVKKVRHMKVRYIIYS					
g247-1	: : : : : : : : : : : : : :					
	-QNGNITRQKHVVVNAYAVGRFGNNEESLFRFQLDDKGKWGNPQLLVKKVRHMDRVRIIYS					
	100	110	120	130	140	
	250	260	270	280	290	300
m247-1.pep	GCPEDDDAGKEETFKYTDKFDSAQNAVTPAGVEVL	LSSGTDTKIAASSDNHIYAYRIDAT				
g247-1	: : : : : : : : : : : : : :					
	GCPEDDEDAGKEEFRTYNKFKDSKNVTPAGVEVL	DLSGLNAKIAASSDNSIYAYRINAT				
	150	160	170	180	190	200
	310					
m247-1.pep	IRGGNVCANRTLX					
g247-1						
	IRGGNVCANRTLX					
	210	220				

a247-1.seq (partial)

1	ATAATACAG	CTAATTGAT	TCCTATTGCT	GAATCCACAG	ATATTAAATA
51	TCGCGGGTTT	GCCAGGCTC	GTCGCGATT	GATTTTCCAA	TACGGCATCG
101	ATGACTTTGA	TGCCAGTGCT	GAGCTGCTTG	TAGTCACAGC	CTGTTCCAAA
151	ATAGCAAAAC	CGGGTAAGAA	AATATCTACC	TTGCAAGAAG	CAAAGAGTGC
201	ATTACAGATT	ACTAATGATG	ATAAAACAAA	TGAAAATATC	ACCCGTCAAA
251	GGCATGTGGT	CAATGCCTAT	CGCGTCGGCA	GGATTGCCGC	TGAGGAAGGT
301	TTGTTCCGCT	TCCAATTGGA	TGATAAGGGC	AAGTGGGGTA	ATCCTCAGTT
351	GCTCGTGAAA	AAGATTAGAC	ATATGAAAGT	GCGGTATATC	TATGTTTCCG
401	ACTGTCCTGA	AGATGACGAT	CGCCGGCAAG	AGGAAAAATT	CAATATACAG
451	GGTACATTGC	ACAGCTCCAC	AAATGCTGTT	ACGCCGCCGC	GGGTGGAGGT
501	TTTATTGAGT	AGCGGCTACTG	ATACCAAGAT	TGCCGCTTCT	TCAGACAATC
551	ATATTATATG	TTACCGTATC	GATGCGACAA	TACGCGGGGG	AAATGTATGC
601	GCAAAACAGAA	CACTTTGA			

a247-1.pwp (partial).

1	NNTAKLIPIA	ESTDIKYPGF	AQARPALIFQ	YGIDDLDSA	ETVVVSSCSK
51	IAKPGKKIST	LQEAKSALQI	TNDDKQONGNI	TRQRHVVNAY	AVGRIAGEEG
101	LFRFQLDDKG	KWGNPQLLVK	KIRHMKVRYI	YVSDCPEDDD	AGKEEKFKYT
151	FTGDSSTNAV	TPAGVEVLLS	SGTDTKIAAS	SDNHIYAYRI	DATIRGNVNC
201	ANRTL*				

[illegible]

570

```

m247-1      YAVGRIADEEGLFRFQLDDKGKWNQPLLKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFSSTNAVTTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            | |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1   atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggtcccga ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgccagc tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggtttgctg
201 ggagggcgaa tttcagggtt tggatttggg atatgctgct gacagtaaag
251 ttacgtttag cgaaaactgt gaaaaagggt tgtgtaccgc agtgaatgtg
301 cggacaaata ataatggtag tgaagaggct tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgccct gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaggcgcgcg caggcgctcg caaaatgccg cgctatatta tcgaatatatt
501 aggcgtgaag aacggacaaa atgtttatcg gggtactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcataaat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1   MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFVVVTAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNNGSEEA FGNIVVQKQP AVEAVKRSCP AKSGKNSTDL CIDNKGMEYN
151 KGAAGVSKMP RYIIIEYLVK NGQNVYRVTA KAWGKNANTV VVLQSYVGNN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1   ..GGGTTTGCAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.TyWT
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGCTT TGGCCGAGKc GkCTwTGCGG
151 GAAGGCGAAC TTCAGGTTTT GGATTTGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAAACGTGT GAAAAGGTCT GTsTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCACCG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GGwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCAC.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGtAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1   ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXR
51  EGELQVLDLE YDTSKVTFs ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGXKEYKKG TRSVTKMPRY IIEYLVGXNG
151 ENVYRVTAKA WGKNANTVVV LQSYVSNND *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

```

m248/g248
            10      20      30      40
m248.pep  GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
            | ||: |||| | |||| | ||||| ||||| ||||| ||||| |||||

```

571

```

g248      MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNND-NEEAFDNIVVQGKP
           50      60      70      80      90      100
g248      LAEAAALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQGKP
           70      80      90      100      110      120
m248.pep  TVEAVKRSCPA-----NSTDLCLDKKXKEYKKGTRSVTKMPRYIIIEYLGXNGENVYRVTA
           110      120      130      140      150
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYIIIEYLGXNGENVYRVTA
           130      140      150      160      170      180
m248.pep  KAWGKNANTVVVLQSYVSNNDEX
           160      170      180
g248      KAWGKNANTVVVLQSYVGNNDQX
           190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51 GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEAAALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCTA KSTGLCIDNK GMEYKKGTQS
151 VSKMPRYIIE YLGXNGENV YRVTAKAWGK NANTVVVLQS YVSNNDE*

```

m248/a248 89.4% identity in 180 aa overlap

```

m248.pep      GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
                10      20      30      40
a248      MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS
                10      20      30      40      50      60
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNNDNEEAFDNIVVQGKPT
                50      60      70      80      90      100
a248      LAEAAALREGEFQVLDLEYDTSKVTFSENCGKGLCTAVNVRTNNDNEEAFDNIVVQGKPT
                70      80      90      100      110      120
m248.pep  VEAVKRSCPANSTDLCIDKKXKEYKKGTRSVTKMPRYIIIEYLGXNGENVYRVTAKAWGK
                110      120      130      140      150      160
a248      VEAVKRSC TAKSTGLCIDNKGMEYKKGTQSVSKMPRYIIIEYLGXNGENVYRVTAKAWGK
                130      140      150      160      170      180
m248.pep  NANTVVVLQSYVSNNDEX
                170      180

```


|||||
a248 NANTVVVLQSYVSNNDX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```

1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGTTTGTAACTGCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAGGTC TGTGTGCCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```

1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEAAALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCPA NSTDLCKDKK GMEYKKGTRS
151 VSKMPRYIEE YLGVKNGENV YRVTAKEGK NANTVVVLQS YVSNNDX*

```

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGSAFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	119
m248-1.pep	LAEAAALREGELQVLDLEYDTDSKVTFSENCGKGLCAAVNVRTNND-NEEAFDNIVVQGKPT					
g248	LAEAAALREGELQVLDLEYAADSKEVTFSENCGLCTAVNVRTNNGSEAFGNIVVQGKPT					
	70	80	90	100	110	120

	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA---NSTDLCKDKKMEYKKGTRSVSKMPRYIEEYLGKNGENVYRVTA					
g248	AVEAVKRSCPAKSGKNSTDLCKDKKMEYKKGTRSVSKMPRYIEEYLGKNGQNVYRVTA					
	130	140	150	160	170	180

	180	190
m248-1.pep	KAWGKNANTVVVLQSYVSNNDX	
g248	KAWGKNANTVVVLQSYVGNNDQX	
	190	200

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m248-1.pep	LAEAAALREGELQVLDLEYDTDSKVTFSENCGKGLCAAVNVRTNNDNEEAFDNIVVQGKPT					
a248	LAEAAALREGELQVLDLEYDTDSKVTFSENCGLCTAVNVRTNNDNEEAFDNIVVQGKPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCKDKKMEYKKGTRSVSKMPRYIEEYLGKNGENVYRVTAKEGK					
a248	VEAVKRSCPAKSTGLCKDKKMEYKKGTRSVSKMPRYIEEYLGKNGENVYRVTAKEGK					
	130	140	150	160	170	180

```

                190
m248-1.pep    NANTVVVLQSYVSNNDEX
              |||||
a248          NANTVVVLQSYVSNNDEX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```

g249.seq
1   atgaagaata atgattgctt ggcctgaaa aatccccagt ccggtatggc
51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtattttgg
101 cattgctgtc cgtacagttg cggacagtcg cttccgctag ggaggcggaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaatggt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcgggtgt
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagttag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga

```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```

g249.pep
1   MKNNDCLRLK NPQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDLDSNKK YSLYMGKQTL SAVDGEFMLD
101 AEKSKAQLAE EQLKRFSHEL KNALPDAVAI HYAVCKDSSG DAPTLSDSGA
151 FSSNCDNKAN GDTLIKVLWV NDSAGDSDIS RTNLEVSGDN IVYTYQARVG
201 GRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```

m249.seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATT TGCATTGAT
301 GCCATGAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTCGGCAG GGGATTCCGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCCGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```

m249.pep
1   MKNNDCFRLLK DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVXXXXXXXX
51  XXXXXXXXXXX XLMEGMLMNP TIDSDSNKK YNLYMGNHTL SAVDGDFAID
101 AMKTKGQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLGNAF
151 SSNCDNKANG DTLIKVLWVN DSAGDSISR TNLEVSGDNI VYTYQARVG
201 RE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

```

m249/g249
                10      20      30      40      50      60
m249.pep      MKNNDCFRLLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXX
              |||::|::|: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60
           70      80      90     100     110     120
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTKGQLAEALKRFSYEL
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g249      NLMEGMLMNPTIDLDSNKKNYSLYMGKQ-TLSAVDGEFMLDAEKSQAQLAEELKRFSHEL
           70      80      90     100     110     120
           130     140     150     160     170     179
m249.pep  KNALPDAAAIHYAVCKDSSGNAP-TLSGN-AFSSNCDNKANGDTLIKVLWVND-SAGDS-DIS
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g249      KNALPDAAVAIHYAVCKDSSGDAP-TLSDSGAFSSNCDNKANGDTLIKVLWVND-SAGDS-DIS
           130     140     150     160     170     180
           180     190     200
m249.pep  RTNLEVSGDNIVYTYQARVGGREX
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51 GCTGATAGAA GTCTTGCTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCACTTG CGGACAGTCG CTCCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCACGCAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AAATAAGAC GCAGTTGGCA GAGGCACAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TCGGCAGGCC ATCCATTACG
401 CCGTCTGCAA GGATTCTGCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGCAAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1  MKNNDCFRLK NPQSGMALIE VLVAMLVLTIGILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAP-TLSAGS
151 TFSSNCDGSA NGDTLIKVLW VND-SAGDS-DI ARTNLETNGN NIVYTYQARV
201 GGRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

           10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60
           70      80      90     100     110     119
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTKGQLAEALKRFSYE
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a249      NLMEGMLMNPTIDSDSNKKNYNLYMGNH-HALSVVDGDFQVDAIKTKTQLAEALKRFSYE
           70      80      90     100     110     120
           120     130     140     150     160     170
m249.pep  LKNALPDAAAIHYAVCKDSSGNAP-TLS-GNAFSSNCDNKANGDTLIKVLWVND-SAGDS-DI
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a249      LKNALPDAAAIHYAVCKDSSGVAP-TLSAGSTFSSNCDGSANGDTLIKVLWVND-SAGDS-DI
           130     140     150     160     170     180

```

```
m249.pep      180          190          200
               SRTNLEVSGDNIVYTYQARVGGRGX
               :|:|||||:|||||
a249           ARTNLETNGNNIVYTYQARVGGRGX
               190          200
```

m249-1.seq

m249-1.pep

m249-1/g249 90.1% identity in 203 aa overlap

a249/ L36117

Query: 13 QSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQIVSQITONLMEGMLMNPFI 72
 QSG ++IEVLVA+L+++IG+L ++++Q +T+ ++ + + + NL+E M +P
 Sbjct: 12 QSGFSMIEVLVALLLISIGVLGMIAMQGKTIQYTADSVERNKAAMLGSNLLESMRASPKA 71

Query: 73 DSDSNKKKNYNLYMGNHHALSVDVGDFQVDAIKTKTOLAEA---OLKRFSYELKNALPDAA 129

576

D + M G A + T L +A +L ++ ++KN LP A
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAKGSAPFTAPSSCTPLPDAIKDRLGCVAEQVKNELPGAG 126
 Query: 130 AI---HYAVCKDSSGVAPTLASGSTFSSNCDGSANGDTL-
 + Y +C+ S +CDG G L I++ W + A ++
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLERLAWRGKQACVNAADSSA 172
 Query: 186 ETN 188
 +T+
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLK	DSQSG	MALIE	VLVAM	LVLTIG
a249	MKNND	CFRLK	DSQSG	MALIE	VLVAM	LVLTIG
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLM	EGMLM	NPTID	SDSNK	KNYNL	YMGNH-
a249	NLM	EGMLM	NPTID	SDSNK	KNYNL	YMGNH-
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKN	ALPDAA	AIHYA	VC	CKDSS	GNA
a249	LKN	ALPDAA	AIHYA	VC	CKDSS	GNA
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRT	NLEV	SGDN	IV	TYQAR	VGGREX
a249	ART	NLET	NGNN	IV	TYQAR	VGGREX
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1 atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51 aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggta
101 tgcagggcgg gcaaaaaggt atggggccggc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcgcatat cctgatggg ggcgcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgtgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1 MHTTASPRDE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51 GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRRARV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1 ATGCACACCT TCCCCGCATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51 CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAACTACT CGGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCACTAT
151 GAACCTTCGCC GGCGGCTCCG AGTTGCCAC GGTCAACCTG TGGGCGGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1 MHTPSPHNEF IRGIKESSPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51 MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRRARTVF YV*
  
```

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

```

      10          20          30          40          50          59
m250.pep    MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGSWLEMLLMTSMNFAGGSEF
             |||::||| | | | | | | | | | | | | | | | : | | | | | : | | | | |
g250         MTHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNFAGGSEF
              10          20          30          40          50          60

      60          70          80          90          100         110
m250.pep    ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRRARTVFYVX
             ||| | | | | | | | | : | | | | | | | | | | | | | | | : | | | | |
g250         ATVNLWAEPLPILLIATITFMINSRHILMGGGACHAHERNTAEKSRRARAVFYV
              70          80          90          100         110

```

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTGCCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGGCGG	CTCCGAGTTT	GCCACGGTCA	ACCTGTGGGC
201	GGAACTCTG	CCGATACTGG	TTATCGCCAC	CGTAACCTTA	ATGATTAATT
251	CTCGGCATAT	CCTGATGGGG	G.CGGCACTT	CCCCCGCACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACTGTT	TTTTATGTGT	GA

```

1  MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMQGQKG MSWLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTC PAPERN
101 TAEKSARTV FYV*

```

```

59          10          20          30          40          50
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTSMNFAGGSEF
          |
||:|||||||||||||||||||||||||||||||||:|||||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMSWLEMLLMTGMNFAGGSEF
          10          20          30          40          50
60
          60          70          80          90          100          110
m250.pep
ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAAPERNTAEKSRARTVFYVX
|||||
a250
ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAAPERNTAEKSRARTVFYVX
          70          80          90          100          110

```

1	atgcctgacc	caatagggat	tcttttcgct	gccgtcgggg	ttgatttttt
51	tgccgttgtt	ttgagggggc	gttttcaacg	aataggcgcg	gttggcatgt
101	tqataataat	aatcctgatg	gcggaqgtcq	qaacaaaac	ggtcqtaacc

g251.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pep

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/q251

m251.pep TVDAARRAVRISIVAQAADLPRNDISPAYGDP
IGAGFTAVGADFFAVVLRGRVRRIGAVG
g251 MPDPIGILFAAVGVDFFAVVLRGRFQIRIGAVG

```
a251.seq
1  ATGCGTGCTG CGGTAGTCGT AGCGCAACCC CGCGCCGACA TCCGCCACC
51  TGCCCAAACG GACATTGTCC CGAAGTCGCG CGTAATAGCT TTTGCCGTTG
101 ATGTCGCGCG CGGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACCACATTTC CCCTGCCTAT GCTGACCCAA TAGGGTTGGT
201 CCTTGCCGCC GTTGGGGTTG GCGGTTTTAG GGGGCGTTTT CGACGAATAG
251 GCGCGGTTGG CATGTTGATA ATAATAATCC TGATGGCGGA GATTAGAGTC
301 AAAGCGGTCA AAACCGAGAT TCACGCTCAG GTTGTGGCGG ATTTTGGCGC
351 TATCGAAGGA TTTTTTGAAT GCCGCCTGCA AGAGCTCTGT GCTTCCCCG
401 TAAATCACGC GGTCGGATTT GTAGTAGGAA AACGGCTTGT CGGCACTCGG
451 GCGGCAATAT TTGTCCGAAC CGTCGGCAGA ACAGTGCGTC TGCTGAAAAT
501 GATTGTCCAA ACCGATGCCC TGCCGGTCGT AAGAGAGCCG GGCATAATCC
551 ACCCAAGTGT CTTTATCGCG ATTGGTATAG ACATATTGCA AACCGTAGCG
601 GCTTTTGGTG TGCGTCTCGT CTTAAAACAC GCCCGTACCG TATTCCGCGC
651 CCACCAGCGC ACCGTTTTCG CCGTTGGTAA ACAGACCGCC GTATTTGTGG
701 TCGCCGCGCT ATTTGCCGTT GCCTCTTATC GGTCCGTATT TTCTATTTTC
751 ATCAAAAACC GCCTTGGTCA GGAATGCCGG AACCGTCATA TCGCGCGTGT
801 CGAAAGTTTG TTGCGTGTGT TCGAGTATGC CGCCGATGTA GTGCCGTTTG
851 TTTTCAAACG GAAAACCCGG CGGGAACAGC CACGATCGGC TTTCGTATGA
```

a251.pep

1	MRAAVVVAQP	RADIRPPAQT	DIVPNCRVIA	FAVDAARRAV	RISIVAQAAD
51	LPRNHISPAY	ADPIGLVLAA	GVGQFGRGF	RRIAGVGLI	<u>IIILMAEIRV</u>
101	KAVKTEIHAQ	VVADFGGIEG	VFECRLQEPV	AFPVNHAVGF	VVGKRLVGTR
151	AAIFVRTVGR	TVRLCLKMIVQ	TDALPVVREA	GIHPSVFIG	<u>IGIDIFQTVA</u>
201	AFGVRLVKH	ARTVFRAHQF	TVFAVGKQTA	VFVVARVFAV	ASYRSVFVF*
251	IKNRLGOECR	RNHRIARVESL	LVFEYGAADV	VPVFVKTKTR	AEOPRSFVF*

	10	20	30	40	50	60
m251.pep	MRAAVVVAQARADIRPPAQT	DIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY				
			:			
a251	MRAAVVVAQPRADIRPPAQT	DIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY				
	10	20	30	40	50	60
	70	80	90	100	110	120
m251.pep	GDPIGAGFTAVGADFFAVVLRGRVRRIGAVGMLIIIIILMAEIRAKAVKPEIHAQVVADFG					
	:	:	:	:	:	

580

```

a251      ADPIGLVLAAVGVGGF----RGRFRIRIGAVGMLIIIIILMAEIRVKAVKTEIHAQVVADFG
              70              80              90              100             110

              130             140             150             160             170             180
m251.pep  GIEGFFECRLQEPVAFPVNHAIGFVIGKRLVGTRAAIFVRTVGR TVRLLKMIQT DALPV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      GIEGFFECRLQEPVAFPVNHAIGFVIGKRLVGTRAAIFVRTVGR TVRLLKMIQT DALPV
              120             130             140             150             160             170

              190             200             210             220             230             240
m251.pep  VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVF AVGKQSAVFVVAR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVF AVGKQSAVFVVAR
              180             190             200             210             220             230

              250             260             270             280             290             300
m251.pep  VFAVTGQRTLFFICIKNRLGQECNRNRIARVESLLRVFEYAADV VPLILKTKTRAEQPR
              ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a251      VFAVASYRS-VFSIFIKNRLGQECNRNRIARVESLLRVFEYAADV PFVFKTKTRAEQPR
              240             250             260             270             280             290

m251.pep  PAFVX
              ||||
a251      SAFVX
              300

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 987>:

```

g253.seq
1   atgatcgaca gggaccgtat gttgcgggac acgttggaac gtgtgctgctg
51  ggggtcgcttc tggttatggg tgggtggtggc atcgatgatg tttaccgccg
101 gatttttcagg cacttatctt ctgatggaca atcaggggct gaatttcttt
151 ttagtttttg cgggagtgtt gggcatgaat acgctgatgc tggcagtatg
201 gttggcaacg ttgttcctgc gcgtgaaagt gggacggttt ttcagcagtc
251 cggcgacgtg gtttcggggc aaaggccctg taaatcaggc ggtgttgctg
301 ctgtatgcgg accagtggcg gcaaccttcg gtacgatgga aaataggcgc
351 aacggcgcac agcttggtggc tctgcacgct gctcggaatg ctggtgtcgg
401 tattgctgct gcttttggtg cggcaatata cgttcaactg ggaaagcacg
451 ctggtgagca atgccgcttc ggtacgcgcg gtggaaatgt tggcatggct
501 gccgtcgaaa ctcggtttcc ctgtccccga tgcgcggcg gtcatcgaa
551 gtcgtctgaa cggcaatatt gccgatgcgc gggcttggtc ggggctgctg
601 gtcggcagta tcgtctgcta cggcatcctg ccgcgcctct tggcttgggt
651 agtggtgtaa atccttttga aaacaagcga aaacggattg gatttggaaa
701 aaacctatta tcaggcggtc atccgcgcgt ggcagaacaa aatcaccgat
751 gcggatacgc gtcgggaaac cgtgtccgcc gtttcgccga aaatcgtctt
801 gaacgatgcg ccgaaatggg cgctcatgct ggagaccgag tggcaggacg
851 gccaatggtt cgagggcagg ctggcgcagg aatggctgga taagggcggt
901 gccgccaatc gggaacagg tgcgcgcgtg gagacagagc tgaagcagaa
951 accggcgcaa ctgcttatcg gcgtacgcgc ccaaactgtg ccggaccggg
1001 gcgtgctgcg gcagattgtg cggctttcgg aagcggcgca gggcggcgcg
1051 gtggtgcagc ttttgccgga acaggggctt tcagacgacc tttcggaaaa
1101 gctggaacat tggcgtaacg cgctgaccga atgcggcgcg gcgtggcttg
1151 agcctgacag ggtggcgag gaaggccgtt tgaaagacca ataa

```

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

```

g253.pep
1   MIDRDRMLRD TLERVAGSF WLWVVASMM FTAGFSGTYL LMDNQGLNFF
51  LVLAVGLGMN TLMLAVLAT LFLRVKGRF FSSPATWFRG KGPVNQAVLR
101 LYADQWRQPS VRWKIGATAH SLWLCTLLGM LVSVLLLLLV RQYTFNWEST
151 LLSNAASVRA VEMLAWLPSK LGFPVPDARA VIEGRLNGNI ADARAWSGLL
201 VGSIVCYGIL PRLLAWVCK ILLKTSENGL DLEKTYQAV IRRWQNKITD
251 ADTRRETVSA VSPKIVLNDK PKWALMLETE WQDQWFEGR LAQEWLDKGV

```

581

301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGGA
 351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRAVAQ EGRLKDQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 989>:

m253.seq

```

1   ATGATTGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
51  GGGGTCGTTT TGGTTGTGGG TGGTGGCGGC GACGTTTGCA TTTTTCACCG
101 GTTTTTCAGT CACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT
151 TTGGTTTGGG CGGGCGTGTT GGGCATGAAT ACGCTGATGC TGGCAGTATG
201 GTTGGCAATG TTGTTCTGCG GTGTGAAAGT GGGGCGTTT TTCAGCAGTC
251 CGGCGACGTG GTTTCGGGGC AAAGACCTCG TAAATCAGGC GGTGTTGCGG
301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC
351 AACGTGCGAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTCTGG
401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAAGCACG
451 CTGTTGAGCA ATGCCGCTTC GGTACGCGCG GTGGAAATGT TGGCATGGCT
501 GCCGTCGAAA CTCGTTTCC CTGTCCCGCA TCGCGGGGCG GTCATCGAAG
551 GCCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGCTC GGGGCTGCTG
601 GTCGGCAGTA TCGCCTGCTA CGGCATCTCG CCGCGCCTGC TGGCTTGGGT
651 AGTGTGTAAG ATCCTTTTGA AAACAAGCGA AAACGGATTG GATTTGGAAA
701 AGCCTATTA TCAGGCGGTC ATCCGCCGCT GGCAGAACAA AATCACCGAT
751 GCGGATACGC GTCGGGAAAC CGTGTCCGCC GTTTCACCGA AAATCATCTT
801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAG TGGCAGGACG
851 GCCAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGCGGTT
901 GCCACCAATC GGGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
951 ACCGGCGCAA CTGCTTATCG GCGTGCAGCG CCAAACTGTG CCGGACCGCG
1001 GCGTGTTCG GCAGATTGTC CGACTCTCGG AAGCGGCGCA GGGCGGCGCG
1051 GTGGTGACAG TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTCGGAAAA
1101 GCTGGAACAT TGGCGTAACG CGCTGGCCGA ATGCGGCGCG GCGTGGCTTG
1151 AGCCTGACAG GCGGCGCAG GAAGGGCGTT TGAAAGACCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 990; ORF 253>:

m253.pep

```

1   MIDNRNMLRE TLERVRAGSF WLWVVAATFA FFTGFSVTYL LMDNQGLNFF
51  LVLAVGLGMN TLMLAVWLAM LFLRVKVRGF FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSVLLLLLV RQYTFNWEST
151 LLSNAASVRA VEMLAWLPSK LGFPVPDARA VIEGRLNGNI ADARAWSGLL
201 VGSIAICYGIL PRLLAWVVCK ILLKTSENGL DLEKPPYQAV IRRWQNKITD
251 ADTRRETUSA VSPKIIILNDA PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
301 ATNREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGGA
351 VVQLLAEQGL SDDLSEKLEH WRNALAECGA AWLEPDRAAQ EGRLKDQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/g253

```

          10      20      30      40      50      60
m253.pep  MIDNRNMLRETLEVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAVGLGMN
          |||:||||:|||||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g253      MIDRDRMLRDTLEVRAGSFWLWVVASMMFTAGFSGYLLMDNQGLNFFLVLAVGLGMN
          10      20      30      40      50      60

          70      80      90      100     110     120
m253.pep  TLMLAVWLAMFLRVKVRGFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH
          |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g253      TLMLAVWLATLFLRVKVRGFFSSPATWFRGKGPVNQAVLRLYADQWRQPSVRWKIGATAH
          70      80      90      100     110     120

          130     140     150     160     170     180
m253.pep  SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA
          |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g253      SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA
          130     140     150     160     170     180

```

582

	190	200	210	220	230	240
m253 . pep	VIEGRNLNGNIADARAWSGLLVGSIA CYGILPRLLAWVVKILLKTSENGLDLEKPYQAV					
g253	VIEGRNLNGNIADARAWSGLLVGSIVCYGILPRLLAWVVKILLKTSENGLDLEKTYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 . pep	IRRWQNKITDADTRRET VSAVSPKII LNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
g253	IRRWQNKITDADTRRET VSAVSPKIVLNDAPKWALMLETEWQDGGWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 . pep	ATNREQVA ALET ELKQKPAQLLIGVRAQTV PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
g253	AANREQVA ALET ELKQKPAQLLIGVRAQTV PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253 . pep	SDDLSEKLEHWRNALAECGA AWLEPDRAAQEGRLKDQX					
g253	SDDLSEKLEHWRNALTECGA AWLEPDRAAQEGRLKDQX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

a253 . seq	1	ATGATCGACA	GGAACCGTAT	GCTGCGGGAG	ACGTTGGAAC	GTGTGCGTGC
	51	GGGGTCGTTC	TGGTTGTGGG	TGGCGGCGGC	GACGTTTGCG	TTTTTTACCG
	101	GTTTTTCAGT	TACTTATCTT	CTAATGGACA	ATCAGGGTCT	GAATTTCTTT
	151	TTGGTTTTGG	CGGGCGTGTT	GGGCATGAAT	ACGCTGATGC	TGGCAGTATG
	201	GTTGGCAATG	TTGTTCTCTG	GCGTGAAAGT	GGGGCGTTTT	TTCAGCAGTC
	251	CGGCGACGTG	GTTCGGGGG	AAAGACCCCTG	TCAATCAGGC	GGTGTTCGGG
	301	CTGTATGCGG	ACGAGTGGCG	GCAACCTTCG	GTACGTTGGA	AAATAGGCGC
	351	AACGTGCGAC	AGCCTGTGGC	TCTGCACGCT	GCTCGGAATG	CTGGTGTCTG
	401	TATTGTTGCT	GCTTTTGGTG	CGGCAATATA	CGTTCAACTG	GGAAAGCACG
	451	CTGTTGGGCG	ATTCGTCTTC	GGTACGGCTG	GTGGAAATGT	TGGCATGGCT
	501	GCTTCGCAAA	CTGGGTTTTT	CCGTGCCTGA	TGCGCGGGCG	GTCATCGAAG
	551	GTCGTCTGAA	CGGCAATATT	GCCGATGCGC	GGGCTTGGTC	GGGGCTGCTG
	601	GTCGGCAGTA	TCGCCTGCTA	CGGCATCCTG	CCGCGCCTCT	TGGCTTGGGC
	651	GGTATGCAAA	ATCCTTTTGA	AAACAAGCGA	AAACGGCTTG	GATTTGGAAA
	701	AGCCCTATTA	TCAGGCGGTC	ATCCGCCGCT	GGCAGAACAA	AATCACCGAT
	751	GCGGATACGC	GTCGGGAAAC	CGTGTCGCGC	GTTTCGCCGA	AAATCGTCTT
	801	GAACGATGCG	CCGAAATGGG	CGGTCATGCT	GGAGACCGAA	TGGCAGGACG
	851	GCGAATGGTT	CGAGGGCAGG	CTGGCGCAGG	AATGGCTGGA	TAAGGGCGTT
	901	GCCGCCAATC	GGGAACAGGT	TGCCGCGCTG	GAGACAGAGC	TGAAGCAGAA
	951	ACCGGCGCAA	CTGCTTATCG	GCGTGCGCGC	CCAAACTGTG	CCCGACCGCG
	1001	GCGTGTTGCG	GCAGATCGTC	CGACTTTCGG	AAGCGGCGCA	GGGCGGCGCG
	1051	GTGGTGCAGC	TTTTGGCGGA	ACAGGGGCTT	TCAGACGACC	TTTCGGAAAA
	1101	GCTGGAACAT	TGGCGTAACG	CGCTGACCGA	ATGCGGCGCG	GCGTGGCTGG
	1151	AACCCGACAG	AGCGGCGCAG	GAAGGCCGTC	TGAAAACCAA	CGACCGCACT
	1201	TGA				

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

a253 . pep	1	MIDRNRMLRE	TLERVAGSF	WLWVAATFA	FFTGFSVTYL	LMDNQGLNFF
	51	LVLAVLGMN	TLMLAVWLAM	LFLRVKVGFR	FSSPATWFRG	KDPVNQAVLR
	101	LYADEWRQPS	VRWKIGATSH	SLWLCTLLGM	LVSVLLLLLV	RQYTFNWEST
	151	LLGDSSSVRL	VEMLAWLPAK	LGFPVPDARA	VIEGRNLNGNI	ADARAWSGLL
	201	VGSIACYGIL	PRLLAWAVCK	ILLKTSENGL	DLEKPYQAV	IRRWQNKITD
	251	ADTRRET VSA	VSPKIVL NDA	PKWAVMLETE	WQDGEWFEGR	LAQEWLDKGV
	301	AANREQVAAL	ETELKQKPAQ	LLIGVRAQTV	PDRGVLRQIV	RLSEAAQGGA
	351	VVQLLAEQGL	SDDLSEKLEH	WRNALTECGA	AWLEPDRAAQ	EGRLKTNDR
	401	*				

583

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLERVAGSFVLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
a253	MIDRNRMLRETLERVAGSFVLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m253.pep	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWVVKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRETIVSAVSPKIILNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWQNKITDADTRRETIVSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253.pep	ATNREQVAAELETKQKPAQLLIGVRAQTVPDGRVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVAAELETKQKPAQLLIGVRAQTVPDGRVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRDKQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcaggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg tttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactggttt ctttgagaaa cgggcccgggc
301 tggacgggat tttcactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggctcttg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtatttg gcggcagcat aacccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

584

```

51  LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLL SIAIYIVMGW MVLAVMKSLT
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

```

m254.seq (partial)
1  ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT
51  GTACCACGGA ATTGCAGCCG GAAACTGAA AAGCATTTTG AAAAAACCG
101 ACCACTGCAT GATTTATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA
151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG
201 GCTGCTGGCG GCTGCAGGAA TCGACAAGA ACTCACCATC GGACGGAAAA
251 GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG
301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT
351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTCGGC ATTTACTGGT
401 TTGTAAACGA TGAAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTC
451 GTATTGGGCG GCAGCATCAC CCAATTGTG AGCGTGTACG GTTACGTAAT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

```

m254.pep (partial)
1  ..VSVYGISLLL LYLSSWLYHG IAAGKLKSIL KKTDHCMYV LIAGSYTPFA
51  LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IVIYVVMGWM
101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGHGIWHLF
151 VLGGSITQFV SVYGYVI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254 . pep					10	20	30
					VSVYGISLLLLYLSSWLYHGIAAGKLKSIL		
g254							
	20	30	40	50	60	70	
m254 . pep		40	50	60	70	80	90
		KKTDHCMYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS					
g254							
	80	90	100	110	120	130	
m254 . pep		100	110	120	130	140	150
		IVIYVVMGWMVLAVMKSLTASLPSAGLAWLAAGGMLYSVG IYWFVNDEKIRHGHGIWHLF					
g254		: :					
	140	150	160	170	180	190	
m254 . pep		160					
		VLGGSITQFVSVYGYVIX					
g254							
		VLGGSITQFVSVYGYVIX					
		200					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

```

a254 . seq
1  ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTTGA GCGGTTTGAT
51  TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG
101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAAACCT
201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTTAT GTGCTGATTG
251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGGCCGGGC

```

301	TGGACGGTAT	TTTCACTGTC	CTGGCTGCTG	GCGGCTGCAG	GAATCGCACA
351	AGAACTCACC	ATTGGACGGA	AAAGCGAAAA	ACGACTGCTG	TCTATTGCGA
401	TTTATATCGT	AATGGGCTGG	ATGGTCTTGG	CGGTAATGAA	ATCCCTGACA
451	GCCTCACTCC	CGCCGGCAGG	ACTGGCTTGG	CTGGCGGCAG	GCGGTATGCT
501	GTACAGCGTC	GGCATTTACT	GGTTTGTA	CGATGAAAAA	ATCCGACACG
551	GGCAGCGAAT	CTGGCACTCT	TTCGTATTGG	GCGGCAGCAT	CACCCAATTT
601	GTCAGCGTGT	ACGGTTACGT	AATCTGTA		

a254 . pep

1	MYTGERFNTY	SHLSGLILAA	AGLALMLLKT	IGHGDGYRIF	SVSVYGISLL
51	LLYLSSSLYH	GIAAGKLKSI	LKKTDHCMYI	VLIAGSYTPF	ALVSLRNGPG
101	WTVFSLSWLL	AAAGIAQELT	IGRKSEKRL	SIATYIVMGW	MVLAVMKSLT
151	ASLPPAGLAW	LAAGGMLYSV	GIYWFVNDEK	IRHGGIWHL	FVLGGSITQF
201	VSVYGYVI*				

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

586

g255.seq
 1 atggttggac aggaagcctt gcggggtcag ttcgtcgccg tgttcgctgc
 51 cgcgttgcgt tacgctgtca aaacctgcgc cgatttccac gcctttgacg
 101 gcgttgatgc ccatcatcgc gtaggcgatt tcggcatcga ggcggtcgaa
 151 aacgggttcg cccaaaccga cggggacgtt ggcggttcg atatgcagtt
 201 tcgcgccgac ggaatccaag gatttgcgca caccgtccat atagtgttcc
 251 agttcggcga tttggctttg gttggcggca aaaaaaggat tttgggaaat
 301 gtgttcgctg ccttcaaacc ggattttttt ttcgcccact tgggtaacgt
 351 aggcggtgat ttccgtgccg aatttttctt tcagccattt tttggcaacg
 401 gctccggcgg caacgcgggc tgcggtttcg cgggcggaac tcctgccgcc
 451 gccccggtag tcgcgctac cgtatttctg ccaataggta tagtcggcgt
 501 gtccggggcg gaagcggtg gcgatgtcgc cgtagtcttc gctgcgctgg
 551 tcggtgttgc ggattag

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

g255.pep
 1 MVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVE
 51 NGFAQTDGDV GGFDMQFRAD GIQGFATVH IVFQFGLAL VGGKKRILGN
 101 VFAAFKPDPF FADLGNVGGD FRAEFFFQPF FGNGSGGNAG CGFAGGTPAA
 151 APVVARVVFV PIGIVGVSGA EGGDVAVVF AALVGVAD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

m255.seq
 1 GTGGTTGGAC AGGAAGCCTT GCGGGGTCAG TTCGTGCGCG TGTTGCTGCG
 51 CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
 101 GCGTTGATGC CCATCATCGC GTAGGCGATT TCGGCATCGA GGCGGTCAAA
 151 AACAGGTTTCG CCCAAGCCGA CAGGGACATT GGCTGCTTCG ATATGCAGCT
 201 TCGCGCCGAC GGAATCCAAG GATTGCGCA CGCTGTCCAT ATAGTTTTC
 251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
 301 GTGTTGCGAG CTTCAAACC GGATTCTTT TTCGCCGACT TGGGTAACGT
 351 AGGCGGTGAT TTCCGTGCCG AATTTTCTT TCAACCATT TTTGGCAACG
 401 GCTCCGGCAG CAACGCGGGC GCGGTTTCA CGGGCGGAGC TCCTGCCGCC
 451 GCCCGGCTAG TCGCGCTGC CGTATTGTG CCAATAGGTA TAGTCGGCGT
 501 GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTT GCTGCGCTGG
 551 TCGGTATTGC GGATTAA

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

m255.pep
 1 VVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVK
 51 NRFAQADRI GCFDMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
 101 VFAAFKPDPF FADLGNVGGD FRAEFFFQPF FGNGSGSNAG GGFTGGAPAA
 151 AAVVARAVVF PIGIVGVAGA EAGDVAVVF AALVGIAD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/g255

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAAHRVGDFGIEAVKNRFAQADRI					
g255	MVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAAHRVGDFGIEAVENGFAQTDGDV					
	10	20	30	40	50	60
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDPFFADLGNVGGD					
g255	GGFDMQFRADGIQGFATVHIVFQFGLALVGGKKRILGNVFAAFKPDPFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	FRAEFFFQPF FGNGSGSNAGGGFTGGAPAAAAVVARAVFVPIGIVGVAGAEAGGDVAVVF					
g255	FRAEFFFQPF FGNGSGGNAGCGFAGGTPAAAPVVARVVFPIGIVGVSGAEGGDVAVVF					

587

	130	140	150	160	170	180
	189					
m255 . pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```

a255 . seq
  1  GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCGG TGTTTCGCTGC
 51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
101  GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GGCGGTCGAA
151  TACGGGTTTCG CCCAAGCCGA CGGGGACGTT GGCGGCTTCA ATATGCAGCT
201  TCGCGCCGAC GGAATCCAAG GATTTCGCA CGCTGTCCAT ATAGTTTCC
251  AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301  GTGTTTCGAG CCTTCAAACC GGATTCTTT TCGCCGACT TGGGTAACGT
351  AGGCGGTGAT TTCCGTGCCG AATTTTCTT TCAACCATTT TTTGGCAACG
401  GCTCCGGCGG CAACGCGGGC GCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451  GCCCCGGTAG TCGCGCGTGC CGTATTGTG CCAATAGGTA TAGTCGCGCT
501  GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551  TCGGTATTGC GGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```

a255 . pep
  1  VVGQEALRGE FVAVFAAALR YAVKTCADFH AFDGVDHHR VGDFGIEAVE
 51  YGFAQADGDV GGFNMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
101  VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNGSGNAG GGFAGGTPAA
151  APVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*

```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255 . pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVKNRFAQADRDI					
a255	VVGQEALRGEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVEYGFADGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m255 . pep	GCFDMLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m255 . pep	FRAEFFFQPF FGNGSGSNAGGGFTGGAPAAA VVARAVFVPIGIVGVAGAEAGGDVAVVF					
a255	FRAEFFFQPF FGNGSGSNAGGGFTGGAPAAA VVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
	189					
m255 . pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```

g256 . seq
  1  atgctcgcgg tacgcaatcg gggttggcac ggcgcagtcg tccatttcgg
 51  cagctgcggc ggcgtagcga acaccgcccc ggtgttctac cacttgggtg
101  ataccgccga aatcgccctt gctttggaca cgctaccgcg gcgttaccgt
151  gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201  tttgggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgccgtat
251  ccgccccgt tgatgcagag gcggcaggca gccgcttcga cagcggcatc
301  acgcggctgc tctacacgcg ctacttcttc cgcacactga taccctaaag

```


588

```

351 acgttcgctc caaggttttc agacggcatt tgccgcaggg tgcaaaacac
401 tgggcgagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451 cggcacgact actaccgcca aacttcctgc aaaccgctgc tcaaacacgt
501 tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttcctgccgc
551 ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601 caacctgcac acggcgggca cgcgggcttt gtgagcagca ccggcggcag
651 gctgcacctg caatggctgc cgcgaccgt cctgtcctat tttgacagct
701 tccgcacaaa caggcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

```

g256.pep
  1 MLAVNRNGWH GAVVHFRSCG GVANTAPVFY HLGDTAEIAF ALDTLTARYR
 51 EIYAVGVSLG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNAANDP FLPPEALPRA DEASEAVTLF
201 QPAHGGHAGF VSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

```

m256.seq
  1 ATGCTTGCGG TACGCGATCG GGGTTGGCAC GCGGTAGTCG TCCATTTCGG
 51 CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTtGGCG
101 ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTCGCCGC GCGTTACCGT
151 GAAAtATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAATA
201 TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTCATCT
251 CCGCCCCCGT CGATGCAGAG GCGGCAGGCA GACGCTTCGA CAGCGGCATC
301 ACGCGGCTGC TCTACACGCG CTACTTCCTC CGCACCTGA TACCCAAAGC
351 AAAATCGCTC CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCCCT GCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCCTGTTC
601 CAGCCGGCAT ATGGTGGTCA TGTGGGCTTT GTCAGCAGCA CCGGCGGCAG
651 GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

```

m256.pep
  1 MLAVRDRGWH GVVHFRSCG GIANTAPVFY XLGDTAEIAF TLDTFAARYR
 51 EIYAVGVSLG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRRFDSGI
101 TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPAYGGHGVF VSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

```

m256/g256
      10      20      30      40      50      60
m256.pep MLAVRDRGWHGVVHFRSCGGIANTAPVFYHLGDTAEIAFTLDTFAARYREIYAVGVSLG
      |||||:|||||:|||||||:|||||||:|||||||:|||||||:|||||||
g256      MLAVNRNGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAFALDTLTARYREIYAVGVSLG
      10      20      30      40      50      60

      70      80      90     100     110     120
m256.pep GNALAKYLGEQGKKALPQAAVISAPVDAEAAGRRFDSGITRLLYTRYFLRTLIPKAKSL
      ||| |||||:|||||:|:|:|:||||| |||||:|||||:|||||:|
g256      GNAPAKYLGEQGKKALPHASAAVSAPVDAEAAGSRFDSGITRLLYTRYFLRTLIPKARSL
      70      80      90     100     110     120

      130     140     150     160     170     180
m256.pep QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLNNAVNDP
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|
g256      QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLNNAANDP

```

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256 . pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```

a256 . seq
1   ATGCTCGCGG TACGCGATCG GGGTTGGAAC GGCCTAGTCG TCCATTTCCG
51  CAGCTGCGGC GCGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACCGCCGA AATTGCCTTT ACTTTGGACA CGCTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGCC GCCGTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCCTGTTC
601 CAGCCGACAC ACGGTGGTCA TGTCGGCTTT GTCGGCAGCA CCGGCGGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```

a256 . pep
1   MLAVRDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EIYAVGVSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSCI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG FVSTGGRLHL QWLPQTVLSY FDSFRTNRR*

```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256 . pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVFYXLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWNHGVVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256 . pep	GNALAKYLGEQKKALPQAAVISAPVDAEAAGRRFDSGITRLLYTRYFLRTLIPKARSL					
	: : : : :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAAGNRFDSDGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256 . pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256 . pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```

g256-1 . seq
1   ATGATTTTGA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACA CCGGCACCC GCATACCGCC

```

590

```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTTCGCC CGATGCGCCG CTGGTCGTGC TGTTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTCGAACTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GCGCAGTCG TCCATTTCGG CAGCTGCGGC
301 GCGGTAGCGA ACACCGCCC GGTGTTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACCGC GCGTTACCGT GAAATATACG
401 CCGTCGCGGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCCGCCGTAT CCGCCCCGGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCTGCGCGC CCGAAGCCCT
801 GCGCCGTGCA GACGAAGCGT CCGAAGCCGT TACCCTGTTT CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTTGACAGCT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SRSYHAYVEL MLAVNRGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EIYAVGVSLG GNAPAKYLGE
151 QGKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG KTLGEFDDR FTAPLHGFAF RHDYRQTSC KPLLKHVAKP
251 LLLNAANDP FLPEALPRA DEASEAVTLF QPAHGGHAGF VSSTGGRLHL
301 QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCCGCGCCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTGCCCCGA TCGCGCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCAGCC ATTACGCGGT CGAACTGATG CTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTCCGCGAG CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAATATTT GGGCGAACAG
451 GGCACAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCGTCGA
501 TGAGAGGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAGC CGGCTGTCTT
551 ACACGCGCTA CTCTCTCCGC ACCCTGATAC CCAAAGCAA ATCGCTCCAA
601 GGTTTTCAGA CGCATTTCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCTGCAAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCGGCCCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CCTGTTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCGC AGACCGTCCT GTCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSYHAYVEL LAVDRGWHG VVVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYR IYAVGVSLGG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFAFR HDYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHVGFV SSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

10 20 30 40 50 59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g256-1 MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
10 20 30 40 50 60
60 70 80 90 100 110 119
m256-1.pep LVVLFHGLEGSSRSYHAYVELMLAVDRGWHG VVVHFRSCGG IANTAPVYFHLGDTAEIAF

```

591

```

g256-1      |||||:|||||:|||||:|||||:|||||:|||||
            LVVLFHGLEGSSRSHYAVELMLAVRNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
            70      80      90      100     110     120

m256-1.pep  120      130      140      150      160      170      179
            TLDTF AARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAGRFRFDSGI
            :|||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      ALDTLTARYREIYAVGVSLGGNAPAKYLGEQKKALPHASAAVSAPVDAEAAGSRFDSGI
            130      140      150      160      170      180

m256-1.pep  180      190      200      210      220      230      239
            TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRF TAPLHGFADRHDYYRQTSC
            |||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      TRLLYTRYFLRTLIPKARS LQGFQTAFAAGCKTLGEFDDRF TAPLHGFADRHDYYRQTSC
            190      200      210      220      230      240

m256-1.pep  240      250      260      270      280      290      299
            KP LLKHVAKP LLLNAVNDPFLPPEALPRAD E VSEAVTLFQPAYGGHVGFVSSTGGRLHL
            |||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1      KP LLKHVAKP LLLNAANDPFLPPEALPRAD EASEAVTLFQPAHGGHAGFVSSTGGRLHL
            250      260      270      280      290      300

m256-1.pep  300      310      319
            QWLPQTVLSYFDSFRTNRRX
            |||||:|||||:|||||
g256-1      QWLPQTVLSYFDSFRTNRRX
            310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1.seq
1  ATGATTTTGA CACCGCCGGA CACACCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACG CTCCGCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAACCGC CTACGACTTT
151 TCAGACGGCA TTTGCCCCGA TCGCGCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGCGGT CGAACTGATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGCGCGC
301 GTAGCGAACA CCGCCCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAAATATT GGGCGAACAG
451 GCGGAAAACG CGTGCCGCA AGCCGCGGCC GTCATCTCCG CACCCGTCGA
501 TGCAGAGGCG GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGC AACTGATAC CCAAAGCAGG GTCGCTCCAA
601 GGTTCGAGA CGGCATTTGC CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGTTTC ACCGACCCGC TGCAGGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCGCTGCC
801 CCGCGCAGAC GAAGTGTCG AAGCCGTTAC CCTGTTCCAG CCGACACACG
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGTTGCCG AGACCGTCCT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1.pep
1  MILTPPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVDRGWNG VVVHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLI PKARSLQ
201 GFQTAFAGC KTLGEFDDRF TAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PTHGGHVGFV GSTGGRLHLO
301 WLPQTVLSYF DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

a256-1.pep  10      20      30      40      50      60
            MILTPPDTPFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFS DGISPDAPL
            |||||:|||||:|||||:|||||:|||||:|||||
m256-1      MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS DGISPDAPL
            10      20      30      40      50      60

a256-1.pep  70      80      90      100     110     120
            VVLFHGLEGGSGSHYAVELMLAVDRGWNGVVVHFRSCGGVANTAPVFYHLGDTAEIAFT
            |||||:|||||:|||||:|||||:|||||:|||||
m256-1      VVLFHGLEGSSRSHYAVELMLAVDRGWNGVVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAGNRFDSGIT					
m256-1	130	140	150	160	170	180
	LDTFAARYREIYAVGVSLGGNALAKYLGEQGGKALPQAAAVISAPVDAEAAGRRFDSGIT					
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAGCKTLGEFDDRFTAPLHGFADRHDIYRQTSC					
m256-1	190	200	210	220	230	240
	RLLYTRYFLRTLIPKAKSLQGFQTAFAGCKTLGEFDDRFTAPLHGFADRHDIYRQTSC					
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNVAVDPFLEPEALPRADEVSEAVTLFQPTHGGHVGFVSGTGGRHLQ					
m256-1	250	260	270	280	290	300
	PLLKHVAKPLLLNVAVDPFLEPEALPRADEVSEAVTLFQPAYGGHVGFVSSTGGRHLQ					
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	310					
	WLPQTVLSYFDSFRTNRRX					

```
g257.seq
1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgcggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151 aaagtggtcg cgctgggttc cggcgcgagg ctgcgcctgt tcggcgagg
201 cgacagacag gcggcggatt tggtaataaa ggttttggcg gaagtggcgc
251 gtttgaaaaa aatggttcag ctttaccgtg aagacagcct gatcagccgt
301 ctgaaccgcg acggttatct gacttcgcct ccggcggatt ttttggaaat
351 qttgaqcctg qccqcqatat tcacgcgcctg a
```

g257.pep

1	MGRHFGRRRF	LTAAAVAVAG	AAVSFLPNPF	AAGGEKRNMD	KKRDENVFFW
51	KGVALGSGAE	LRLFGVDDRQ	AADLVNKLVA	EVARLEKMFS	LYREDSLISR
101	LNRDGYLTSP	PADFLELLSL	AAIFTR*		

```
m257.seq
1  ATGGGCAGGC  ATTTCTGGGCG  .CAGCGTTTT  CTGACGGTTG  CCGCCGTTGC
51  GGCGGGGaC.  GCGGcGGTTT  CTTTCCTGCC  GAATCCTTTT  GCCGCCGATG
101 ATGAAAAACG  CAACGGGGAT  GAAAAACGCA  ATGAAAATGT  GTTTTTCTGG
151 AAAGGTGTCG  CACTGGGTTC  CGGTGCGGa.  CTCCGTCTGT  TCGGTGTGGA
201 CGACAGGCGT  GCGGCGGATT  TGGTCAACAA  GGTTTTGGCG  GAAGTGGCGC
251 GTTTGAAAAA  ATTGTTTACG  CTTTACCGTG  AAGACAGCCT  GATCAGCCGC
301 CTGAACAGGG  ACGGTTATCT  GACTTCGCG  TCGGCGGATT  TTTTGAAC
351 GkTGAGCCTG  GCCGCGATAT  TCACGkCTG  A
```

m257.pep

1	MGRHFGXQRF	LTVAAVAAGX	AAVSFLPNPF	AADDEKRNKD	EKRNEVFFW
51	KGVALGSGAX	LRLFGVDDRR	AADLVNKLVA	EVARLEKLFS	LYREDSLISR
101	LNRDGYLTSP	SADFLELXSL	AAIFTX*		

m257/q257

593

```

m257.pep  MGRHFGQRFLTVAAVAAGTAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALGSGAD
          |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      MGRHFGRRRFLTAAAVAVAGAASFLPNPFAAGGEKRNMDKKRDENVFFWKGVALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRAADLVNKVLAEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      LRLFGVDDRQAADLVNKVLAEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC  ATTTTCGGGCG  CAGGCGTTTT  TTGACAGTTG  CCGCCGTTGC
51  GCGGCGGGGC  GCGGCGGTTT  CTTTCCTGCC  GAATCCTTTT  GCCGCCGATG
101 ATGAAAAACG  CAATAAAGAT  GAAAAACGCA  ATGAAAATGT  GTTTTTCTGG
151 AAAGGTGTCG  CACTGGGTTC  CGGTGCGGAG  CTCCGTCTGT  TCGGTGTGGA
201 CGACAGGCGT  GCGGCGGATT  TGGTCAACAA  GGTTTGGCG  GAAGTGCGCG
251 GTTTGAAAAA  AATGTTTCAGC  CTTTACCGTG  AAGACAGCCT  GATCAGCCGT
301 CTGAACCGTG  ACGGTTATTT  GACTTCGCCG  CCGGCGGATT  TTTTGGAAC
351 GTTGAGCCTG  GCCGTGATAT  TCACGCGCTG  A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF  LTVAAVAAAG  AAVSFLPNPF  AADDEKRNKD  EKRNENVFFW
51  KGVALGSGAE  LRLFGVDDRR  AADLVNKVLA  EVARLEKMFS  LYREDSLISR
101 LNRDGYLTSP  PADFLELLSL  AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALGSGAX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
a257      MGRHFGRRRFLTVAAVAAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAE
          10      20      30      40      50

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRAADLVNKVLAEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
a257      LRLFGVDDRRAADLVNKVLAEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTXX
          |||||
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

```

g258.seq
1   atgcgccgct tcctaccgat cgcagccata tgcgccgtcg tcctgtgtga
51  cggattgacg gcggcgaccg gcagcaccag ttcgctggcg gattattttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctgggtgt gtccgccggt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcgtggt
201 cggttcgtag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttcctg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggccgcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgcccc
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgaccaattt cgaccagccg cttcccgaca aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgtaa agcataggcg gcgtattgta
651 cgcgcaggga tggttgtcgg caggtacgca caacggggcg gattacgcgc
701 tgttcttccg ccagccgatt cccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gaaaaaagg
801 tttgcagacc ttttttctgg taaccctgct gattgcctcg ctgctgtcga
851 ttttcttgcg gctggtaatg gcaactgtat ttgcccgcgg tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaag gcggtggcgc aggggtgattt
951 cagccagacg cgccccgtat tgcgcaacga cgagttcgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcgga ggaagccgcc cgtcactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctentacccc ctctcttggt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctcccctct ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

```

g258.pep
1   MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVL SAV
51  LARYVILLK  DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVVPQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LDPKEHWEQI
201 QQTGVSRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKKGLQT FFLVTLIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLDG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

```

m258.seq
1   ATGCGCCGTT TTCTACCGAT CGCAGCCATA TCGCCCGTCG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTCT
101 GGTGGATTGT TCGGTCAGC GCAATGCTGC TGCTGGTGTG GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTCGCAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCCG CGTGTTTCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTTG AGCAAGTCCG CATTGAATTT GCGGCGAGAC AACGCCCTCG
401 GCAACGCCGT CCCCCTGCAG ATAGACCTCA TCGGCGCGCG TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCCA
701 TGTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GAAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTTC ACTGGTCATG GCACTGTATT TCGCCCGCGG TTTCGTCGAA
901 CCCGTCCTAT CGCTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGAGTTCGGA CGCTTGACCA

```

m258 . pep

1	<u>MRRFLPIAAI</u>	<u>CAVVLLYGLT</u>	<u>AATGSTSSLA</u>	<u>DYFWWIVAFS</u>	<u>AMLLLVLSAV</u>
51	<u>LARYVILLLK</u>	<u>DRRDGVFGSQ</u>	<u>IAKRLSGMFT</u>	<u>LVAVLPGVFL</u>	<u>FGVSAQFING</u>
101	<u>TINSWFGNDT</u>	<u>HEALERSLNL</u>	<u>SKSALNLAAD</u>	<u>NALGNAVVPVQ</u>	<u>IDLIGAASLP</u>
151	<u>GDMGRVLEHY</u>	<u>AGSGFAQLAL</u>	<u>YNAASGKIEK</u>	<u>SINPHKLDQP</u>	<u>FPKGARWEKI</u>
201	<u>QRAGSVRDLE</u>	<u>SIGGVFLYAQQ</u>	<u>WLSAGTHNGR</u>	<u>DYALFRQPV</u>	<u>PKGVAEDAVL</u>
251	<u>IEKARAKYAE</u>	<u>LSYSKKGLQT</u>	<u>FFLATLLIAS</u>	<u>LLSIFLALVM</u>	<u>ALYFARRFVE</u>
301	<u>PVLSLAEGAK</u>	<u>AVAQGDFSQT</u>	<u>RPVLRNDEFG</u>	<u>RLTKLFNHMT</u>	<u>EQLSIAKEAD</u>
351	<u>ERNRRREEAA</u>	<u>RHYLECVLEG</u>	<u>LTTGVVVFDE</u>	<u>QGCKTFNKA</u>	<u>AEQILGMPLT</u>
401	<u>PLWGSSRRHG</u>	<u>HGVSQAQSSL</u>	<u>AEVFAAIGAA</u>	<u>AGTDKPVHVK</u>	<u>YAAPDDAKIL</u>
451	<u>LKGATVLPED</u>	<u>NGNGVVMVID</u>	<u>DITVLIHAAK</u>	<u>EAAWGEVAKR</u>	<u>LAHEIRNPLT</u>
501	<u>PIQLSAERXA</u>	<u>XKLGGLKDEQ</u>	<u>DAQILTRSTD</u>	<u>TIVQGVAAAK</u>	<u>EMVEAFRNYA</u>
551	<u>RSPSLKLENQ</u>	<u>DLNALIGDVL</u>	<u>ALYEAGPCRF</u>	<u>AADLPANR*</u>	

Homology with a predicted ORF from *N. gonorrhoeae*

m258/g258

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVAFSAMPLLLVLSAVLARYVILLKK					
g258	MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVSFSAMPLLLVLSAVLARYVILLKK					
	10	20	30	40	50	60
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL					
g258	DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSLNL					
	70	80	90	100	110	120
m258.pep	SKSALNLAADNALGNVPVQIDLIGAASLPGDMGRVLEHYAGSGFAQLALYNAASGKIEK					
g258	SKSALDLAADNAVSNAVVPVQIDLIGTASLSGNMGVSLEHYAGSGFAQLALYNAASGKIEK					
	130	140	150	160	170	180
m258.pep	SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV					
g258	SINPHQFDQPLPDKEHWEQIQQTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI					
	190	200	210	220	230	240

596

	250	260	270	280	290	300
m258 . pep	PKGVAEDAVLIEKARAKYAELSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
g258	PENVAQDAVLIEKARAKYAELSYSKKGLQTFVLVTLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258 . pep	PVLSLAEGAKAVAQGDIFSQTRPVLNRNDEFGRLLTKLFNHMTEQLSIAKEADERNRRREEAA					
g258	PILSLAEGAKAVAQGDIFSQTRPVLNRNDEFGRLLTKLFNHMTEQLSIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258 . pep	RHYLECVLEGLTTGVVVFDEQGCLTKFNKAAEQILGMPLTPLWGSSRHGWHGVSAQQSLL					
g258	RHYLECVLDGLTTGVVVSYPVLSCCRRTAVFSTCHSSPLSYFX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1027>:

```

a258 . seq
1   ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTCT
101 GGTGGATTGT TGC GTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGCAG ATTGCCAAAC GCCTTTCGCG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT TATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATCT GGCGGCAGAC AACGCCCTTG
401 GCAACGCCAT CCCCCTGCAG ATAGACCTCA TCGCGCGCGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACAGGCGG GTTCGGTCAG GGATTTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCCG CAGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAAG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAAGG
801 TTTGCAGACC TTTTTCCTGG CAACCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCCGCCG TTTCGTCGAA
901 CCCGTCCTAT CGCTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGAGTTCGGA CGCTTGACCA
1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGACATTATC TCGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACCTT CAACAAAGCG GCGGAACAGA TTTTGGGGAT GCCGCTTACC
1201 CCCCTGTGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACG GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAAA GAAGCCGCGT
1451 GGGGCGAAGT GGCAAAACGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCTGCCGA ACGGCTGGCG TGGAAATTGG GCGGGAAGCT
1551 GGACGAGCAG GACGCGCAA TCCTGACACG TTCGACCGAC ACCATCATCA
1601 AACAAGTGGC GGCATTAAAA GAAATGGTCG AGGCATTCCG CAATTACGCG
1651 CGTTCCCTT CGCTCAAATT GGAAAAATCAG GATTTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTACG AAGCTGGTCC GTGCCGTTT GCGGCGGAAC
1751 TTGCCGGCGA ACCGCTGATG ATGGCGGCGG ATACGACCGC CATGCGGCAG
1801 GTGCTGCACA ATATTTTCAA AAATGCCGCC GAAGCGGCGG AAGAAGCCGA
1851 TGTGCCCCGAA GTCAGGGTAA AATCGGAAGC GGGGAGGAC GGACGGATTG
1901 TCCTGACAGT TTGCGACAAC GGCAAGGGGT TCGGAGGGA AATGCTGCAC
1951 AATGCCTTCG AGCCGTATGT AACGGACAAA CCGGCTGGAA CGGGATTGGG
2001 ACTGCCCGTG GTGAAAAAAA TCATTGAAGA ACACGGCGGC CGCATCAGCC
2051 TGAGCAATCA GGATGCGGGC GGCGCGTGTG TCAGAATCAT CTTGCCAAAA
2101 ACGGTAGAAA CTTATGCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```

a258.pep
  1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
 51 LARYVILLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TIIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFKNAA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIIEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*

```

m258/a258 99.0% identity in 584 aa overlap

```

              10      20      30      40      50      60
m258.pep      MRRFLPIAAICAVVLLYGLTAATGSTSSLAADYFWWIVAFSAMLVLSAVLARYVILLK
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a258           MRRFLPIAAICAVVLLYGLTAATGSTSSLAADYFWWIVAFSAMLVLSAVLARYVILLK
              10      20      30      40      50      60

              70      80      90     100     110     120
m258.pep      DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a258           DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
              70      80      90     100     110     120

              130     140     150     160     170     180
m258.pep      SKSALNLAADNALGNAPVQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a258           SKSALNLAADNALGNAIPVQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK
              130     140     150     160     170     180

              190     200     210     220     230     240
m258.pep      SINPHKLDQPFPGKARWEKIQAGSVRDLESIGGVLYAQGWLSAGTHNGRDIYALFFRQPV
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a258           SINPHKLDQPFPGKARWEKIQAGSVRDLESIGGVLYAQGWLSAGTHNGRDIYALFFRQPV
              190     200     210     220     230     240

              250     260     270     280     290     300
m258.pep      PKGVAEDAVLIEKARAKYAE LSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a258           PKGVAEDAVLIEKARAKYAE LSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
              250     260     270     280     290     300

              310     320     330     340     350     360
m258.pep      PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a258           PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA
              310     320     330     340     350     360

              370     380     390     400     410     420
m258.pep      RHYLECVLEGLTTGVVVFDEQGCLKTFNKAAEQILGMPLTPLWGSSRHGW HGVSAQQSLL
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a258           RHYLECVLEGLTTGVVVFDEQGCLKTFNKAAEQILGMPLTPLWGSSRHGW HGVSAQQSLL
              370     380     390     400     410     420

              430     440     450     460     470     480
m258.pep      AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a258           AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK

```

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258.pep	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDITIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDITIKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258.pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIFKNAAEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

g259.seq

```

1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  ttgatatttc tttgccggtt ttttgaccgc gcaaactctg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaattgctc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccg acgacgaaga cgcgcgcacg attgccgccg
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgcctcg
451 ggcgaaacct atgggcgcgt gttcgccgat attttcgagt tgctggcggc
501 tttggaagg cgcgcttca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

g259.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVVGFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

m259.seq (partial)

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTCGTG TCGGCGCGTT CAAAGGCCAA
201 GCGGGAAGG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGCTsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACkGACGC GGTGCGCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGmGGC
501 TTTGGAAGGG CGCGGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGmGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

m259.pep (partial)

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```

599

151 GETYGRVFAD IFELSALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG
 201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGKMAEQVRFKAE					
	:					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGKMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSALEGRAFKGMLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALERRAFKGILKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRC LPFGNGVGVRTQSGVAGDFKNIR					
g259	AEYKXHLRRC LPFGNGVGFGRQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1	ATGATGATGC	ACGCTTCTGT	CCAAAGCCGT	TTCGCACCGA	TACTTTATGT
51	TTTGATTTTC	TTTGCCGGTT	TTTTGACCGC	GCAAATCTGG	TTCAATCAGA
101	AAGCCTATAC	TGAAGAGCTG	CCTCCGCTTC	TGTCCGCATT	GTCCGCCGTC
151	GCGCTGGTGT	GGCTGGCGTG	GGCGTTCGTG	TCGGCGCGTT	CAAAGGCTAA
201	GGCGGAAAAG	TTCTACCGCG	AAAAAATGAT	ACAGAACGAA	AGCATACACC
251	CCGTCCTGCA	CGCTTCTTTG	CAACACTTGG	AACACAAGCC	GCAAATGCTC
301	GCCCTGCTGG	TCAAAAACCA	CGGCAAAGGG	ATGGCGGAAC	AGGTCAGGTT
351	CAAGGCGGAA	GTGCTGCCCG	ACGACGAAGA	CGCGCGCACG	ATTGCCGCCG
401	AGTTGGCAAA	AATGGATATG	TTTGCAATTG	GGACGGACGC	GGTCGCCTCG
451	GGCGAAACCT	ATGGACGCGT	GTTCGCCGAT	ATTTTCGAGT	TGTCGGCGGC
501	TTTGGAAGGG	CGCGCGTTCA	AAGGAATGTT	GAAACTGACG	GCGGAATATA
551	AAAA.CATCT	TCGCGGATGC	CTGCCGTTTC	GAAACGGCGT	TGGAGTTGGG
601	CGCGCTCAAT	CAGGCGTTGC	AGGAGATTTC	AAAAACATCG	GAAAAGTCCA
651	A				

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1	MMMHASVQSR	FAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALSAV
51	ALVWLAWAFV	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML
101	ALLVKNHKGK	MAEQVRFKAE	VLPDDEDART	IAAELAKMDM	FALGTD AVAS
151	GETYGRVFAD	IFELSALEG	RAFKGMLKLT	AEYKXHLRRC	LPFGNGVGVG
201	RAQSGVAGDF	KNIGKVQ			

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAWAFV					

600

	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHVPVXHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
a259	:					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSALEGRAFGMLKLT					
a259	:					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRCLPFGNGVGVGRTQSGVAGDFKNIR					
a259	:					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCGTG TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCAGAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCAGAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGCGCATGCC TGCCGTTCGG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTC A AACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGLMLKT AEYKNIFGDA CRSETALELG
201 ALNQALQEIS KTSEKSKRIF Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

```

      10      20      30      40      50      60
g259-1.pep  MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV
|||||
m259-1      MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV
      10      20      30      40      50      60

      70      80      90      100     110     120
g259-1.pep  SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE
|:|||||
m259-1      SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE
      70      80      90      100     110     120

      130     140     150     160     169
g259-1.pep  VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSAALE
|||||
m259-1      VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSAALEGRAFGMLKLT
      130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

```

a259-1.seq
1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTATC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCGATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGCGCGGTT CAAAGGCTAA
201 GCGCGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGCGGCG
501 TTTGGAAGGG CCGCGGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AAACGCGGTT GGAGTTGGGC
601 GCGCTCAATC AGCGGTTGCA GGAGATTTC AAAAAATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

```

a259-1.pep
1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLAQEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

```

      10      20      30      40      50      60
a259-1.pep  MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV
|||||
m259-1      MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV
      10      20      30      40      50      60

      70      80      90      100     110     120
a259-1.pep  SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE
|||||
m259-1      SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE
      70      80      90      100     110     120

      130     140     150     160     170     180
a259-1.pep  VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSAALEGRAFGMLKLT
|||||
m259-1      VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSAALEGRAFGMLKLT
      130     140     150     160     170     180

      190     200     210     220
a259-1.pep  AEYKNIFGDACRSETALELGALNQLAQEISKTSKSKRIFYX
|||||
m259-1      AEYKNIFGDACRSETALELGALNQLAQEISKTSKSKRIFYX
      190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

602

```

1  atgggtgctg  gtgtagtatt  cgttgtcttt  cagccgttct  tcagcctgtt
51  ttcgagcggtg  ttcgagggcg  gagtcggtat  agtcgagggg  gcgcacgatg
101 ccgctgaatg  cgacttcttg  tccgaggaat  ttaccctgat  ccggatcggg
151 gatgttttta  ttgattcggg  aggtcagata  acggccccgg  tctttcaggc
201 ctttggtgta  aaccctggcg  cctttgggtg  acagcagcct  gccttccggg
251 cccgagagca  ggcgcgggcg  ggcagcggtt  tctttgctgg  aaacgatttg
301 cgggtgctgc  ataaagacgc  ggtagaagtt  gacatcgatg  gcgggaatac
351 cgtatccgga  cacttcctta  tccggactga  ttttgacgac  ggggatgccg
401 tctgtctgtt  ccaagccgag  gcgcgggttc  ccgccaacgt  agcgcaacac
451 caatacctgg  cccggataaa  tcaggtcggg  attgtggatt  tgatcccggt
501 tcgcgcccc  caggggggga  ccattgccac  gggctgtaca  ggtatttgcc
551 cgaaataccc  cacagggtgt  cgccctgttt  ga

```

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pep

```

1  MGAGVVFVVF  QPFFSLFRAL  FEGGVGIVEG  AHDAAECDL  SEEFTRIRIG
51  DVFIDSVGQI  TARFFQAFGV  NPGAFGVQQP  AFRAREQARR  GSGFFAGNDL
101 RVLHKDAVEV  DIDGGNTVSG  HFLIRTFD  GDAVCLFQAE  ARFAANVAQH
151 QYLARINQVG  IVDLIPVRAP  QGGTIATGCT  GICPKYPTGC  RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

```

1  ATGGGTGCGG  GTATGGTATT  CGTTGTCTTT  CGGCCGTTCT  CCAGCCTGTT
51  TCGAGCGTTG  TTCGAGGACA  GAGTCGGTAT  AGTCGAGGGA  GCGCACGATG
101 CCGCTGAATG  CGACTTCCTG  CCCGAGGAAT  TTACCCGTAT  CCGGATCGGT
151 GATGTTTFTA  TTGATTCGGT  AGGTCAGGTA  GCGGCCCGGC  TCTTTCAGGC
201 CTTTGGTGTA  AACCCTGGTG  CCTTGGTGT  ACAGCAGCCT  GCCTTCCGGG
251 CCCGAGwCA  SGCGCGGyGC  GGCAGCGGTT  TCTTTCGGG  AAACGATTTG
301 CGGATCCGCG  ATAAAGATGC  GGTAGAAGTT  GACATCGATG  GCGGGAATAC
351 CGTATCCGGA  CACTTCCTTA  TCCGGACTCA  TTTTGACGAC  GGGGATGCCG
401 TCTGTCTGTT  CCAAGCCGAG  GCGCGGTTTC  CCGTCAACGT  GGCGCAACAC
451 CAATACCTGG  TCCGATAAAA  TCAGGTCGGG  ATTGTGGATT  TGATCCCGGT
501 TCGCGTyCCA  CAG

```

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260.pep

```

1  MGAGMVVFVVF  RPFSSLFRL  FEDRVGIVEG  AHDAAECDL  PEEFTRIRIG
51  DVFIDSVGVQ  AARLFQAFGV  NPGAFGVQQP  AFRARXXARX  GSGFFAGNDL
101 RMPHKDAVEV  DIDGGNTVSG  HFLIRTHFD  GDAVCLFQAE  ARFAVNVAQH
151 QYLVRINQVG  IVDLIPVRVP  Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRLFEDRVGIVEGAHDAAECDLPEEFTRIRIGDVFIDSVGVQV					
	: : :					
g260	MGAGVVFVVFQPFSSLFRLFEGGVGIVEGAHDAAECDLSEEFTRIRIGDVFIDSVGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
	: : :					
g260	TARFFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVLHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDGDAVCLFQAEARFAVNVAQHQYLVRINQVGIVDLIPVRVPQ					
	: : :					
g260	HFLIRTFDGDGDAVCLFQAEARFAANVAQHQYLARINQVGIVDLIPVRAPQGGTIATGCT					
	130	140	150	160	170	180

603

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

```
a260.seq
  1 ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
 51 TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CCACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCCTGGTG CCTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GGCGCGGCGC GGCAGCGGTT TCTTTGCGGG AAACGATTTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTTC CCGTCAACGT GGCGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTTGCC
551 CGAAATGCCC CACAGGTGTG CGCCCTGTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

```
a260.pep
  1 MGAGMVFVVF RPFSSLFRAL FEDRVGIVEG AHDAAECDLF PEEFTRIRIG
 51 DVFIDSVGQV AARLFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*
```

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVFVVF	RPFSSLFRAL	FEDRVGIVEG	AHDAAECDLF	PEEFTRIRIG	DVFDISVGQV
a260	MGAGMVFVVF	RPFSSLFRAL	FEDRVGIVEG	AHDAAECDLF	PEEFTRIRIG	DVFDISVGQV
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGV	NPGAFGVQQP	AFRAREQARR	GSGFFAGNDL	RVPHKDAVEV	DIDGGNTVSG
a260	AARLFQAFGV	NPGAFGVQQP	AFRAREQARR	GSGFFAGNDL	RVPHKDAVEV	DIDGGNTVSG
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDD	GDAVCLFQAE	ARFAVNVAQH	QYLVRINQVG	IVDLIPVRVP	
a260	HFLIRTHFDD	GDAVCLFQAE	ARFAVNVAQH	QYLVRINQVG	IVDLIPVRVP	QAAXIATGCT
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX 190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

```
g261.seq
  1 atggagcttg ggcataatcgt attccttctg ctttgcgcg gttcagacgg
 51 cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctccggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctgttcgagg atgtagtcca acacgcccac ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtag atcagcgagg tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcacg gatttgacga acacgcccgcg
301 gcagtcggga tagcccgaaa aatcgggttc gcacacgccc gcgatgatgt
351 gccggatacc ctgcccttgg gcaaaaatgg cggcgtaaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggtttc
451 gatggcggcg gtttcgatgg cggcggtttc gtccatcagg gcgttgtgag
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttccagc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggcgt ggacgttttc gcgccgtag gtttgagattg
```


604

651 cctgaatcag gcaggtgggtc gaatcctgac cgcccagaaa gatgaccaag
 701 gctttttggt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep
 1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG
 51 LFADVQHAH FVRQRPRLRL GQVHQRRVDL KIVVHRQIKG NVHGFDEHAA
 101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF
 151 DGGGFDGGGF VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP
 201 VSEGDGLDVF APVGLDCLNQ AGGRILTARE DDQGLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq
 1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTCGCGCT GTTCAGACGG
 51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTTCGCG CAAGATACAG
 101 CTCGGGCATT CGCGcCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
 151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TTCGTCCGCC AACGCCACG
 201 TTTGCGCCTT GGTCAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
 251 TCCATCGCCA AATTAAGGGT AACGTTTCATC GATTTGACAA ACACGTCGCG
 301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCCG GCGATGATGT
 351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
 401 gCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTT CGGCAGTTTC
 451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
 501 GgCTcAAGTC GAGTACGGTT TGTTTGACGC CCAAATCCTG CGCAATCCAG
 551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
 601 GCCTTGGACG TTTTCGCGCC CGTAGGTTT GATTGCCTGA ATCAGGCAGG
 651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep
 1 MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
 51 LLADIVQHAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHRFDKHVA
 101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
 151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
 201 GLDVFAPVGL DCLNQAGGRI LTARKDDQGL LV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
	::					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVQHAH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA AVGIAGEVGF AHARDDVPYP					
g261	FVRQRPRLRLGQVHQRRVDLKIVVHRQIKGNVHGFDEHAA AVGIARKIGF AHARDDVPDT					
	70	80	90	100	110	120
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGV-----VHQGIVRNLPHQAVQVEYGLF					
	:: : :					
g261	LPFGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAQIEYGLT					
	130	140	150	160	170	180
	180	190	200	210	220	230
m261.pep	DAQILRNPAFTQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGLLVX					
	: :					
g261	DTQILRDPLCAFQLDGMALPVSEGDGLDVFAPVGLDCLNQAGGRILTAREDDQGLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1   ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAAG
201 TTTGCGCCTT GGTCAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTTCGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1   MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFDKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAQV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAPVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQRAH					
	10	20	30	40	50	60
m261.pep	FVRQRPRRLRGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAGVIAGEVGFHAHARDDVPYP					
a261	FVRQRPSLRLRGQIHQRRVDLKIIVHRQIKGNVHGFDKHVTAVGIAGEVGFHAHARDDVPYP					
	70	80	90	100	110	120
m261.pep	FVRQRPRRLRGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAGVIAGEVGFHAHARDDVPYP					
a261	FVRQRPSLRLRGQIHQRRVDLKIIVHRQIKGNVHGFDKHVTAVGIAGEVGFHAHARDDVPYP					
	70	80	90	100	110	120
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAQVEYGLFDAQIL					
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAQVEYGLFDAQIL					
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAQVEYGLFDAQIL					
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAQVEYGLFDAQIL					
	130	140	150	160	170	180
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGFLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGFLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1   atggcacggt taaccgtaca caccctcgaa accgccccg aagccgcca
51  accgcgcgta gaggcgtac ccaaaaaaa cggctttat cccaacctca
101 tcggcgattt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgcccgaac cagcctgacc gccggcgaa tccaagtgat
201 ccggatcatc gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgcccgcg ctttggcggc aggtaaatct gacgatgcca aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

451 gtcgaagtcg taatgggcgt agccttggca actttgtgca actacgccaa
 501 caacctcgcc caaacgaaa tcaaccccaa attgcaggca tacgcctaa

This corresponds to the amino acid sequence <SEQ ID 1054; ORF 263.ng>:

g263.pep
 1 MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIGVLANA PEALAFYQEV
 51 GKLNAANSLT AGEVEVIRII AVRTNQCSFC VAGHTKLATL KLLSEQSLN
 101 AARALAAGKS DDAKLGALAA FTQAVMAKKG AVSDEELNAF LEAGYNRQQA
 151 VEVVMGVALA TLCNYANNLA QTEINPKLQA YA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1055>:

m263.seq (partial)
 1 ..GCAGCAGCGC AATTGACGA TGCCAAACTC GGC GCGCTCG CCGCCTTCAC
 51 CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
 101 CATTTTTCGA TCGGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
 151 GGCGT.AsyC TgGCAACCCT GTGCAACTAC GTCAACAACC TCGGACAAAC
 201 CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

This corresponds to the amino acid sequence <SEQ ID 1056; ORF 263>:

m263.pep (partial)
 1 ..GCAGCAGCGC AATTGACGA TGCCAAACTC GGC GCGCTCG CCGCCTTCAC
 51 CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
 101 CATTTTTCGA TCGGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
 151 GGCGT.AsyC TgGCAACCCT GTGCAACTAC GTCAACAACC TCGGACAAAC
 201 CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263/g263

				10	20	30
m263.pep				AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
				:		
g263	QCSFCVAGHTKLATLKLLSEQSLNAARALAAGKSDDAKLGALAAFTQAVMAKKGAVSDD					
	80	90	100	110	120	130
		40	50	60	70	
m263.pep	ELKAFFDAGYNQQQAVEVVMGVXLATLTCNYVNNLGQTEINPELQAYAX					
	: :					
g263	ELNAFLEAGYNRQQA VEVMGVALATLTCNYANNLAQTEINPKLQAYAX					
	140	150	160	170	180	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1057>:

a263.seq
 1 ATGGCACGTT TAACCGTACA CACCCTCGAA ACCGCCCCCG AAGCCGCCAA
 51 AGCGCGCGTC GAGGCGGTAC TTCAAAACAA CGGCTTTATC CCCAACCTTA
 101 TCGGCGTATT ATCAAACGCC CCCGAAGCCT TGGCGTTTTA CCAAGAAGTC
 151 GGCAAGCTCA ACGCCGCCAA CAGCCTGACC GCCGGCGAAG TCGAAGTAAT
 201 CCAGATTATT GCCGCCCGCA CCAACCAATG CGGCTTCTGC GTGGCAGGGC
 251 ACACCAAAC TCGCAACCCTG AAAAACTCC TTTCCGAACA ATCCGTCAA
 301 GCCGCGCGCG CTTGGCGGCG AGGCGAATTT GACGATGCTA AACTCGGCGC
 351 GCTCGCGGCC TTTACCCAAG CCGTAATGGC AAAAAAGGC GCGGTATCCG
 401 ACGAGGAAC TCAAAGCATTT TTTGATGCGG GCTACAACCA GCAGCAGGCA
 451 GTCGAAGTCG TGATGGGCGT AGCCTTGCGA ACTTTGTGCA ACTACGTCAA
 501 CAACCTCGGA CAAACCGAAA TCAACCCCGA ATTGCAGGCT TACGCCTGA

This corresponds to the amino acid sequence <SEQ ID 1058; ORF 263.a>:

a263.pep
 1 MARLTVHTLE TAPEAAKARV EAVLQNNNGFI PNLIGVLSNA PEALAFYQEV
 51 GKLNAANSLT AGEVEVIQII AARTNQCGFC VAGHTKLATL KLLSEQSVK
 101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA
 151 VEVVMGVALA TLCNYVNNLG QTEINPELQA YA*

607

m263/a263 97.4% identity in 77 aa overlap

					10	20	30
m263.pep					AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
a263	QCGFCVAGHTKLATLKKLLSEQSVKAARALAAGEFDDAKLGALAAFTQAVMAKKGAVSDE						
	80	90	100	110	120	130*	
		40	50	60	70		
m263.pep	ELKAFFDAGYNQQQAVEVVMGXLLATLCNYYVNNLQGTEINPELQAYAX						
a263	ELKAFFDAGYNQQQAVEVVMGVALATLCNYYVNNLQGTEINPELQAYAX						
	140	150	160	170	180		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

g264.seq

1	ttgactttaa	cccgaataaac	ccttttcttc	ctcaccgccc	cgttcggcac
51	acactccctt	cagacggcat	ccgcccgcgc	agtgggtcaag	ccggaaaaaac
101	tgcacgcctc	cgccaaccgc	agctacaaag	tcgccgaatt	cacgcaaac
151	ggcaacgcct	cgtggtacgg	cggcagggtt	cacgggacga	aaacttccgg
201	cggagaccgc	tacgatatga	acgcctttac	cgccgcccac	aaaaccctgc
251	ccatccccag	ccatgtgcgc	gtaaccaaca	ccaaaaacgg	caaaagcgtc
301	atcgctccgc	tcaacgaccg	cgcccccttc	cacggcaacc	gcacatcaga
351	cgtatccaaa	gccgcccgcg	aaaaattggg	ctttgtcagc	caaggacgg
401	cacacgtcaa	aatcgaaaca	atcgctccgc	gccaatccgc	accggttgcc
451	gaaaacaaag	acatctttat	cgacttgaaa	tctttcggtg	cggaacacga
501	agcacaagcc	tatctgaacc	aagccgccc	aaatttcgcc	gcttcgcat
551	caagcccga	cctctcggtt	gaaaaacgcc	gttacgaata	cgttgtcaaa
601	atgggcccgt	ttgcctcgca	ggaacgcgc	gccgaagccg	aagcgcaggc
651	acgcggtatg	gttcgggcgc	tactgacctc	cggttgga	

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

1	<u>LTLTRKTLFL</u>	<u>LTAAFGTHSL</u>	<u>QTASADAVVK</u>	PEKLHASANR	SYKVAEFTQT
51	GNASWYGGRF	HGRKTSGGDR	YDMNAFTA AH	KTLPIPSHVR	VTNTKNGKSV
101	IVRVNDRGPF	HGNRIIDVSK	AAAQKLGFVS	QGTAVHKIEQ	IVPGQSAPVA
151	ENKIDIFIDLK	SFGTEHEAQA	YLNQAAQNFA	ASSSSPNLSV	EKKRYEYVVK
201	MGPFSQERA	AEAEAQARGM	VRAVLTS*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264.seq

1	TTGACTTTAA	CCCAGAAAAC	CCTTTTCCTT	CTCACCGCCG	CATTCCGGCAC
51	ACACTCCCTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAAG	GCAGAAAAAC
101	TGCACGCCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAG	ACGCTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTACGCAA	ACCGGCAACG	CCTCGTGGTA
201	CGGCGGCAGG	TTTCACGGGC	GCAAACTTC	CGCGGAGAG	CGATACGATA
251	TGAACGCCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTATCGTCC	GCGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCCG
401	CGCAAAATTT	GGGCTTTGTC	AACCAAGGGA	CGGCACACGT	CAAAATCGAA
451	CAAATCGTCC	CGGGCCAATC	CGCACCGGTT	GCCGAAAACA	AAGACATCTT
501	TATCGACTTG	AAATCTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAACTTTC	GCCGTTTCGT	CATCGGGTAC	GAACCTCTCG
601	GTTGAAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTACCTC
651	GCAGGAACGC	GCCGCCGAAG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTGAC	CGCCGGCTGA			

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

1	<u>LTLTRKTLFL</u>	<u>LTAAFGTHSL</u>	<u>QTASADAVVK</u>	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGF	FHGRKTSGGE	RYDMNAFTA	HKTLPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAAQKLGFV	NQGTAVHKIE
151	QIVPGQSAPV	AENKIDIFIDL	KSFGEHEAQ	AYLNQAAQNF	AVSSSGTNLS
201	VEKKRYEYV	KMGPFSQER	AAEAEQAARG	MVRAVLTA*	

608

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTS GGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHGRKTS GGDYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAAQKLGFVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFGEHEAQ					
g264	FHGNRIIDVSKAAAQKLGFVSQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFGEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAEAQARGMVR AVLTAGX					
g264	AYLNQAAQNFAASSSSPNLSVEKRRYEYVVKMGPF ASQERAAEAEAQARGMVR AVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCCGAAAAAC	CCTTTTCCTC	CTCACC GCG	CATTCCGCAT
51	ACATTCC TTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAGG	GCAGAAAAAC
101	TGCACGCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGA	ACGCTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTCACGCAA	ACCGGCAACG	CCTCGTGGTA
201	CGGCGGCAGG	TTCACGGGC	GCAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCATCGTCC	GCGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCCG
401	CGCAAAAATT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAAATCGTCC	CGGGCCAATC	CGCACC GGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTGCCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTAAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTAAFGIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTS GGE	RYDMNAFTA	AHKTLPISYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAAQKLGFV	NQGT AHVKIE
151	QIVPGQSAPV	AENKDIFIDL	KSFGTEHEAQ	AYLNQAAQNL	ASSASNP NLS
201	VEKRRYEYVV	KMGPFASQER	AAEAEAQARG	MVRAVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

609

	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAAQKLGFVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
a264	FHGNRIIDVSKAAAQKLGFVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRREYEVVKMGPFTSQERAAEAEQAQGMVRAVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRREYEVVKMGPFASQERAAEAEQAQGMVRAVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265 . seq
  1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
 51  GCGCGGCTG ATGATTTTGT CTTGTTTGTT GTGTTGGTGT GCGGCGTGTC
101  CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151  ATGCTCAGCA GTGCGGTTGC GCGCGAGGTC AAGAGAAGGT GTTTGATGTT
201  CATAT .TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251  AGGTATCAAA TAACCGTCAG CCGCGCGTCA ATACCGCCCG AACCATACCG
301  CGCGCCTGAG CTTCGGCTTC GCGCGCGCGT TCCTGCGAGG TAAACGGTCC
351  CATTTTGACG ACGTATTCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265 . pep
  1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
 51  MLSSAVAAEV KRRCLMFI XF AFVNRGLENV DINKVSNRQ PAVNTARTIP
101  RAXASASAAR SCEVNGPILT TYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGAEMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFAFVNRGLENVDINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

```
a265.seq
1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTGCGCTTG
51  GGC GCGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... . . . . . GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACGCGCG
301 GCCTGAGCTT CGGCCTCGGC GCGCGGTTCC TGCAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

```
a265.pep
1   MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKAGHQP AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*
```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANAFAFWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSAVAAEV					
a265	MSVILPPTRANAFAFWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMPISAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFIKFAFVNRLGNVDINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
	: : : : : : : : : : : : : : : : : : : :					
a265	KRRRLKFI---FAPAKYLXCLKDVKAGHQP VNTARTIPRAXASASAARSCEANGPILT					
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

```
g266.seq
1   agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccattcatg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcttc acgaccagac tggtcggcgt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgatc gagctggcgg caggtttcgc gctgaccgcc
201 tctcttgcc acatcctcga atcccgtagc ggagcggtac acaatcaggc
251 ttgggagttt tacgccaccg tcgtctgcct gtacctatt ttcgccttcc
301 cgtgtttcgt gcggcggtat ttttggcaca cgcgcaacag ggaataa
```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

```
g266.pep
1   MQFRRHRRRQ CPNRKPIMTA SMYILLVLAL IFANAPFLT RLFGVAALKR
51  KHFGHHLIEL AAGFALTASL AYILES RAGA VHNQGWEPYA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

```
m266.seq
1   ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGCC
151 rCACTCAAGC GCAAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAGGAT
251 CGGTACACGA TCAGGGTTGG GAGTTTATG CCACAGTCGT CTGCCTGTAC
301 CTGATTTTGG CGTTTCCATG TTTTGTGTGG CCGTATTTT GGCACACGCG
351 CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||
g266      MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
          10      20      30      40      50

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          :|||
g266      LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVR RYFWHTRNREX
          60      70      80      90      100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCCT
101  TGATTTTTGC CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTG CGTTCCCTG TTTCTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKLGIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          :|||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          70      80      90      100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

```
g267.seq
```


612

```

1   atgcaagtcg ccttttttct cgccgtggta ttcaaaaata tgggtttcca
51  caatcgcatc ggtcgggcag gcctcttcgc agaaaccgca gaagatgcac
101 ttggtcaggt cgatgtcgta acgcttgggtg cggcgggtgc cgtcttcgcg
151 ttcttccgat tcgatgttga tcgccattgc cggacacacc gcctcgaca
201 atttacacgc gatgcagcgt tcctctccgt tcggaaaacg gcgttgcgcg
251 tgcagaccgc ggaaacgcac ggattgcggc gttttctctt cgggaaaata
301 aattgtgtct ttgcgggcaa aaaagttttt gagcgttacg cccatgcctt
351 tgaccagttc gccaaagcaga aaggttttta ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1076; ORF 267.ng>:

g267.pep

```

1   MQVAFFLAVV FKNMGFHNRI GRAGLFAETA EDALGQVDVV TLGAAGAVFA
51  FFRFDVDRHC RTHRLAQFTR DAAFLSVRKT ALRVQTAETH GLRRFLFGKI
101 NCVFAGKKVF ERYAHAFDQF AKQKGFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1077>:

m267.seq

```

1   GTGCAAGTCG CCTTTTTTCT CGCCGTGGTA TTCAAAAATA TGGGTTTCCA
51  CAATCGCATC AGTCGGGCAT GCCTCTTCGC AGAAACCGCA GAAGATGCAC
101 TTGgtCAGGT CGATGTCGTA ACGCTTGGTG CGGCGCGTAC CGTCTTCACG
151 TTCTCCGAT TCGATGTTAA TCGCCATTGC CGGACACACT GCCTCACACA
201 ACTTACACGC GATACACCGC TCTTCGCCGT TCGGATACCG CcGCTGCGCG
251 TGCAGACCGC GGAAACGCAC GGATTGCGGC GTTTTCTCTT CGGGGAAATA
301 AATTGTGTCT TTGCGGGCGA AAAAGTTTTT GAGCGTTACG CCCATACCTT
351 TTACCAATTC GCCAAGCAGA AAGGTTTTTA CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1078; ORF 267>:

m267.pep

```

1   VQVAFFLAVV FKNMGFHNRI SRACLFAETA EDALGQVDVV TLGAARTVFT
51  FFRFDVNRHC RTHCLTQLTR DTPLFAVRIP PLRVQTAETH GLRRFLFGEI
101 NCVFAGEKVF ERYAHTFYQF AKQKGFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 267 shows 82.7% identity over a 127 aa overlap with a predicted ORF (ORF 267.ng) from *N. gonorrhoeae*:

m267/g267

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI SRACLFAETAEDALGQVDVVTLGAARTVFTFFRFDVNRHC					
	: : : : : : : : : :					
g267	MQVAFFLAVVFKNMGFHNRI GRAGLFAETAEDALGQVDVVTLGAAGAVFAFFRFDVDRHC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPLFAVRIPPLRVQTAETHGLRRFLFGEINCVFAGEKVFERYAHTFYQF					
	: :					
g267	RTHRLAQFTRDAAFLSVRKTALRVQTAETHGLRRFLFGKINCVFAGKKVFERYAHAFDQF					
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
g267	AKQKGFYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1079>:

a267.seq

```

1   GTGCAAGTCG CCTTTTTTCT CGCCGTGGTA TTCAAAAATA TGGGTTTCCA
51  CAATCGCATC GGTcgggcag GCTTCTTCGC AGAAACCGCA GAAGATGCAC
101 TTGgtCAGGT CGATGTCGTA ACGCTTGGTG CGGCGCGTGC CGTCTTCGCG
151 TTCTCCGAT TCGATGTTGA TCGCCATTGC GGGGCAAACG GCTTCACACA
201 ATTTACACGC GATGCAGCGT TCCTCGCCGT TTGGATAACG GCGTTGCGCG
251 TGCAGACCGC GGAAACGCAC GGATTGCGGC GTTTTCTCTT CGGGAAAATA
301 AATCGTGTCT TTGCGGGCAA AAAAGTTTTT GAGCGTTACG CCCATACCTT
351 TTACCAATTC GCCAAGCAGA AAGGTTTTTA CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLF	FAETAEDALGQVDVV	TLGAARTV	FTFFRFDV	NRHC
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFA	FFRFDVDRHC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTP	FAVRIPPLRVQ	TAETHGLRRFL	FGEINCVFAGEK	VFERYAHTFYQF	
a267	GANGFTQFTRDAA	FLAVWITALRVQ	TAETHGLRRFL	FGKINRVFAGKKV	FERYAHTFYQF	
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaatTT
101 cctgcggaag cgaagagact aaagagattt tgggtcaaact ggtccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atgggtcgaac
251 gtttggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgcagca
351 tggtgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaaagccc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaaagcaa
501 aatctttgccc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctgggtgtc tatggcactg attaaagagc cgttggacaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgaggga
651 ggcagaagaa gcggcggcgc aggaggcatt ggggtcgggag caggaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctgcgagaaa acatggaaaa gcggtatgga caagatctgt gccacaatg
851 cgaaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGINPPFSG KEISCGSEET KEILVKLVRD
51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101 SSKLKCEAAL KLDVPDDVD YAVAANQSIG NSHKKTPDF EPYRKEGAY
151 YVKTISYSVQ PTDDSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAAEA TAQAREAE EAAAQALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLQASQK TWKSGMDKIC ANNAKAEGT PNGIKVSELA
301 CKTAETEARL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGGACAAA GTGAAACAAA GGAACGAAGA
```

614

```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTGCGCG
151  AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACCh TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301  GAACTGGCAT GCAAAACGGC GAAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   .MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAARVS EWEERYKLSR
51  XQFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEAAE-----
                                |||:|||:|||:|||:|||:|||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
          160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  --EAAAQEALGREQEAARVSEWEERYKLSRSQFEQFWKGLPQTQVQNKLPQSQKTWKSMD
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      AEEAAAQEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTQVQNKLQASQKTWKSMD
          220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      KICANNAKAEGETPNNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

a268.seq

```

1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTGCGCG
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

a268.pep

```

1   MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTQVQNKLQA SQKTWKSMD KICANNAKAE GETPNNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEEAAAQEALGREQEAARVSEWEERYKLSRXQFEQFWKGL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a268      MALIKEPLDKAKQRNEELEAAEEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

615

	10	20	30	40	50	60
	70	80	90	100	110	120
m268.pep	PQTVQNKLQPSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
	: : : : :					
a268	PQTVQNKLQASQKTWKSMDKICANNAKAEGETPNGIKFSELACKTAETEARLEELHNRK					
	70	80	90	100	110	120
	130	140				
m268.pep	KALIDEMXREADKKELSKRLX					
	:					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAAGCCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAGCC CTTATCGACG AATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHK FKHICSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLQASQ KTWKSMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

		10	20	30	
m268-1.pep		VQSRDGLHKFKHICSAAMALIKEPLDKVKQRNE			
		: : :: :			
g268	KEGAYVVKTISYSVQPTDDKSKIFAELSQAHDIIHPLSELVS--MALIKEPLDKAKQRNE				
	150 160 170 180 190 200				
	40 50 60 70 80				
m268-1.pep	ELEAAE-----EAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	:				
g268	KLEAAEATAQEAREAEAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	210 220 230 240 250 260				
	90 100 110 120 130 140				
m268-1.pep	KLQASQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE				
	: : : : :				
g268	KLQASQKTWKSMDKICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDE				
	270 280 290 300 310 320				
	150 159				
m268-1.pep	MAREADKKELSKRLX				
	:				
g268	MVREEDKKELPKRLX				
	330				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAAGCCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```

616

401 TGCACAACCG TAAAAAGCC CTTCTCGACG AAATGGCCAG GGAAGCGGAC
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep

1 VQSRDGLHK FKHICSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR
 51 EQEVDVSEW EERYKLSRSE FEQFWKGLPQ TVQNKQASQ KTWKSGMDKI
 101 CANNAKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LLEDEMAREAD
 151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHICSAAMALIKEPLDKAKQRNEELEAAE	EAEEAAAEALGREQ	EQEVDVSEW			
m268-1	VQSRDGLHKFKHICSAAMALIKEPLDKVQRNEELEAAE	EAEEAAAEALGREQ	EAARVSEW			
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKQASQKTWKSMDKICANNAKAEGE	TPNGIKFSEL				
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKQASQKTWKSMDKICANNAKAEGK	TPNGIKFSEL				
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAKTEARLEELHNRKKALLDEMAREADKKELSKRLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq

1 atggttttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgct
 51 cagcccttgg atttgggcgg tgggtgtgggt gtggtcgcgg tcggcttttt
 101 cctgcaaac ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttggcg
 151 gtttcgccgt gggactttat ccggaacacg gtttcgccca aggtgtcggc
 201 ggctttgatg cacagtttta aaaccagggc tttggggcgg tttctgcgc
 251 cgcccggttg cattttgctg tccaatcgcg gggttaaaaa accgttgcg
 301 ttaagtgcg cgtccgtcca agtcgatacg agcgcgcttc tttgccttcc
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep

1 MWVRVNCAAT AALIFSSSPW IWAVVWWSR SAFSCKPCAS LDASSAPALA
 51 VSPWDFIRNT ASPKVSALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS
 101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq

1 ATGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
 51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTTGT
 101 CTTGCAAAACC TTGCGCcaCG TGCCCGCGTC CAGCGCCTGC GTTGATGTT
 151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTCGGCGGC
 201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC
 251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCGTTT
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGTTCTCT GCCTTTCGTT
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep

1 MWVRVNCAAT AVLIFSSSPW IWAIVWWSR SALSCKPCAT CPRPAPALMV
 51 SPWDFIQNTA SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
 101 KFSSVQVDT SALLCLSLRS *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269 . pep      MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT      59
                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269            MVWRVNCAATAALIFSSSPWIWAVVWVWSRSASFCKPCASLDASSAPALAVSPWDFIRNT      60

m269 . pep      ASPKVS AALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT SALLCLSLRS      119
                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269            ASPKVS AALMHSFKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDT SALLCLSLRS      120

m269 . pep      SX      121
                ||
g269            SX      122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269 . seq
1   ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51  CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCGCGCGT CCAGCGCGCC GCGGTTGACG
151 GTTTCGCGGT GGGACTTTAT CCAGAACACG GCTTCGCCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGGCGG TTTTCGTCGC
251 CGCCTGTGCG CATTGTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTCTG
301 TTTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269 . pep
1   MVWRVNCAAT AVLIFSSSPW IWAAVWVWAR SALSWRFCAS VPASSAPALT
51  VSPWDFIQNT ASPKVS AALM HSFKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

                10      20      30      40      50      59
m269 . pep      MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a269            MVWRVNCAATAVLIFSSSPWIWAAVWVWARSALSWRFCASVPASSAPALTVSPWDFIQNT
                10      20      30      40      50      60

                60      70      80      90      100     110     119
m269 . pep      ASPKVS AALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT SALLCLSLRS
                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a269            ASPKVS AALMHSFKTRALGRFSSPPVAILLSGRGVKKPLSFKFSSVQVDT SALLCLSLWS
                70      80      90      100     110     120

m269 . pep      SX      120
                ||
a269            SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270 . seq
1   atgaataaaa accgcaaatt actgcttgcc gcactgctgc tgactgcctt
51  tgccgccttc aagctcgttt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg agggttgcac gctgccggac
151 ggaagccgtg tccgcgcccgc cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccgc ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcata cgctgcccgc tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgcccga taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

g270.pep

```

1  MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTTGCAATG GTGGCAGGCG Ca. CAGCCGC
101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTC
401 AGACGGCATT TACCGCCGAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep

```

1  MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
g270	MNKNRKLLLAALLLTAFAAFCLVLLQWWQAQQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARIRLPVCVEGRR					
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTTGCAATG GTGGCAGGCG CAGCAGCCGC
101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTC
401 AGACGGCATT TACCGCCGAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep

```

1  MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
```

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRLLLLAALLLIAFAAVKLVLQWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAS					
a270	MNKNRLLLLAALLLIAFAAVKLVLQWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
a270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAE					
a270	DFTADITIGSRTFQTAFTAE					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

1	atgttcagtt	cgcgatggc	gaggatttgg	gcgacggggg	taacgtttgtg
51	tatggtcagt	ccgtgtccgg	cgttgacgac	caagcccaaa	tcgccggcga
101	aatgcgcgcc	gttttgatg	cgctcgaaact	gcctgatttg	ttcggcggtg
151	ctttgtgcgt	cgccatatgc	gccggtgtgc	agctcgacaa	cgggcgcgcc
201	gacatcacgg	gcggcttga	tttgccgtgc	gtcggcatcg	ataaacaagg
251	acacgcgat	gcccgcgtcg	gtcaggattt	tggcgaattc	ggcgattttt
301	tcctgttgcg	ccaatacgtc	caaaccgcct	tcggtcgtga	tttcctgccc
351	tttttcaggc	acgatgcaca	cgtcttccgg	catcacttta	agcgcgtttt
401	cgagcatttc	ttccgtcaac	gccatttcaa	ggttcaggcg	cgtgcggatg
451	gcgtttttga	cgccaaatac	atccgcgtct	ttgatgtggc	ggcggtcttc
501	gcgcaggtgc	atggtaatca	ggtctgcacc	gtgcgtttcg	gcaaccagtg
551	ccgcctccac	ggggctggga	taa		

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

1	MFSSRMARIW	ATGVTLCMVS	PCPALTTKPK	SPAKCAPFWM	RSNCLICSAW
51	LCASAYAPVC	SSTTGAPTSR	AAWICLSSAS	INKDTRMPAS	VRILANSAIF
101	SCCANTSKPP	SVVISCRFSG	TMHTSSGITL	SAFSSISSVN	AISRFRVRM
151	AFLTANTSAS	LMWRRSSRRC	MVIRSAPCVS	ATSAASTGLG*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

1	AwGTTCAgTT	CGCGGATGGC	GAGGATTtGG	GCGATGGGGG	TAACGTTGTG
51	TATGGTCAGT	CCGTGTCCGG	CGTTGACGAC	CAAGCCCAAA	TCGCCGGCGA
101	AATGCGCGCC	GTTTTGGATG	CGCTCGAACT	GCCTGATTtG	TTCCGGCGTG
151	CTGCGCGCGT	CGGCATACGC	GCCTGTGTGC	AGCTCGACAA	CGGGCGCGCC
201	GACATCACGG	GCGGCTTGA	TTTGCCTGTC	GTCGGCATCG	ATAAACAAAG
251	ACACGCGTAT	GCCTGCGTCG	GTCAGGATTt	TGGTGAACCC	GGCGATTtTT
301	TCCTGTTGCG	CCAATACGTC	CAAACCGCCT	TCGGTCGTGA	TTTCCTGACG
351	TTTTTCAGGC	ACGATGCACA	CGTCTTCCGG	CATCACTtTC	AAAGCGTTtT
401	CCAACATTTC	TTCCGTCAAC	GCCATTtCAA	GGTTcAGGCG	CGTGCGGATG
451	GCGTTTTTGA	CGGCAACAC	GTCCGCGTCT	TTGATGTGGC	GGCGGTCTTC
501	GCGCAGGTGC	ATGGTAATCA	AATCCGCACC	GTGCGTTTCG	GCAACCAGTG
551	CCGCCTCCAC	GGGGCTGGGA	TAA		

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

1	XFSSRMARIW	AMGVTLCMVS	PCPALTTKPK	SPAKCAPFWM	RSNCLICSAW
51	LRASAYAPVC	SSTTGAPTSR	AAWICLSSAS	INKDTRMPAS	VRILVNPAIF
101	SCCANTSKPP	SVVISXRFSG	TMHTSSGITF	KAFSNISSVN	AISRFRVRM
151	AFLTANTSAS	LMWRRSSRRC	MVIKSAPCVS	ATSAASTGLG *	

Computer analysis of this amino acid sequence gave the following results:

620

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLCASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSAIFSCCANTSKPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITLFAFSNISVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAAPCVS					
g271	TMHTSSGITLSAFSSISVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

1	ATGTT	CAGTT	CGCGG	ATGGC	GAGGA	TTTGG	GCGAT	GGGGG	TAACG	TTGTG
51	TATGG	TCACT	CCGTG	TCCGG	CGTTG	ACGAC	CAAGC	CCCAA	TCGCT	GGCAA
101	AATGC	GCGCC	GTTTG	GATG	CGCTC	GAACT	GCCTG	ATTG	TTCGG	CGTGG
151	CTGCG	CGCGT	CGGCAT	ACGC	GCCTG	TGTC	AGCTC	GACAA	CGGGC	CGGCC
201	GACAT	CACGG	GCGGCT	TGGA	TTTGC	CTGTC	GTCGG	CATCG	ATAAA	CAAGG
251	ACACG	CGTAT	GCCCG	CGTCG	GTCAG	GATTT	TGGTG	AATTC	GGCAAT	TTTG
301	TCTTG	TTGCG	CCAAT	ACGTC	CAAGC	CGCCT	TCGGT	CGTGA	TTTCT	GACG
351	TTTTT	CCGGC	ACGAT	GCACA	CGTCT	TCCGG	CATCA	CTTTA	AGCGC	GTTTT
401	CGAGC	ATTTC	TTCCG	TCAAC	GCCAT	TTCAA	GGTTC	AGGCG	CGTGC	GCGATG
451	GCGTT	TTTTGA	CAGCAA	ACAC	GTCCG	CGTCT	TTGAT	GTGGC	GGCGG	TCTTC
501	GCGCA	GGTGC	ATGGTA	ATCA	GGTCG	GCACC	GTGCG	TTTCG	GCAAC	CAGTG
551	CCGCT	CCAC	GGGCT	TGGGA	TAA					

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

1	MFSSRMARIW	AMGVTL	CMVS	PCPAL	TTKPK	SLAKCAP	FWM	RSNCLICSAW
51	LRASAYAPVC	SSTTGAPT	SR	AAWICL	SSAS	INKDTRMP	PAS	VRILVNSAIL
101	SCCANTSKPP	SVVIS*	RFSG	TMHTSSGITL	SAFSSIS	SVN	AISRFRVRM	
151	AFLTANTSAS	LMWRRSS	RRRC	MVIRSA	PCVS	ATSAASTGLG	*	

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTSKPPSVVISXRFSG					

621

	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVKSAPCVS					
a271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1  atgactgcaa aggaagaact gttcgcgatg ctgcgccata tgaacaaaaa
51  caaagggttcc gacctgtttg tgacgaccca tttcccgcgcc gctatgaagc
101 tggacggcaa aatcacccgc atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgcacc aacgagtgca atttcgccat cagcctgccg gacaccagcc
251 gcttcgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccctgaag gatgttgccg tgaaaaaacg cgggctggtt atttttgtcg
401 gcggcaccgg ctcgggcaaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaag atccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgc gaggtcggcg
551 tggacacgga aaactggatg gcggcggtga aaaatacgct gcgtcaggcg
601 ccggatgtga tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctcgaccgca tcatcaactt cttccccgag
751 gagcggcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatttcgcaa cgctcggtc cgcgagacgg cggcaaggcg aggggtggcg
851 cagtgcaggt gctgctcaat tcgcccctga tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgctg
1051 ttggcggtac agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1  MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RAITSKIPKF ESLNLPALK DVALKKRGLV IFVGGTGSBK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMDT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAWCCAAAA
51  CAAAGGTTCG GACCTGTTTCG TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GCGGAAAAAA
151 TGTATGGAAA TCgccttttc GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAaaaaacg CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG

```

622

```

551 TGGATACGGA AAACCTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATTG GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCAAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTGA TTTGGAGTT GATTCAACA
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAaAGTTyCA GCCCCGATT
1101 GGnACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272.pep

```

1  MTAKEELFAW LRHMxQNKGs DLFVTTTFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAM IORGATALVF
101 RTITSKIPKF ESLNLPVLK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAlA FAETGHLcMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLyQLYE KGDISLQEAL KNADSAHDLR
351 LAVQLRSRRA QSXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272.pep	10	20	30	40	50	60
	MTAKEELFAWLRHMxQNKGsDLFVTTTFPPAMKLDGKITRITDEPLTAEK					
g272	MTAKEELFAWLRHMxQNKGsDLFVTTTFPPAMKLDGKITRITDEPLTAEK					
m272.pep	70	80	90	100	110	120
	AKQAEFSSTNECNFAISLPDTSRFRVNAMIORGATALVFRTITSKIPKFESLNLPPVLK					
g272	AKQAEFSSTNECNFAISLPDTSRFRVNAMIORGATALVFRAITSKIPKFESLNLPPALK					
m272.pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
m272.pep	190	200	210	220	230	240
	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAlAFAETGHLcMATLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAlAFAETGHLcMATLHANSTNQA					
m272.pep	250	260	270	280	290	300
	LDRIINFFPEERREQLLTDLSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
g272	LDRIINFFPEERREQLLTDLSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
m272.pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMQTFDQHLyQLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMQTFDQHLyQLYEKGDISLQDALKNADSAHDLRLAVQLRSRRA					

623

```

          370
m272.pep  QXSPDLXLLX
          || :||| |||
g272      QSSDPDLELLX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1   ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCG TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GCGGAAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTTCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AAAGTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTTC TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCCCTTGA GGATGCCTTG AAAAAATGCC ATTCCGCACA CGATTGTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATTT
1101 GGAAGTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1   MTAKEELFAW LRHMNKNKGS DLFVTTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RAITSKIPKF ESLNLPVLK DVALKKRGLV IFVGGTGSGK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLVQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272.pep  MTAKEELFAWLRHMXQNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEKCM EIAFSIMS
          ||||| :|||||
a272      MTAKEELFAWLRHMNKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEKCM EIAFSIMS
          10      20      30      40      50      60

          70      80      90      100     110     120
m272.pep  AKQAEFFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRITITSKIPKFESLNLPVLK
          ||||| :|||||
a272      AKQAEFFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRAITSKIPKFESLNLPVLK
          70      80      90      100     110     120

          130     140     150     160     170     180
m272.pep  DVALKKRGLVIFVGGTGSGKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          ||||| :|||||
a272      DVALKKRGLVIFVGGTGSGKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          130     140     150     160     170     180

```

624

	190	200	210	220	230	240
m272 . pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272						
	190	200	210	220	230	240
	250	260	270	280	290	300
m272 . pep	LDRIINFFPEERREQLLDLSLNQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272						
	250	260	270	280	290	300
	310	320	330	340	350	360
m272 . pep	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G D I S L Q E A L K N A D S A H D L R L A V Q L R S R R A					
a272						
	310	320	330	340	350	360
	370					
m272 . pep	Q S X S P D L X L L X					
	:					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

g273 . seq

```

1  atgagtccttc aggcgggtatt tatatacccc ccaagccgta ccgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcaccg tttccctgcc gttcttgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcggca gccgcgccc acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcgcc gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcgggcgc gtgccgctga aatcaaggcg
351 gtttgagaag tgttccnacc gcgcccgcc tatgtgccga aatattatct
401 tgcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttcacgt
451 tgcccaattg ttcatacgg cgtttgccg cttttgttt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

g273 . pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ QSGKHTDRR QDIGVFEAGT
51  PFTVFLPFLV AFEIKDDAGK QRGSRARWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRFEK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

m273 . seq

```

1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCCG TTTTCCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGCAAG CAGCGCGGCA GCCGCGCCG ACATTAGCAT TGTGTTCATT
251 GTTGTTCTCTT AATGCTTAAA AACC CGCCTG TCCGTGCAAC CGTTTAAAGG
301 CGGCAAATTG CAAAATTGT TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTTCCCGAC GCGCCGCCCT GTGTGCCGGA GTTATTGTGTC
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACCTGTTT CATACGGCGT TTACCTGCCT TTTGTkTwTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

m273 . pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ QSGKHADRC QDIGVFKAGT
51  PFPVFLPLL V AFEIKDDAGK QRGSRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY A*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRCQDIGVFKAGTPFPVFLPLL					
	: : :					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHTDRRQDIGVFEAGTPFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFE					
	: : :					
g273	AFEIKDDAGKQGRSRARHWHCVHCCSLTVKNPPGRATVLRREIAKFVCGRVPLKSRRFEK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSRRA-ALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVYLPFVXQAVFSYAX					
	: : :					
g273	CFXRARPMCRNIICRSPAKSPRTRFAEFPRCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

1	ATGAGTCTTC	AGGCGGTATT	TGTATACCCC	CCAAGCCGTA	CCGCACAATA
51	CAACGAAAAT	CAGGAAAACG	GCGGTAAAGC	TCATAAACAG	GGACAAAGCG
101	GCAAACACGC	CGACCGCCGT	CAGGATATAG	GCGTATTCCA	GACCGGAAC
151	CCATTACCG	TTTTCCTGCC	GCTTTTGTG	GCTTTTGAAA	TAAAGGATGA
201	TGCCGGCAAG	CAGCGCGGCA	GCCGCGCCCG	ACATTAGCAT	AATGTTTCATT
251	GTTGTTCTT	AACGGTTAAA	AACCCGCCCG	TCCGTGCAAC	CGTTTTTAAG
301	AGGCGGTAAG	TCACAAAGTT	TGTTGGCGGA	CGTGCTCTCT	TACAATCAGG
351	GCGGTTTAAG	GGGCATGATG	CACTGCCCCG	TGTGCCGGAT	ATTATTTGTC
401	GCTCACCTGC	AAAATTGCCA	AGAACGCGCT	TTGCGGGATT	TCCACATTGC
451	CCACTTGTTT	CATACGGCGT	TTGCCTGCTT	TTTGTTTTTC	AAGCAGTTTT
501	TTCTTACGCG	TAA			

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

1	MSLQAVFVYP	PSRTAQYNEN	QENGGAHKQ	GQSGKHADRR	QDIGVFQTGT
51	PFTVFLPLFV	AFEIKDDAGK	QGRSRARH*	NVHCCSLTVK	NPPVRATVEK
101	RR*ITKFVGG	RALLQSGRFK	GHDALPRVPD	IICRSPAKLP	RTRFAGFPHC
151	PLVSYGVCLL	FVFQAVFSYA	*		

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRCQDIGVFKAGTPFPVFLPLL					
	: : :					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQGGSGKHADRRQDIGVFQTGTPFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFE					
	: : :					
a273	AFEIKDDAGKQGRSRARHXHNVHCCSLTVKNPPVRATVFKRRXITKFVGGALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRAALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVYLPFVXQAVFSYAX					
	: :					
a273	GHDALPRV-PDIICRSPAKLPRTFRAGFPHCPLVSYGVCLLFVFQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

```
g274.seq
  1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTGT
 51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101  GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151  CATATCGGGG TGCAGGTCCT CATTCTCTCC GATATGAATG CGGCAAAAGT
201  GTTTGTCCGgC ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251  TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301  GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTgt tcaaAACCT
351  TCCGCCGGCC AACCCTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401  GGCgCGTCGA GAACAAATGG ATTACCAGCC AGGGCAATGC GGTGATTG
451  ACCCCGATGG ACAAACTTTT CAATAATGCA GGAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

```
g274.pep
  1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
 51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101  GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVVRVENKW ITSQGNVAVL
151  TPMDKLFNNA GSK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

```
m274.seq
  1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
 51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101  GCAAACATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151  CATATCGGGG TGCAGGTTCT CATTCTCCCC GATATGAATG CGGCAAAAGT
201  GTTTGTCCGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251  TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301  GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAAACCCT
351  TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401  GCGCGCTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTG
451  ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

```
m274.pep
  1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
 51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101  GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVVRVENKW ITSQGNVAVL
151  TPMDKLFNNT ESK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

```
g274/m274

      10      20      30      40      50      60
g274.pep  MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP
          |||
m274      MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP
          |||

      10      20      30      40      50      60
g274.pep  DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA
          |||
m274      DMNAAKVFGVGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT
          |||

      70      80      90     100     110     120
g274.pep  NHWYVRVEDAAGVVRVENKWITSQGNVAVLTPMDKLFNNAGSKX
          |||
m274      NHWYVRVEDAAGVVRVENKWITSQGNVAVLTPMDKLFNNNTESKX
          |||

      130     140     150     160
g274.pep  NHWYVRVEDAAGVVRVENKWITSQGNVAVLTPMDKLFNNAGSKX
          |||
m274      NHWYVRVEDAAGVVRVENKWITSQGNVAVLTPMDKLFNNNTESKX
          |||
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCCCC GATATGAATG CGGCAAAAGT
201 GTTGTGTCGGC GCGCAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAACCCT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTGT
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1  MAGPIFVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
a274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFGVGEFDGKQPLNLLMHPTKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
a274	DMNAAKVFGVGEFDGKQPLNLLMHPTKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFGVGEFDGKQPLNLLMHPTKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
a274	DMNAAKVFGVGEFDGKQPLNLLMHPTKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		
m274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1  atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tgggcgacga tgatgccggt gcggttttcc atcaggcgtt
101 cgagcgcttg ttggacgagg cgttcgatt cgttgtccaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgctct ttcaaatgg cgcgggcgat
201 ggcgacgcgt tgcgctgtc cgccggataa gttgctgccg ttcgatccga
251 tgggctggtg cagtccgagc ggggatgcgt cgatcaggct ttgcaggttg
301 gcggttgga gggcgacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcggagc ttttcaaaca ggggtgtcgtc aaacaggaat acgtcttggtg
401 agacgagggc gaattggcg cgaggcagt cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccgca gacggttcga caaagcggg
501 cagaagggtg acgacggtg atttgccgct gccggaacgt ccgaccaggg
551 cgagcgcttc gccttgctg atgtcgaggt tgaagttgtc gagggctttg
601 atgctgctg aacggtatt gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcggcgca gcgtgcctt gtcctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcgcgca ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct tttgatggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

m276.seq

1	ATGATTTTGC	CGTCGTCCAT	CACGATGATG	CGGTCGGCCC	CTTCGATGGT
51	GGTCAGGCGG	TGGGCGACGA	TGATGCCGGT	GCGGTTTTCC	ATCAGGCGTT
101	CGAGCGCCTG	TTGGACGAGG	CGTTCGGATT	CGTTGTCTAA	TGCGCTTGGT
151	GCTTCGTCCA	ATAATAATAT	CGGCGCGCTT	TTCAAAATGG	CGCGGGCAAT
201	GGTCAGCGGT	TGCCGTGTCT	GCGCCGATAA	GTTGTCTGCC	TTCCGATCCGA
251	TGGGCTTGGT	CAGTCCGAGC	GGGGAGCTGT	CAATCAGGCT	TTGCAGGTTG
301	GCGGTTTGGG	GGGCGAACAG	GACTTCGGCT	TCGCCC CGGT	CGGGACGGCT
351	GTATCGGACG	TTTTCAAACA	GGGTGTCGTC	AAACAGGAAT	ACGTCTTGGG
401	AGACGAGGGC	GAATTGGGGC	CGCAGGCGAT	CGAGTTTGAT	GTCCGCCGAT
451	TCGATACCGT	CTATGCAGAT	GTTGCCGGCA	GACGGTTCGA	CAAGCGGGGG
501	CAGCAGGTTG	ACGACGGTGG	ATTTGCCGCT	GCCGGAACGT	CCGACCAGGG
551	CGACGCGTTC	GCCTTGTCTG	ATGTCGAGGT	TGAAGTTGTC	GAGGGCTTTG
601	ATGCCGTCTG	AACGGTATTC	GACATCGACG	TTGCGGAAGC	TGATGCGCCC
651	TTCGACACGC	TGCGGTGCGA	GCGTGCCCTT	GTCTGTTCG	GGCGGGGTGT
701	CGAGAAATGC	ACATACACCG	TCGGCGGCGA	GGAACATCGT	CTGCATAGGG
751	ATGCTGATGT	TGGCAAGGCT	TTTGATGGGG	GCGTACATT	GCAGCATCGC
801	GACGATGAAT	GCCATAAAAT	CGCCGATGGT	GGTGTAG	

m276 . pep

1	MILPSSITMM	RSAPSMVVR	WATMPVRF	IRRSSACWTR	RSDSLSNALV
51	ASSNNNIGAS	FKMARAMATR	CRCPPDKLLP	FDPMGWCSPS	GELSIRLCRL
101	AVWRANRTSA	SPASGLYRT	FSNRVSSNRN	TSWETRANWA	RRQSSILMSAM
151	SIPSMQMLPA	DGSTKRGSR	TTVDLPLPER	PTRATRSPCL	MSRLKLSRAL
201	MPSERYSTST	LRKLMRPST	CASVPSPSCS	GGVSRNAHTP	SAARNIVCIG
251	MLMLARLLMG	AYICSITATMN	AINSPMVV*		

Homology with a predicted ORF from *N.gonorrhoeae*

m276/q276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRRWATMMPVRF	SIRSSACWTRRSDSLSNALVASSNNNIGAS				
g276	MILPPSMTMMRSADSTVVRRWATMMPVRF	SIRSSACWTRRSDSLSNALVASSNNNIGAS				
	10	20	30	40	50	60
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCS	PSGELSIRLCRLAVWRANRTSASPASGR	LYRT			
g276	FKMARAMATRCRCPPDKLLPFDPMGWCS	PSGDASIRLCRLAAWRADRTSASPASGR	LYRT			
	70	80	90	100	110	120
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLS	AMSIPSMQMLPADGSTKGRSRLTTVDL	PLPER			
g276	FSNRVSSNRNTSWETRANWARRQSSLS	AMSIPSMQMLPADGSTKGRRLTTVDL	PLPER			
	130	140	150	160	170	180
m276.pep	PTRATRSPCLMSRLKLSRALMPSE	RYSTSLRKLMPSTRCGASVPLSCSGG	VSRNAHTP			
g276	PTRATRSPCLMSRLKLSRALMPSE	RYSTSLRKLMPSTRCGASVPLSCSGG	VSRNAHTP			
	190	200	210	220	230	240

629

	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIA TMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIA TMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```
a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTGCTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGGTGCGA GCGTGCCTTT GTCCTGTTCT GGCGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATTG GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```
a276.pep
1  MILPSSITMM RSAPSMVVRW WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGSR LTTVDLPLPER PTRATRSPLC MSRLKPSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIA TMNAINSPMVV*
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSI RLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSI RLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSI PSMQMLPADGSTKRGSR LTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSI PSMQMLPADGSTKRGSR LTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPLCMSRLKLSRALMPSERYSTSLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPLCMSRLKPSRALMPSERYSTSLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIA TMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIA TMNAINSPMVVX					

630

250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
  1  ..atggtacacg tcgccgtagc ttacgggtatt gccgtccggc gtttttgcgc
 51  aaacgagggtc atagacgttt tccacgcctt gcaggtagat cgccaagcgt
101  tcgatgccgt aggtaatctt gccgagtagc ggcgtgcaat cgataccgcc
151  gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201  cttcccagcc caaacccac gcaccgaggg tgggggtttc ccagtcgtct
251  tcgacaaagc ggatgtcgtg gactttggga tcgatgcca attcgcgcag
301  ggagtcgaga tagaggtctt ggatattggc gggggcgggt ttgagggcga
351  cttggaattg gtaatagtgt tgcaggcggg tgggggtgtc gccgtagcgg
401  ccgtctttgg ggcggcggct ggggttgacg taggcggcaa accaaggctc
451  gggggccgagc gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
501  cttccatgtc gaagggttg atgacgggtc agcctttgtc tgcccagaag
551  gtttgcagtt tgaagatgat ttggttgaag gtaagcatgg cttattgttc
601  gataaaataa aggttttatt ttactgtttc catagccgct tgaatagatt
651  tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
  1  ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
 51  DLLEIGKLG Y FHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101  GVEIEVL D I G G G F E G D L E L V I V L Q A V G V V A V A A V F G A A A G L D V G G K P R L
151  GAERAQAGG MGCAGTDFHV EGLDDGA FV CPEGLQFEDD LLEGKHGLLF
201  DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
  1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
 51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101  CGCAGCAGCC AGTCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGCTC
151  GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTGCA
201  GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251  ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301  GTCGATGCCG CCGACTTGTT GGAAATAGGT AAAGTGGGTT ACTTCCATGC
351  CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401  TCCCAGTCGT CTTGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451  CAATTCGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501  GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGACGGCG GTTGGGGTTG
551  TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601  AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651  TGCCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701  TCTGCCCAGA ATGTTTGCA TTTGAAGAT ATTTGTTGGA AGTAAGCAT
751  GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
  1  MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQPVG I AVFEVVGGLL
 51  DFVLVVHVA V GDGVAVERF PNEVVDV F Y T L Q V H R Q A F D A V G D F A E Y G R A
101  VDAADLLEIG KLG Y F H A V E P D F P A Q T P R A E G G V F P V V F D K A D V V D F G I D A
151  QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201  KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251  GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

```
g277.pep                                10          20          30
MVHVAVAYGIAVRRFCPNEVIDVFHALQVH
```

631

```

m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVHVAVGDGVAVERFCPNEVVDVFTLQVH
           30      40      50      60      70      80
g277.pep  RQAFDAVGNFAEYGRAIDTADLLEIGKLGYPHAEVPDFPAQTPRTEGGVFPVVFADKADV
           40      50      60      70      80      90
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAEVPDFPAQTPRAEGGVFPVVFADKADV
           90     100     110     120     130     140
g277.pep  DFGIDAQFAQGVEIEVLDIGGGGFEGLDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPR
           100     110     120     130     140     150
m277      DFGIDAQFAQVVEIEVLDIGGSGLEGLDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPR
           150     160     170     180     190     200
g277.pep  GAERAQAGGGMGCAGTDFHVEGLDDGAAAFVCPPEGLQFEDDLLEGKHGLL
           160     170     180     190     200
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCPPECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1  ATGCCCCGCT TTAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51 TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGTTT
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTGACAAA GCGGATGTCG TGCACTTTGG GGTGATGCC
451 CAATTGCGCG AGGGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DEVLVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVFPVVFAD ADVVHFGVDA
151 QFAQGVEIEV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

m277.pep  10      20      30      40      50      60
MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPVGIAVFEVVGGLLDFVLVHVAV
a277      10      20      30      40      50      60
MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPVGIAVFEVVGGLLDFVLVHVAV

m277.pep  70      80      90      100     110     120
GDGVAVERFCPNEVVDVFTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAEV
a277      70      80      90      100     110     120
SYCITVQRFCPNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP

m277.pep  130     140     150     160     170     180

```

632

```

m277.pep      DFPAQTPRAEGGVFPVVFDDKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQA
a277          DFPAQTPRAEGGVFPVVFDDKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQA
              130      140      150      160      170      180

m277.pep      VGVVAVAAVFGAAAGLDVGGKPRLLGAECAQAGGGMGCGAGTDFHVEGLDDGAAAFVCPECLQ
a277          VGVVAVATVFGAAAGLDVGGKPRLLGAECAQTGGGMCAGTDFHVEGLDDGAAAFVCPECLQ
              190      200      210      220      230      240

m277.pep      FEDDLLEGKHGLX
a277          FEDDLLEGKHGLX
              250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1   ttgctgtcaa tcacgcccgg tgcgattttt tcgacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaaat acggccggta
151 caggtaacgg tgtcgccctt tttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gagtgcgcgt ccaggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatTTACA gacagatttt cgatcctggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1   LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1   TTGCGCGCAA TCACGCCCGG TGCATTTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1   LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VQVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRDFD DRDFQLAVET LIQHLHQLAD
201 LFGVQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

q278/m27.8

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

1	TTGCGCGCAA	TCACGCCCGG	TGCGATTTTT	TCGATAGGGG	CGGTCAAAGT
51	TGTATTAATC	GGGCCTTTGC	CGTCGATAGG	CCGACCCAAT	GCATCAACGA
101	CGCGTCCGAC	CAGTTCGCGT	CCGACCGGCA	CTTCCAAGAT	ACGACCGGTA
151	CAGGTAACCG	TGTCGCCTTC	TTTAATATGT	TCGTGCTCGC	CCAACACTAC
201	GGCGCCGACG	GAGTCGCGCT	CCAGGTTTCAT	CGCCAAGGCC	AAAGTGTTAC
251	CCGGGAATTC	GAGCATCTCA	CCTTGCATTG	CATCTGACAA	ACCATGGATG
301	CGAACGATAC	CGTCAGTTAC	CGAAATCACC	GTACCACGGG	TACGCATCTC
351	GGCATTTTACA	GACAGATTTT	CGATCTTGGC	TTTAATCAAA	TCGCTAATTT
401	CAGCAGGATT	AAGCTGCATG	AAAACCTCTC	TAATTTCGTC	TAGTCGTGTA
451	CAAGGCACTC	AATTTGCCTT	GTACAGACAA	ATCCAAAACC	TGATCACCCA
501	CTTCAACTTT	TATGCCGCCA	ATCAGCTCCG	GTTTCGATTTC	GACAGAGATT
551	TTCAGCTCGC	TGTCGAAACG	CTTATTCAGC	ATTTGCGCCA	ACTCGCCGAC
601	CTGTTTGTGC	GTCAACGGAT	AGGCACTGTA	AATGACGGCA	GATTTGATAT
651	GGTTGAATGA				

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

1	LR	AITPGAIF	SIGAVKVVLI	GPLPSIGRPN	ASTTRPTSSR	PTGTSKIRPV
51	QV	TVSPSLIC	SCSPNTTAPT	ESRSRFIAKP	KVLPGNSSIS	PCIASDKPWM
101	RT	IPSVTEIT	VPRVRTSAFT	DRFSILALIK	SLISAGLSCM	KTLLIRHSRV
151	QGTQFALYRQ	IQLNLTSHNF	YAANQLRFDF	DRDFQLAVET	LIQHRLQLAD	
201	LFVGGORIGTV	NDGRFDMVE*				

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNAST	TRPTSSRPTGTSKIR	VPVQTVSPSLMC		
a278	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNAST	TRPTSSRPTGTSKIR	VPVQTVSPSLIC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYPNTTAPTESRSR	FIAPKVLPGNSSIS	PCIASDKP	WMRTIPSVTEIT	VPQVR	TSFT
a278	SCSPNTTAPTESRSR	FIAPKVLPGNSSIS	PCIASDKP	WMRTIPSVTEIT	VPRVR	TSFT
	70	80	90	100	110	120

634

	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
a278	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHLHQLADLFVQGRIQTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLHQLADLFVQGRIQTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1  atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgtcg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgctg ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcggcggc gttgcctgca atcacgactt gtccgggcga
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcattc tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcattcag tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcggcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgcccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNSAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1  ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTCT GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGCGAGCGG CAGGCGCGCT TTGGCACC GGCTTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCTGCA ATCACGATT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACCTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCACACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAA SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

a279.seq

1	ATGACNCNGA	TTTGC GGCTG	CTTGATTTC A	ACGGTTTNN A	GGGCTTCGG C
51	GAGTTTGTC G	GCGGCGGGT T	TCATGAGGCT	GCAATGGGA A	GGTACNGACA
101	CNNGCAGCGG	CAGGCGCGCT	TTGGCGCCGG	CTTCTTTGG C	GGCAAGCATA
151	GCGCGCTCGA	CGGCGGCGGC	ATTGCGTGC A	ATCACGACTT	GTCCGGGCGA
201	GTTGAAGTTG	ACGGCTTCAA	CCACTTCATC	CTGTGCGGAT	TCGGCGCAAA
251	TTTGTTTTAC	CTGTTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	NGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	CCAATGCGCC	GGCGGCAACN	AGTGCGGTGT
401	ATTCGCCGAN	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCCGAATAG				

a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	ARSTAAALPA	ITTCPGELKL	TASTTSSCAD	SAQICFTCSS	SKPRIAAIAP
101	TPCGTADCIS	SARXRSLTA	SAKSNAPEAT	SAVYSPXLCP	ATAAGVLPPA
151	SE*				

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:					
a279	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTFCGTADCISSARRRTSLTA					
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTFCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
a279	SAKSNAPAATSAVYSPXLCPPATAAGVLPPASEX					
	130	140	150			

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttccgg ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggg gagcgcgtag ccgtacaaag cctcgtcggg
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgcgcgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat caccgaccac atcatgacca cgaaggacac caccacgacc
401 acggcggaata tgaccccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccata acgtcgtctga aacctgata aaggccgatc ccgaaggcaa
501 agttttattat caacaacgct tgggcaacta ccaaattgcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcattttaatg ccgtccctgc cgccaaacgc
601 aaagtctctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtgag cagcgaagcc gagccgtccg
701 ccaacaagat cgccgccatc atccggcaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtg accgcatcgc
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcggca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAKQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADIQRAV KQSKVSYAEA
101  TKGIQPLKAE EGGHHHDH HDHDHDEHGH HHDHGEYDPH VWNDPVLMSD
151  YAQNVAETLI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQAFNAVPAAKR
201  KVLTHGDAFS YMGNRYNISF IAPQGVSSSE EPSAKQVAAI IRQIKREGIK
251  AVFTENIKDT RMDRIAKET GVNVSGLKLYS DALGNAPADT YIGMYRHNVE
301  ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAATCAC CTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTCAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAACTCG TCCTGCTCAA CGGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCAAGAT CATGACCACG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGCACGATG CTTTTCCTA TATGGGCAA CATTACCATA TCGAATTCAT
651 CGCCCCGCAA GGCGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAACATCA AGGACACCCG TATGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGGCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADVQRAV KQSKVSYTEA
101  TKGIQPLKAE EGGHHHDH HDHGHHDH GEYDPHVWND PVLMSAYAQN
151  VAKALIKADP EGKVYYQQL GNYQMLKKL HSDAQAAFNA VPAKRKVL

```

Homology with a predicted ORF from *N.gonorrhoeae*

m280/q280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

1	ATGAAACACC	CCAAACAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AACTGCCGCG	CCCCTGCCGG	TTGTAAACAG	CTTCAGCATT	TTAGGCCAGC
101	TAGCCAAACA	AATCGGCGGA	GAGCGCGTAT	CCACACAAAG	TTTGGTCGGA
151	GCCAAACCAAG	ATACGCACGC	CTATACATATG	CCATAGCGCGG	ACATTAFAAAA
201	AATCCGCGAGT	GCAAAACTCG	TCCTGATTAA	CGGCTTAGGA	CTTGAAGCTG
251	CGACATCCCA	ACGTGCCGTC	AAACAGAGCA	AAGTATCTCA	TGCCGAAGCG
301	ACCAAAGGCA	TCCAAACCCCT	CAAAGCCGAA	GAAGAAGCGC	GACACCATCA
351	CGACCACGAT	CATGACCACG	ACCATGACCA	CGAAGGACAC	CACCACGACC
401	ACGGCGAATA	TGACCCCCAC	GTCTGGAACG	ACCCCGTCTCT	TATGTCGGCC
451	TATGCCCAAA	ACGTGCGCCA	AGCCCTGATA	AAGCGATGAC	CCGAAGGCCAA
501	AGTTTATTAT	CAACAACGCT	TGGGCCAATA	CCCAATGCAG	CTCAAAAAAC
551	TGCACAGTGA	CGCACAAGCC	GCATTTAATG	CGCTCCCTGC	CGCCAAACGC
601	AAAGTCCTGA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTTACCA
651	TATCGAATTG	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTCAG
701	CCAAACAAGT	CGCGCCCATC	ATCCGACAAA	TCAAACGCGA	AGGCATCAAA
751	GCGGTATTTA	CCGAAAATAT	CAAAAGACCC	CGCATGGTTG	ACCGCATCGG

638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep
 1 MKHPKLTLIA ALLTTAATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
 51 ANQDTHAYHM TSGDIKKIRS AKLVLLINGLG LEAADIQRAV KQSKVSYAEA
 101 TKGIQPLKAE EEGGHHHDHD HDHDHDHEGH HHDHGEYDPH VWNDPVLMSA
 151 YQNVAEALI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQA AFNAVPAAKR
 201 KVLTGHDFAF YMGKRYHIEF IAPQGVSSA EPSAKQVAI IRQIKREGIK
 251 AVFTENIKDT RMVDRIAKET GVNVSGLYS DALGNAPADT YIGMYRHNK
 301 ALTNAMKQ*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVT	SFSILGDVAKQIGGERVSIQSLVG	ANQDTHAYHM			
a280	MKHPKLTLIAALLTTAATAAPLPVVT	SFSILGDVAKQIGGERVSIQSLVG	ANQDTHAYHM			
	70	80	90	100	110	120
m280.pep	TSGDIKKIRSAKLVLLINGLGLEAADVQRAVKQSKVSYEAT	TKGIQPLKAE	EEGGHHHDHD			
a280	TSGDIKKIRSAKLVLLINGLGLEAADIQRAVKQSKVSYEAT	TKGIQPLKAE	EEGGHHHDHD			
	130	140	150	160	170	
m280.pep	HDH---EGHHHDHGEYDPHVWNPVLMSA	YQNVAKALIKADPEGKVYY	QQRLGNYQMQ			
a280	HDHDHDHEGHHHDHGEYDPHVWNPVLMSA	YQNVAEALIKADPEGKVYY	QQRLGNYQMQ			
	190	200	210	220	230	
m280.pep	LKKLHSDAQA	AFNAVPAAKRKVL	TGHDFAFSYMGKRYHIEF	IAPQGVSSA	EPSAKQVAI	
a280	LKKLHSDAQA	AFNAVPAAKRKVL	TGHDFAFSYMGKRYHIEF	IAPQGVSSA	EPSAKQVAI	
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTR	RMVDRIAKETGVNV	SGKLYSDALGNAPADTY	I	GMYRHNK	
a280	IRQIKREGIKAVFTENIKDTR	RMVDRIAKETGVNV	SGKLYSDALGNAPADTY	I	GMYRHNK	
	300					
m280.pep	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq
 1 atgcactacg ccctcgcatc cgtcttctgc ctgtccctca ggcgcgcacc
 51 cgtcggcgta ttcctcgta tgcgcgctat gagcctgata ggcgacgcat
 101 tgagccacgc cgtcctgccc ggtgcccgcg tcggctacat gtttgccggc
 151 ttgagcctgc ccgctatggg tgtgggcggg tttgcccgcg gtatgctgat
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgctccg
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa
 451 agcatagacc cccttttctt caagtccgtc aacggcaaa ggcgggctttg

639

```

501 gcacgtcatt ttcctcatcc tcgtcggtat gaacctcgta tccggcttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccgtt tatgggcaag aaatatgggg acgctcattc tgttgctcgt
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tcctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgtag cgctctttat
751 cttttttccg tcatactcgg caaagaaggc ggcattctgc ccaaattggt
801 caaaaaccac cgccaccaca ccacctga

```

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.pep

```

1  MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGVGG FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL
101 ISKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE
151 SIDPLFLKSV NGKGLWHVI FLILVVMNLV SGFQALGILM SVGIMMLPAI
201 TARLWARNMG TLILLSVLIA LFCGLIGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILPKWFKNH RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

```

1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCCTCGTCA TCGCCCGTAT GAGCCTGATA GGCGACGCAT
101 TGAGCCACGC CGTCCTGCCC GGTGCCGCGG TCGGCTACAT GTTTGCCGGC
151 TTGAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GCATGCTGAT
201 GGCACGTGCTT GCCGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG CGTAGTCCTC
301 GTCAGCAAAA ACGGGAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC
351 TGTACTTGCC GTCGATATTC CTGCCCTGCA GCTCATCGCC GCCGTCTCCA
401 GCCTACGCT CATTACCCTT GCCGTCATCT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCCGTC GCGGGCAAAG GCGGGCTTTG
501 GCACGTCCCT TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TCATGATGCT GCCAGCCATT
601 ACCGCCCGCC TGTGGGCGAA GCATATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCCTTTAT
751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CC..

```

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

```

1  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTLITL AVIYRPLVLE
151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGILM SVGLMMLPAI
201 TARLWAKHMG ALILLSVLTA LLCGLSGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILT..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/g281

```

              10      20      30      40      50      60
m281.pep      MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGLGG
              | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||
g281           MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGVGG
              10      20      30      40      50      60

              70      80      90     100     110     120
m281.pep      VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL VSKNGSSVDL LHLLFGSVLA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g281           FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL ISKNGSSVDL LHLLFGSVLA
              70      80      90     100     110     120

              130     140     150     160     170     180
m281.pep      VDIPALQLIA AVSSLTLITL AVIYRPLVLE SIDPLFLKSV GKGGLWHVL FLVLVVMNLV

```

640

```

|||||:|||||:|||||:|||||:|||||:
g281  VDIPALQLIAAVSGLTLITLAVIYRPLVLESIDPLFLKSVNGKGGWLWHVIFLILVVMNLV
      130      140      150      160      170      180

      190      200      210      220      230      240
m281.ppep SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP
|||||:|||||:|||||:|||||:|||||:
g281  SGFQALGILMSVGIMMLPAITARLWARNMGTLLLSVLIALFCGLIGLLISYHIEIPSGP
      190      200      210      220      230      240

      250      260
m281.ppep AIILCCSVLYLFSVILGKEGGILT
/ |||||:|||||:
g281  AIILCCSVLYLFSVILGKEGGILPKWFKNHRHHTTX
      250      260      270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1161>:

```

a281.seq
1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCTCGTCA TGCGCCGTAT GAGCCTGATA GGCGACGCAT
101 TGAGCCACGC CGTCTGCCC GGTGCCGCCG TCGGCTACAT GTTTGCCGGC
151 TTAAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GTATGCTGAT
201 GGCACGTCTT GCCGACTCG TCAGCCGCTT CACCACCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG TGTAGTCCTC
301 GTCAGCAAAA ACGGCAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC
351 CGTACTTGCC GTCGATATTC CTGCCCTGCA ACTCATCGCC GCCGTATCCA
401 CCCTCACACT GCTTACCCTT GCCGTCATCT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCTGTC GGCGGCAAAG GCGGGCTTTG
501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TTATGATGCT GCCAGCCATT
601 ACCGCCCGCC TATGGGCGAA GCACATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCC GCCATCATCC TCTGTTGAG CGTCCTTTAT
751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CCAAATGGCT
801 CAAAAACCAC CGCCACCACA CCACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1162; ORF 281.a>:

```

a281.ppep
1  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSTLTLLTL AVIYRPLVLE
151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGLM SVGLMMLPAI
201 TARLWAKHMG ALILLSVLTA LLCGLSGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILTKWLKNH RHHTT*

```

m281/a281 99.2% identity in 264 aa overlap

```

      10      20      30      40      50      60
m281.ppep MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLP GAAVGYMFAGLSLPAMGLGG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a281  MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLP GAAVGYMFAGLSLPAMGLGG
      10      20      30      40      50      60

      70      80      90      100     110     120
m281.ppep VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLHLLFGSVLA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a281  VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLHLLFGSVLA
      70      80      90      100     110     120

      130     140     150     160     170     180
m281.ppep VDIPALQLIAAVSSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGGWLWHVFLVLVVMNLV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a281  VDIPALQLIAAVSTLTLLTLAVIYRPLVLESIDPLFLKSVGGKGGWLWHVFLVLVVMNLV
      130     140     150     160     170     180

```

641

	190	200	210	220	230	240
m281 . pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281 . pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

```

g282 . seq
1   atgggattgg gtatggaat cggcaagctg atttgtgctc ttttgggtgc
51  gatcaatccg tttagcgcgt tgctgcctta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgacg ggcggtgcgc tattgaaggt
201 tttgggcata agcgtcggtt cgtttcagggt cggcggcggg attttgggtg
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggcgatt gccgtcgtgc ccatcgccat accgatcacc atcggtcagg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcgc tgattatcgc ggcggtttg gtggtcagtg cgatttgta
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattccgc aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

```

g282 . pep
1   MGLGMEIGKL IVALVLINP FSALSLYLDL TNGHSTKERR KVARTA AVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYS
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMMLA AVS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

```

m282 . seq
1   ATGGGATTGG GCATGGAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CCGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTAAACCGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

```

m282 . pep
1   MGLGMEIGKL IVAFLVLINP FSALSLYLDL TNGHSTKERR KVARTA AVAV
51  FAVIAVFALI GTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMMLA AVS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

642

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

```

      10      20      30      40      50      60
m282.pep  MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g282      MGLGMEIGKLIVALLVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI
          10      20      30      40      50      60

      70      80      90     100     110     120
m282.pep  GGTLLKVLGISVGSFQVGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g282      GGALLKVLGISVGSFQVGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI
          70      80      90     100     110     120

      130     140     150     160     170     180
m282.pep  AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g282      AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL
          130     140     150     160     170     180

      190     200     210
m282.pep  GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g282      GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX
          190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

```

a282.seq
  1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
 51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101  ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151  TTTGCCGTGA TTGCGGTATT TGCGCTGATC GGCGGTACGC TGCTGAAGGT
201  TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGA ATTTTGGTGT
251  TGCTGATTGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301  AATCTCGGCG CGCAGCCGGA AACGGGGCAG GTGCGCCCCG CCCGCAATGC
351  CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401  GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451  GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTGTGTA
501  TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCTGCTG GGTGCGACGG
551  GGCTGACGAT TTAAACCGT ATCATGGGTA TGATGCTGGC GGCGGTATCG
601  GTGGAGATTA TTGTGTCGGG ACTGAAAATG ATATTCCCGC AACTGGCAGG
651  TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

```

a282.pep
  1  MGLGMEIGKL IVAFLVLINP FSALSPLYDL TNGHSTKERR KVARTAAVAV
 51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101  NLGAQPETGQ VRPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151  DIALIIAAGL VVSAICYAIL IVAGKVSRL GATGLTILNR IMGMLAAVS
201  VEIIVSGLKM IFPQLAG*

```

m282/a282 99.1% identity in 217 aa overlap

```

      10      20      30      40      50      60
m282.pep  MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a282      MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI
          10      20      30      40      50      60

```

643

	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
m282 . pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
m282 . pep	GATGLTILNRIMGMLLAAVSVEIIVSGLKTIFFPQLAGX					
a282	GATGLTILNRIMGMLLAAVSVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

g283 . seq

1	atgaactttg	ctttatccgt	catcacattt	accctcgcct	ctttcctgcc
51	cgtcccgccct	gccggaaccg	ccgtctttac	ttggaaagac	ggcggcgcca
101	acagctattc	ggatgtgccg	aaacagcttc	atcccgacca	gagccaaatc
151	ctcaacctgc	ggacgctcca	aaccaaaccg	gcggtcaagc	ccaaacctgc
201	cgtcgatacg	aatgcggaca	gtgcgaagga	aaacgaaaag	gatatcgccg
251	agaaaaacgg	gcagcttgag	gaagaaaaga	aaaaaatgac	cgaaaccgaa
301	cggcagaaca	aagaagaaaa	ctgccggatt	tcaaaaatga	acctgaaggc
351	ggtgggaaac	tcaaatgcga	aaaacaagga	tgatttgatc	cgtaaataca
401	ataacgccgt	aaacaaatac	tgccgttaa		

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

g283 . pep

1	MNFALSVITF	TLASFLPVPP	AGTAVFTWKD	GGGNSYSDVP	KQLHPDQSQI
51	LNLRTLQTKP	AVKPKPAVD	NADSAKENEK	DIAEKNGQLE	EEKKKIAETE
101	RQNKEENCRI	SKMNLKAVGN	SNAKNKDDLI	RKYNNAVNKY	CR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

m283 . seq

1	ATGAACTTTG	CTTTATCCGT	CATTATGTTG	ACCCTCGCCT	CTTTCCTGCC
51	CGTCCCGCCT	GCCGGAGCCG	CCGTCTTTAC	TTGGAAGGAC	GGCGGCGGCA
101	ACAGCTATTC	GGATGTACCG	AAACAGCTTC	ATCCCGACCA	AAGCCAAATC
151	TTAAACCTGC	GGACGCGCCA	AACCAAACCG	GCGGTCAAAC	CCGCCCAAGC
201	CGACGCAGGG	AAGCGCACAG	ACGGCGCGGC	ACAGGAAAAC	AATCCCGACA
251	CTGCCGAGAA	AAACCGGCAG	CTTGAGGAAG	AAAAGAAAAG	AATTGCCGAA
301	ACCGAACGGC	AGAACAAAGA	AGAAACTGTC	CGGATTTCAG	AAATGAACCT
351	GAAGGCGGTG	GGAAATTCAA	ATGCAAAAAA	CAAGGATGAT	TTGATTCCGA
401	AATACAATAA	CGCCGTAAAC	AAATACTGCC	GTAA	

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

m283 . pep

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGNSYSDVP	KQLHPDQSQI
51	LNLRTRQTKP	AVKPAQADAG	KRTDGAAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNKEENC	RISKMNLKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283 . pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
	10	20	30	40	50	60


```

              70      80      90      100      110      120
m283.pep      AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRIKMNLKAV
              |||| | : | :||| : |||| ||||| : ||||| ||||| ||||| |||||
g283           AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKKIAETERQNKEENCRIKMNLKAV
              70      80      90      100      110

              130      140
m283.pep      GNSNAKNKDDLIRKYNNAVNKYCRX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g283           GNSNAKNKDDLIRKYNNAVNKYCRX
              120      130      140

```

```
a283.seq
1  ATGAAC TTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTCCTGCC
51  CGTCCC GCCT GCCGGA GCCG CCGTCTTTAC TTGGAAGGAC GCGGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCCAGCA AAGCCAAATC
151 TTAAACCTGC GACGCGCCCA AACCAAACCG GCGGTCAAAC CGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAGA AGAAAAC TCGGATTTCAA AAATGAACCT
351 GAAAGCGGTG GAAATTC AAATGCAAAA CAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTA AACAAATACTGCC GTTAA
```

a283.pep

1	<u>MNFALSVIML</u>	<u>TLASFLPVPP</u>	<u>AGAAVFTWKD</u>	GGGNSYSDVP	KQLHPDQSQI
51	LNLRTQRTKP	AVKPAQADAG	KRTDGA AQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNK EENC	RISKMN LKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

		10	20	30	40	50	60
m283.pep		MNFALSVMILTLASFLVPVPPAGAAVFTWKDGGGNSYS	SDVPKQLHPDQSQILNLRTRQTKP				
a283		MNFALSVMILTLASFLVPVPPAGAAVFTWKDGGGNSYS	SDVPKQLHPDQSQILNLRTRQTKP				
		10	20	30	40	50	60
		70	80	90	100	110	120
m283.pep		AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENC	RISKMN	LKAV			
a283		AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENC	RISKMN	LKAV			
		70	80	90	100	110	120
		130	140				
m283.pep		GNSNAKNKDDLIRKYNN	AVNKYCRX				
a283		GNSNAKNKDDLIRKYNN	AVNKYCRX				
		130	140				

```
g284.seq.
1  atgccgtctg aaactcgaaa tcggtttcag acggcattgg tttacgcggc
51  aggttggggc ttagcggctc ttgtaacggc attcgccttt gcctgcaaaa
101 gagtcgccgg ctttcgcgtt gcctttgaag ccttcgccgg tttttttgaa
151 actgtccttc ttaaagcctt ctttctgtaa accttcgccg cgcgttttgc
201 cgccgaagcc ttctttgccg gttttatgat cgccgcgcgg cgcgcgggat
251 ttcctatcgc ccagccgcc tttgcctttc ggcttgccgc ctgcggattt
301 gcgtttgcgg gccggtcca tgccttcgat ggtcagttcg ggcagtttgc
351 ggttaatgta tttttcgatt ttgtggactt tgacgtattc gttcacttcg
401 gcaaacgtaa tcgcaatacc cgtgcgcctt gcgcggccgg tgcgccgat
451 gcggtggacg tagtcttcgc cgtgtttcgg caggttcgtaq tttatgacg
```

645

```

501  gggtaatggt  cggtacgtca  ataccgcgtg  cggcaacgtc  ggtggcaacc
551  aaaattttgc  agcggccttt  acgcaaatcc  gtcagcgtgc  ggttgcgcca
601  gccctgcggc  atatcgccgt  gcaggcagtt  ggcggcgaaa  cttttttcgt
651  acaattcatc  cgcgatgact  tcggtcacgc  ctttggtgga  cgtgaaaatc
701  acacattggt  cgatgttggc  atcgcgcagg  atgtggtcga  gcaggcggtt
751  tttgtggcgc  atatcgtcgc  agtacaacaa  ctgctcttcg  attttgcctt
801  ggcgcgtccac  gcgttcgact  tcgataattt  cagagtcttt  ggtcagtttg
851  cgcgccagtt  tgccgactgc  gccgtcccaa  gtggcggaga  acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRVAGFAF  AFEAFAGFFE
51  TVFLKAFFLE  TFAARFAAEA  FFARFMIAAP  AAGFPIAPAA  FAFRLAACGF
101 AFAGRLHAFD  GQFGQFAVNV  FFDFVDFDVF  VHFGKRNNT  RAACAAGAPD
151 AVDVVFRLEF  QVVVYDVNG  RYVNTACGNV  GGNQNFAAAF  TQIRQRAVAP
201 ALRHIAVQAV  GGETFFVQFI  RDDFGHRFGG  RENHTLVDVG  IAQDVVEQAV
251 FVAHIVAVQQ  LLFDLALAVH  AFDFDNFRVF  GQFARQFADC  AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
1  ATGCCGTCTG  AAACTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCCTT  GCCTGCAAAA
101 GAATCGCCGG  CTTTGCCTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTTTTGAA
151 ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTGC
201 CGCCGAAGCC  TTCTTTGCTC  GGTTTATGAT  CGCCGCGCCA  ACCGCCGGAT
251 TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301 GCGTTTGCGG  GTCGGTTCCA  TGCCTTCGAT  GGTCAGTTCG  GGCAGTTTTC
351 GGTAAATGTA  TTTTTCGATT  TTGTGACTT  TGACGTATTC  GTTCACTTCG
401 GCAAACGTAA  TCGCAATACC  CGTGCGGCC  GCGCGGCCGG  TGCGCCCGAT
451 GCGGTGGACG  TAGTCTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501 GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACATC  GGTGGCAACC
551 AAAATTTTGC  AGCGGCCTTT  ACGCAAATCC  ATCAGCGTGC  GGTTGCGCCA
601 GCCTTGCGGC  ATATCGCGGT  GCAGGCAGTT  TGCGGCGAAA  CCTTTTTTCG
651 ACAGTTTCATC  CGCAATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701 ACGCATTGAT  CGATATTGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751 TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801 GATCGTCCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTCAGTTTG
851 CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901 CTGACGGTCG  CTCGGCGTTG  CTTCCACGAT  GGTTCGATG  TCGTCGATAA
951 AGCCCATATC  CAACATACGG  TCGGCTTCGT  CAAAATCAG  CACTTCCAAA
1001 CGTTCAAAAT  CAACTTTGCC  GCTTTGCATC  AGGTCCATCA  GACGGCCCGG
1051 CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCACGG  GTTTGGTAGC
1101 CGAAAGACGC  GCCGCCGACG  ATGCTGACGG  TGCGGAACCA  ACGCATATTT
1151 TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  GTTCGCGGGT
1201 CGGGGTCAAC  ACCAAAGCAC  GCGGGCCTTT  GCCCGGTTT  TCGCTGCGTT
1251 TGGTCAGTTT  TTGCAAAGTC  GGTA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE
51  TVSLKAFFLE  TFAARFAAEA  FFARFMIAAP  TAGFTIAPAA  FAFRLAACGF
101 AFAGRFHAFD  GQFGQFSVNV  FFDFVDFDVF  VHFGKRNNT  RAACAAGAPD
151 AVDVVFRLEF  QVVVDNVNG  RYVDTACGNI  GGNQNFAAAF  TQIHQRAVAP
201 ALRHIAVQAV  CGETFFVQFI  RNDFGHGFVG  RENHALIDIG  IAQDMIEQAV
251 FVAHIVAVQQ  LFFDFALIVH  AFDFDDFRVF  GQFARQFADR  AVPSGGEQQS
301 LTVARRCFHD  GFDVVDKAHI  QHTVGFVQNG  HFQTFKINFA  ALHQVHQFAR
351 RGDNQIDRFA  QGTGLVAERR  AADDADGAEP  THIFGIRQRV  FLDLSRQFAG
401 RGQHQSTRAF  ARFFAAFGQF  LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284 . pep	MPSETRNR FQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNR FQTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284 . pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAAGFPIAPAAFAFRLAACGFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284 . pep	FFDFVDFDV FVHF GKRRNRNTRAACAAGAPDAVDVVFRLFRQVVVDNVGNRGYVDTACGNI					
g284	FFDFVDFDV FVHF GKRRNRNTRAACAAGAPDAVDVVFRLFRQVVVDNVGNRGYVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284 . pep	GGNQNF AAFTQI HQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNF AAFTQI HQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHRFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284 . pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLLDFALAVHAFDFFDFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284 . pep	LTVARRCFH DGFVDV DKAHIQHTVGFVQNQH FQTFKINFAALHQVHQTARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284 . seq
1   ATGCCGTCTG AACTCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCGTTT GCCTTTGAAG CCTTCGCCGG TTTTTTTGAA
151 ACCGTCTCTC TTAAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTTGC
201 CGCCGAAGCC TTCTTTGCTC GGTTCATGAT CGCCGCGCCA ACCGCGGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTGCGG GTCGGTTCCA TGCCTTCGAT GGTCACTTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCAGCCT GCGCGGCCGG TGCGCCCGAT
451 GCGGTGGACG TAGTCTTCGG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACGTC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT GCGCAAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT GGCGGCGAAA CCTTTTTCGT
651 ACAATTCATC CGCGATGACT TCGGTCATGG CTTTGGTGGA CGTGAAAAATC
701 ACGCATTGAT CGATGTCGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTCTTCG ATTTTGCCTT
801 GGTCGTCCAC GCGTTCGACT TCGATGATTT CAGGGTCTTT GGTCACTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCT TCCGGCGTGG CTTTCGACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAATCAG CACTTCCAAG
1001 CGGGCGAAAT CGACTTTGCC GCTTTGCATC AAGTCCATCA GACGGCCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCGCGG GTTTGGTAGC
1101 CGAACGATGC ACCACCGACG ATGCTGACGG TACGGAACCA ACGCATATTT
1151 TTGGCATAAC CCAGCGCGTT TTTCTCGACT TGAGCCGCCA ATTCGCGGGT
1201 CGGCGTCAAC ACCAACGCGC GCGGGCCTTT GCCCGGTTTT TCGCTGCGTT
1251 TGGTCAGTCG CTGCAAAGTC GGTA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284 . pep
1   MPSETRNR FQ TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE

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647

```

FFARFMIAAP TAGFTIAPAA FAFRLAACGF
FDFVDFDVF VHFGRNRNT RAACAAGAPD
RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
RDDFGHGFGG RENHALIDVG IAQDMIEQAV
AFDFFDDFRVF GQFARQFADR AVPSGGEQQS
QHTVGFVQNG HFQAGEIDFA ALHQVHQTAR
TTDDADGTEP THIFGIRQRV FLDLSRQFAG
LQSR*

```

24 aa overlap

```

      30      40      50      60
LAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
|||||
LAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
      30      40      50      60

      90     100     110     120
TAGFTIAPAAFAFRLAACGFAFAGRFHAFDGQFGQFSVNV
|||||
TAGFTIAPAAFAFRLAACGFAFAGRFHAFDGQFGQFSVNV
      90     100     110     120

      150     160     170     180
RAACAAGAPDAVDVVFRVFRQVVVDNVGNRGYVDTACGNI
|||||:
RAACAAGAPDAVDVVFRVFRQVVVDNVGNRGYVDTACGNV
      150     160     170     180

      210     220     230     240
PALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG
|||||:|||||
PALRHIAVQAVGGETFFVQFIRDDFGHGFGGRENHALIDVG
      210     220     230     240

      270     280     290     300
QLFFDFALIVHAFDFFDDFRVFGQFARQFADRAVPSGGEQQS
|||||:|||||
QLFFDFALVVHAFDFFDDFRVFGQFARQFADRAVPSGGEQQS
      270     280     290     300

      330     340     350     360
QHTVGFVQNGHFQTFKINFAALHQVHQTARRGDNQIDRFA
|||||:|||||:|||||
QHTVGFVQNGHFQAGEIDFAALHQVHQTARRGDNQIDRFA
      330     340     350     360

      390     400     410     420
PTHIFGIRQRVFLDLSRQFAGRGQHQSTRAFARFFAAFGQF
|||||:|||||
PTHIFGIRQRVFLDLSRQFAGRRQHQRARAFARFFAAFGQS
      390     400     410     420

```

identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

cgataccgat ccgaccgaaa acggcacgcg
ccccgcccc gccggcaaaa aaacgccgcc
cactgctgt ctgtcctgat tttggcagta

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151 tgtttccctcg gctggatcgc cggtagcgaa gcaggtttgc gcttcgggct
201 gtaccaaatac ccgtcctggg tcggcgtaaa catttcctcc caaaacctca
251 aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc
301 gagggggcag accttaaaat cagccgcttc cgcttcgctg ggaaaccgtc
351 cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca
401 tcgccatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa
451 ggctgcccgc acagcataga cctgcccgcc gctgtctatc tcgaccgctt
501 cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaacgctct
551 atctcgaacg cctcaacgcg gcataccgtt acgaccgtaa agggcaccgc
601 ctcgacctga aggcgcgcca cagcccggtg agcagttcgt cggggtcagc
651 ctcggtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca
701 aaggcggatt cgaaggcgaa accatacaca gtacggcgcg gctgagcgcg
751 agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801 cctctcggga aaatccgtca tccaccggtt tgccgaatca ttggataaaa
851 cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901 gtgccttccc tgcccgatgc cgggctgaat ttcgacctga ccgccatccc
951 gtcgttttca gacggcatcg cgctggaagg ctcgctcgat ttggaaaaaca
1001 ccaaagccgg ctttgccgac cgcaacggca tcccgtccg tcagggttttg
1051 ggcggtcttg tcatccggca ggacggcacg gtgcatatcg gcaatacgtc
1101 cgccgccttg ctcggaaggc ggggcatcag gctgtcgggc aaaatcgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatcaactc cgtcggcgcg
1201 gaagacgtgc tgcaaacgcg gttcaaaagg aggttgagcg gcagcatcgg
1251 catcggcggc acgaccgcct cgcccaaaat ctcttggaac ctcggcaccg
1301 gcacggcacg cagggacggc agcctcccca tcgcaagcga ccccgcaaac
1351 gaacagcgga aactggtgtt cgacaccgtc aacatctccg ccggggaagg
1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgctgtctca
1451 agctggacat ccgttccgcg gcattcgacc cttcgcgcat cgatccgcga
1501 tttccggcag gcaatatcaa cggttcgatt catcttgccg gtgaactggc
1551 aaaagagaaa tttacgggca aaatgcgttt tttgcccggt acgttcaacg
1601 gcgtgccgat tgccggcagc gccgacattg tttacgagtc ccgccacctt
1651 ccgcgcgcgc ccgtcgattt gcggttgagg cggaaacatc tcaaacgaga
1701 cggcggcttc ggcaaaaaag gcgaccggct taacctcaat atcaccgcac
1751 ccgatttatc ccgtttcggg ttcggactcg cggggtcttt aaatgtacgc
1801 ggacaccttt ccggcgattt ggacggcgcg atccgaacct ttgaaaccga
1851 cctttccggc acggcgcgca acttacacat cggcaaacgc gcagacatcc
1901 gttcgctcga ttttaccctc aaaggctcac ccggcacaag ccgcccatg
1951 cgcgccgata tcaaggcgcg ccgcctttcc ctgtcgggcy gcgcggcggt
2001 tgtcgatacc gccggcctga cgctggaagg tacgggcygc cagcacccga
2051 tccgcacaca cgccgcatg acgctggagc gcaaacctgt caaactcgat
2101 ttggacgctt caggcgcat caacagggaa cttaccgat ggaaaggcag
2151 catcgcatc ctgcacatc gcggcgcat caacctcaag ctgcaaaacc
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaag tgcggcaaat
2251 tggcaggcaa tgggcggcag cctcaacctg caacactttt cttgggacag
2301 gaaaaaccggc atatcggcaa aaggcgcgcg acgcggcctg cacatcgccg
2351 agttgcacaa tttcttcaaa ccgcccttcg aacacaatct ggttttaaac
2401 ggcgactggg atgtcgcta cgggcacaaac gcgcgcggct acctaatat
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt
2501 tgaacgcatt ttccctgaaa acgcgcttcc aaaacgaccg catcggaatc
2551 ctgcttgacg gcggcgcgcg tttcgacagg attaacgccg atttgggcat
2601 cggcaacgcc ttcggcgga atatggcaaa tacaccgctc ggcggcagga
2651 ttacagcctc ccttcccgcg ttggcgcat tgaagccctt tctgcccgcc
2701 gccgcgcaaa acattaccgg cagcctgaat gcctccgcgc aaatcggcgg
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggt agcagcaact
2801 acgggaaaat caacggcaat atcaccgtcg ggcaaacgcy ctccctcgat
2851 accgcacctt tgggcggcag gctcaacctg accgttgccg atgccgaagc
2901 attccgcaac ttcctaccgg tcggacaaac cgtcaaaagg agcctgaatg
2951 ccgccgtaac cctcggcggc agcatcgccg acccgcaact gggcggcagt
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatcatctt
3051 ggacaacggc tcgctgcgtt cgcatattgc aggcaggaaa ttggtaatcg
3101 acagcctgaa attccggcac gaaggacgg cggaaactct cggcacggct
3151 agcatggaaa acagcgtgcc cgatgtcgat atcggcgcgg tgttcgaca
3201 ataccgcac ctgtcccgcg ccaaccgcgc cctgacgggt tccggcaaca
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt
3301 aaaactgatc aggggctgtt cggttcgcaa aaatcctcga tgccgtccgt
3351 cggcgacgat gtcgtcgat tgggcgaagt caagaaagag gcggcgccat
3401 cgtccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

649

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3451 ttctccggct acggcgcgga cgttaccata ggccgcaaac tgaccctgac
3501 cgcgcaaccg ggcggaaatg tgcgtggggt gggcacggtc cgcgtcatca
3551 aaggcggtta caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgtc caacgacccc aacctgaaca tccgcgccga
3651 acgcccgcct tccccgcgtg gtgcggggcg ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcgcca gcagcgcgca
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctggtg gatgatttgg gctttaccag caagcgcagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtcgctc aaactgattt accggctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

g285.pep

```

1 MTDTTPTDTD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWIAGTE AGLRFGlyQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRSLHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDRFETG KISMGTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAI LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGTGARTDGL SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTDGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLG TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651 RADIKGGRLS LSGGAADVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKSGSIGI LDIGGAFLNK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSLNL QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFENLVLN
801 GDWDVAYGHN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLLP
901 AAQNITGSLN ASAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSF
951 TAPLGGRNLN TVADAEAFRN FLPVGQTVKG SLNAAVTLGG SIADPHLGG
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 SMENSVPDVG IGAVFDKYRI LSRPNRRLTV SGNTRLRYSY QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GGKLTILTAQP GGNVRGVGTG RVIKGRYKAY GQDLDTIKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SSGELTYTIR FDRFLGSDKK DSAGNGKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

m285.seq

```

1 ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51 CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCTGAT TTTGGCAGTA
151 TGTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAAAT CCGTCTTGGT TCGGCGTAAA CATTTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGACGCG TGCACATTAC CGAAATTTC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CAGCCGCTGG AGCAGTTCGT CGGGGGCGGC
651 CTCGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCTTC
901 GTGCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCCG TCAGGTTTTA
1051 GCGGGCTTTG TCATCCGGCA GGACGGCACG GTGCATATCG GCAATACGTC
1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTTCGACC CTTCGCGCAT CGATCCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTTAAACAGA
1701 CGGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC
1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGTGATTT GGACGGCGGC ATCCGAACCT TTGAAACCGA
1851 CCTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA
1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGGGCG GAGCGGCGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCAGA
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAAT
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAAACCGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GCGGACTGGG ATGTCGCCTA CGGGCGCAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CGGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
2551 CTGCTTGACG GCGGCGGCGG TTTGCGGCGG ATTAACGCCG ATTTGGGCAT
2601 CGCCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
2651 TTACCGCCTC CCTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
2701 GCCGCGCAAA ACATTACCGG CAGCCTGAAT GCCGCCGCGC AAATCGGCGG
2751 ACGGGTAGGC TCTCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGGAAAAT CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCCGCAAC TTCTTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCCGTAA CTTCCGGCGG AGCATCGCCG ATCCGCACTT GGGCGGCAGC
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GCAACAACGG TCCTGCGTTC CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CCGTACGGTC
3151 GGTATGGAAG ACAGCGGACC CGATGTCGAT ATCGGCGCGG GTTTCGACAA
3201 ATACCGCATC CTGTCCCGCG CCAACCGCCG CTTGACGGTT TCCGGCAACA
3251 CCGCCTGCG CTATTGCGCG CAAAAAGGCA TATCCGTTAC CGGGATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTTTCGCA AAATCCTCGA TGCCGTCCGT
3351 CGGCGACGAT GTCGTGCTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
3401 CGTCCCGCT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC
3451 TTCGCCGGT ACGGCGCGGA CGTTACCATA GCGGCGAAAC TGACCTGAC
3501 CGCCCAATCG GGCGGAAGCG TACGGGGCGT GGGCACGGTC CGCGTCATCA
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
3601 GTCTCCTTTG TCGGCCCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA
3651 ACGCCGCTT TCCCCGTCG GTGCGGGCGT GGAAATATTG GGCAGCCTCA
3701 ACAGCCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAAAAGAC
3751 AAGCTCTCTT GGCTCATCCT CAACCGCGCC GGCAGCGGCA GCAGCGGCGA
3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAAATCA
3851 ACGACCGCAT CGGGCTGGTG GATGATTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT
3951 CGGCAACAA CTGACCGGCA AACTCTACAT CCGGTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAATGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTTC TCGGCGGGCG AGCTGACATA

651

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
 4151 GAAACGGCAA AGGAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep
 1 MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRF RFAWKPESELM RRS�HITEIS AGDIAIVTKP TPPKEERPPL
 151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
 301 VPSLPDAGLN FDLTAIPSFS DGIALEGLSD LENTKAGFAD RINGIPVRQVL
 351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSTRIDPQ
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIIKTGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
 601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651 RADIKGSRLS LSGGAHVDT ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKSGSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENLVLN
 801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGDNAFSLK TRFQNDRIGI
 851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLPA
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRFSD
 951 TAPLGGRLNL TVADAEVFRN FLPVGQTVKG SLNAAVTLLG SIADPHLGGS
 1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
 1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
 1151 FAGYGADVTI GGKLTTLTAQS GGSVRGVGT VIKGRYKAY GQDLDTKTGT
 1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
 1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
 1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
 1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNGKKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
g285	MTDTPPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPESELM					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPESELM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMKGAFDK					
g285	RRSLHITDISAGDIAIVTKPTPPKEERPQGLPDSIDLPAAYLDRFETGKISMKGTFDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
g285	QTVYLERLNAAAYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					

[illegible]

653

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g285      |||||:|||||
AAQNITGSLNASAQIGGRVGSPSVNAAVNGSSNYKINGNITVGQSRSFDTAPLGGRNLN
          910      920      930      940      950      960

m285.pep      970      980      990      1000      1010      1020
TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIAADPHLGGSINGDKLYRNQTQGIILDNG
|||||:|||||
g285      TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIAADPHLGGSINGDKLYRNQTQGIILDNG
          970      980      990      1000      1010      1020

m285.pep      1030      1040      1050      1060      1070      1080
SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
|||||:|||||
g285      SLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENSVPDVDIGAVFDKYRILSRPNRRLTV
          1030      1040      1050      1060      1070      1080

m285.pep      1090      1100      1110      1120      1130      1140
SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
|||||:|||||
g285      SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAASLPVNMN
          1090      1100      1110      1120      1130      1140

m285.pep      1150      1160      1170      1180      1190      1200
LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGVRGVGTVRVIKGRYKAYGQDLDTKGT
|||||:|||||
g285      LTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVRGVGTVRVIKGRYKAYGQDLDTKGT
          1150      1160      1170      1180      1190      1200

m285.pep      1210      1220      1230      1240      1250      1260
VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
|||||:|||||
g285      VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
          1210      1220      1230      1240      1250      1260

m285.pep      1270      1280      1290      1300      1310      1320
GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
|||||:|||||
g285      GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
          1270      1280      1290      1300      1310      1320

m285.pep      1330      1340      1350      1360      1370      1380
LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
|||||:|||||
g285      LTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
          1330      1340      1350      1360      1370      1380

m285.pep      1390
DSAGNGKGKX
|||||
g285      DSAGNGKGKX

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1185>:

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a285.seq
1   ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTGCTGTA GCTGTCGGCG GCACTGCTGT CTGTTCTGAT TTTGGCAGTA
151 TGTTCCTCG GCTGGCTCGC CGGCACGGAA GCGGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGGCT GGAAACCGTC
351 CGAATGATG CGCCGCAGCC TGCACATTAC CGAAATTTC GCCGCGGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTCGACCTGA AGGCTGCCGA CACGCCGTGG AGCAGTTCGT CGGGGTCAGC

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651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCCTTC
901 GTGCCTTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGGA AAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGTCCG TCAGT TTTA
1051 GGCAGCTTTG TCATCCGGCA GGACGGCAG GTGCATATCG GCAATACGTC
1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGG AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTGAGC GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTGGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCGCGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTGACCT CTTCGCGCAT CGATCCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTCCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAAGACAGA
1701 CCGCGGCTTC GGCAAAAAG GCGACCGGCT TAACCTCAAT ATCACCACAC
1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CCGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA
1851 CCTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTTCG CCGACACAAG CCGCCGATA
1951 CCGCGCGACA TCAAAGGCG CCGCCTTTCG CTGTCGGGCG GAGCGGAGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCAGC
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAAGGCG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAAT
2251 TGGCAGGCAA TGGGCGGCG CCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAACCAGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGT TTTAAAC
2401 GCGGACTGGG ATGTGCGCTA CCGGCGAAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTCCGGGCG ATTAACGCGG ATTTGGACAT
2601 CGGCAACGCC TTCGGCGGCA ATATGGCAA TGCAACGCTC GCGCGGAGGA
2651 TTACCGCCTC CCTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC
2701 GCCGCGCAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGGAAT CAACGGCAAC ATCACCCTCG GGCAAGGCC CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTGCGG ATGCCGAGT
2901 ATTCCGCAAC TTCCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGACG
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
3151 GGTATGGAAC ACAGCGGACC CGATGTCGAT ATCGGCGCGG GTTTCGACAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGT TCCGGCAACA
3251 CCCGCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CCGGATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTTCGCAA AAATCCTCGA TGCCGTCCGT
3351 CCGCGACGAT GTCGTCGAT TAGGCGAAGT CAAAAAGAG GCGGCGGCGC
3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC
3451 TTCGCCGGCT ACGGCGCGGA CGTTACCATA GCGGCGAAAC TGACCTGAC
3501 CGCCCAATCG GCGGAAGCG TCGGGGCGT GGGCACGGTC CGGTCATCA
3551 AAGGCGTTA TAAGGCATAC GGGCAGGATT TGACATTAC CAAAGGCACG
3601 GTCTCCTTTG TCGGCCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA
3651 ACGCCGCTT TCCCCGTCG GTGCGGGCGT GGAAATATTG GGCAGCTCA
3701 ACAGTCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAGAGAC
3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA
3801 CAATCGGCC CTGTCCGAG CCGCGGCGC GCTGTTGCC GGGCAATCA
3851 ACGACCGCAT CCGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

655

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3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTATT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTG CCCGTATCGG CAGCCGTTG TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

```

a285.pep
  1 MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNIS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPL
151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSF S DGIALEGLD LENTKAGFAD RNGIPVRQVL
351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIIKTGGG GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAEVVDT ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKSGSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENLVLN
801 GDWDVAYGRN ARGYNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFPLA
901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSF
951 TAPLGGRLNL TVADAEVFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGG
1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSMPSVGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGKLTILTAQS GGSVRGVGTV RVIKGRYKAY QDLDITKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNSKKG*

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m285/a285 99.4% identity in 1389 aa overlap

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          10      20      30      40      50      60
m285.pep  MTDTAPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
          |||
a285      MTDTAPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
          10      20      30      40      50      60

          70      80      90     100     110     120
m285.pep  AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM
          |||
a285      AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM
          70      80      90     100     110     120

          130     140     150     160     170     180
m285.pep  RRSLLHITEISAGDIAIVTKPTPPKEERPPSLPDSIDLPAAYLDRFETGKISMKGAFDK
          |||
a285      RRSLLHITEISAGDIAIVTKPTPPKEERPPSLPDSIDLPAAYLDRFETGKISMKGAFDK
          130     140     150     160     170     180

          190     200     210     220     230     240
m285.pep  QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
          |||
a285      QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
          190     200     210     220     230     240

          250     260     270     280     290     300
m285.pep  TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF
          |||

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656

a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTL EEVLVKGFNINPSAF
	250 260 270 280 290 300
m285.pep	310 320 330 340 350 360
	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT
a285	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGSFVIRQDGT
	310 320 330 340 350 360
m285.pep	370 380 390 400 410 420
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGINSVGAEDVLQTAFKGRLDGSIGIGG
a285	VHIGNTSVALLGRGGIRLSGKIDTEKDILDNLIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
m285.pep	430 440 450 460 470 480
	TTASPKISWQLGIGTARTDGLAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
a285	TTASPKISWQLGIGTARTDGLAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
	430 440 450 460 470 480
m285.pep	490 500 510 520 530 540
	RLKLDIRSFADPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
a285	RLKLDIRSFADPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	490 500 510 520 530 540
m285.pep	550 560 570 580 590 600
	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
a285	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
	550 560 570 580 590 600
m285.pep	610 620 630 640 650 660
	GHLSGDLGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
a285	GHLSGDLGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
	610 620 630 640 650 660
m285.pep	670 680 690 700 710 720
	LSGGAHVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
a285	LSGGAHVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
	670 680 690 700 710 720
m285.pep	730 740 750 760 770 780
	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
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	730 740 750 760 770 780
m285.pep	790 800 810 820 830 840
	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
a285	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	790 800 810 820 830 840
m285.pep	850 860 870 880 890 900
	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
a285	TRFQNDRIGILLDGGARFGRINADLDIGNAFGGNMANAPLGGRITASLPDLGTLKPFLPA
	850 860 870 880 890 900
m285.pep	910 920 930 940 950 960
	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYKINGNITVGQSRSFDTAPLGGRNLN
a285	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYKINGNITVGQSRSFDTAPLGGRNLN

657

a285	AAQNITGSLNAAAQIGGRVGS	PSVNA	AVNGSS	NYGKING	NITV	QSR	SFDTAP	LGGR	LNL
	910	920	930	940	950	960			
m285.pep	TVADA	EVFRN	FLPVG	QTVK	GS	LNA	AVTL	GGSI	ADPH
	970	980	990	1000	1010	1020			
a285	TVADA	EVFRN	FLPVG	QTVK	GS	LNA	AVTL	GGSI	ADPH
	970	980	990	1000	1010	1020			
m285.pep	SLRSH	IAGRK	WVIDS	LKFR	HEGT	AELSG	TVGM	ENSG	PDVD
	1030	1040	1050	1060	1070	1080			
a285	SLRSH	IAGRK	WVIDS	LKFR	HEGT	AELSG	TVGM	ENSG	PDVD
	1030	1040	1050	1060	1070	1080			
m285.pep	SGNTR	LRYS	PQKGI	SVTGM	IKTDQ	GLFG	SQKSS	MP	SVGDD
	1090	1100	1110	1120	1130	1140			
a285	SGNTR	LRYS	PQKGI	SVTGM	IKTDQ	GLFG	SQKSS	MP	SVGDD
	1090	1100	1110	1120	1130	1140			
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	1150	1160	1170	1180	1190	1200			
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	1150	1160	1170	1180	1190	1200			
m285.pep	VSVFG	PLNDP	NLNIRA	ERRLS	PVGAG	VEILG	SLNS	PRIT	LTAN
	1210	1220	1230	1240	1250	1260			
a285	VSVFG	PLNDP	NLNIRA	ERRLS	PVGAG	VEILG	SLNS	PRIT	LTAN
	1210	1220	1230	1240	1250	1260			
m285.pep	GSGSS	GDNA	ALSAA	AGALL	AGQIN	DRIGL	VDDL	LGFT	SKRS
	1270	1280	1290	1300	1310	1320			
a285	GSGSS	GDNA	ALSAA	AGALL	AGQIN	DRIGL	VDDL	LGFT	SKRS
	1270	1280	1290	1300	1310	1320			
m285.pep	LTGK	LYIG	YEYS	ISSAE	QSVK	LIYRL	TRAI	QAVAR	IGSR
	1330	1340	1350	1360	1370	1380			
a285	LTGK	LYIG	YEYS	ISSAE	QSVK	LIYRL	TRAI	QAVAR	IGSR
	1330	1340	1350	1360	1370	1380			
m285.pep	DSAG	NGK	GKX						
	1390								
a285	DSAG	NSK	GKX						
	1390								

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCCGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACACTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCAGCA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAAGGCCT
351 GCCCCAGAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTC ACAACAACAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCTGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGGCCGAAC TGACGATCGA CCGCGGCAAT ATCCGCCTCT
701 CGGGAATATC GTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCG GATGCCGGGC TGAATTTCTGA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAAA
901 GCGCGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAAG TTTTGGGCGG
951 CTTTGTCTATC CGGAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCGTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTG GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCTCGCCC AAAATCTCTT GGCAACTCG CACCGGCACG
1201 GCACGCACGG ACGGCAGCCT cgcATCGCA AGCAGACCCG CAAACGAACA
1251 GCGGAAACTG GTGTTGACA CCGTCAACAT CTCCGCGGGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCTTCG CGCATCGATC CGCAATTTCC
1401 GGCAGGCGat atCAACGGTT CGATTCTATC TGCCGGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTGC CCGGTACGTT CAACGGCGTG
1501 CCGATTGCGG GCAGCGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
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1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCCGGC GATTTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTCC
1801 CTCGATTTTA CCTCAAAGG CTCACCCGGC ACAAGCCGCC CGATGCGCGC
1851 CGATATCAAG GCGCGCCGCC TTTCCCTGTC GGGCGGCGCG GCGGTTGTCTG
1901 ATACCGCGG CTTGACGCTG GAAGGTACGG CCGCGCAGCA CCGCATCCGC
1951 ACACACGCCG CCATGACGCT GGACGGCAAA CCGTTCAAAC TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGGCG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GACAGGAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGAAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCGCGG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAACACGCG CTTTCAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGGC CGCGGTTTCG GACGGATTAA CGCCGATTG GGCATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAAATACAC CGCTCGGCGG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 CAAAGAACAT ACCGGCAGCC TGAATGCCTC CGCGCAAACT GGCGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGTAGCAG CAACTACGGG
2701 AAAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCCT TCGATACCGC
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCG GCGGCAGCAT CGCCGACCCG CACTTGGGCG GCAGTATCAA
2901 CCGCGACAAG CTCTATTACC GCAACCAAA CCAAGGCATC ATCTTGGA
2951 ACGGCTCGCT CGGTTGCGAT ATTGCAGGCA GGAAATGGGT AATCGACAGC
3001 CTGAAATTC GGCACGAAG GACGGCGGAA CTCTCCGGCA CGGTCAGCAT
3051 GGAACACAGC GTGCCCGATG TCATATCGG CGCGGTGTTC GACAAATACC
3101 GCATCCTGTC CGGCCCAAC CGCCGCTGA CGGTTTCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAAAAC
3201 TGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGCGGCG GGCATCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCTC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC
3401 AACCGGGCGG AAATGTGCGT GGGGTGGGCA CGGTCCGCGT CATCAAAGG
3451 CGTTACAAAG CATACGGGCA GGATTTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTGCGC CGCTCAACG ACCCAAACCT GAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAA TATTGGGCAG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GTGCCGCGAG CGGCAGCAGC GCGCACAATG
3701 CCGCCCTGTC CCGAGCCGCA GCGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAACC GCGCAACTCA ACCCGCGCGA ACAGGTGCTG ACCGTCGGCA
3851 AACAACGTGAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACCT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCGCCGT ATCGGCAGCC GTTCGTGCGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTCTTC GGTTCGGACA AAAAAGACTC CGCAGGAAAC
4051 GGCAAAGGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:
g285-1.pep

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1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
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101 IVTKPTPPKE ERPPQGLPDS IDLPAAVYLD RFETGKISMG KTFDKQTVYL
151 ERLNAARYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGTTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSHTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAG LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGPSG TSRPMDRADIK GGRSLSSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSGILDIGG AFNLKLQNRM
701 TLEAGAHEVA ASANWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 HNFVKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPPGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRRIT
851 ASLPDLGALK PFLPAAQNI TGSNLASAQI GGRVGSPPSVN AAVNGSSNYG
901 KNGNITVVGQ SRSFDTAPLG GRNLTLVADA EAFRNFLPVG QTVKGS LNAA
951 VTGGSIADP HLGGSINGDK LYRNQTQGI ILDNGLSLRH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRSYSPQKIS VTMGIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAASL
1101 PVNMNLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPPGNVR GVGTVRVIK
1151 RYKAYGQDL ITKGTVSFVG PLNDPNLNIR AERRLSPPVA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
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101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTCCGCGCCG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAACAC CGCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG GCGGCCTCGG
551 TCGGCTTGAA AAAACGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA CGGCGAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGCGCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGAC TGAATTTTGA CCTGACCGCC ATCCCGTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGTTTCG TCGATTTGGA AAACACCAAA
901 CGCGGCTTTG CGGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCGG
951 CTTTGTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCAGCG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCGCGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGCGGAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG CGAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGCTG GATTGCGGCG TGGGGCGGAA CATTATTAAT ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGT GATTGAGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
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1951 ACACACGCGG CATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGCGG GCAAGTGCGG CAAATTGGCA

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAA
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2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGGACGGG
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3351 CGGCTACGGC CGGACGTTA CCATAGGCGG CAACTGACC CTGACCGCC
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3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pep

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151 ERLDASYRYD RKHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
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651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
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751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPPGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSINAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRLNLTVADA EVFRNFLPVG QTVKGSNLAA
951 VTLLGSIADP HLGGSSINGDK LYRNTQTQGI ILDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKDSAGN
1351 GKKG*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

g285-1 . pep	LKLSAALLSVLILAVCFGLGWIAGTEAGLRFLGYQIPSWFGVNISSQN	LKLTGTLDDGFGDGN				
m285-1	LKLSAALLSVLILAVCFGLGWLAGEAGLRFLGYQIPSWFGVNISSQN	LKLTGTLDDGFGDGN				
	10	20	30	40	50	60
g285-1 . pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPPLSLPDS					
	70	80	90	100	110	120
g285-1 . pep	IDLPAAVYLDRLFETGKISMGKTFDKQTVYLERLNAAVRYDRKGHRLLDLKAADTPWSSSSG					
m285-1	IDLPAAVYLDRLFETGKISMGKAFDKQTVYLERLDASVRYDRKGHRLLDLKAADTPWSSSSG					
	130	140	150	160	170	180
g285-1 . pep	SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
g285-1 . pep	PFAESLDKTLLEEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK					
m285-1	PFAESLDKTLLEEVLVKGFNINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK					
	250	260	270	280	290	300
g285-1 . pep	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGI					
m285-1	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGI					
	310	320	330	340	350	360
g285-1 . pep	NSVGAEDVLQTAFAKGRLDGSGIGIGTTASPKISWQLGTGTARTDGS LAIASDPANEQRKL					
m285-1	NSVGAEDVLQTAFAKGRLDGSGIGIGTTASPKISWQLGTGTARTDGS LAIASDPANGQRKL					
	370	380	390	400	410	420
g285-1 . pep	VFDTVNISAGEGSLTAQGYLELFKDRLLKLDIRSRADFSPRIDPQFPAGDINGSIHLAGE					
m285-1	VLDTVNIAAGQGSLSLAQGYLELFKDRLLKLDIRSRADFSPRIDPQLPAGNINGSINLAGE					
	430	440	450	460	470	480
g285-1 . pep	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDRLGRNIVKTDGGFGKKG					
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDRLGRNIIKTDGGFGKKG					
	490	500	510	520	530	540
g285-1 . pep	RLNLNITAPDLRSRFGFLAGSLNVRGHLSGDLGGIRTFTDLSGTARNLHIGKAADIRS					
m285-1	RLNLNITAPDLRSRFGFLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS					
	550	560	570	580	590	600
g285-1 . pep	LDFTLKGSPGTSRPMRADIKGGRSLSLSGGAAVVDTAGLTLEGTAQHRIIRTHAAMTLDGK					
m285-1	LDFTLKGSPDTSRPIRADIKGSRSLSLSGGAAVVDTAGLMDGTGVQHRIRTHAAMTLDGK					
	610	620	630	640	650	660
g285-1 . pep	PFKLDLDASGGINRELTRWKSGSIGILDIGGAFNLKLQNRMTLEAGA EHVAASAANWQAMG					
m285-1	PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLQNRMTLEAGA ERVAASAANWQAMG					
	670	680	690	700	710	720
g285-1 . pep	GSLNLQHFSWDRKTGISAKGGARGLHIAELHNFFKPPFEHNLVLNGDWDVDVAYGHNARGYL					
m285-1	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVDVAYGRNARGYL					
	730	740	750	760	770	780

	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAAQNTGSLNAAQIGGRVGSVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAAQNTGSLNAAQIGGRVGSVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVGQSRSFDTAPLGGRLNLTVADAEAFRNFLPVGQTVKGSLNAAVTLGGSIAADP					
m285-1	KINGNITVGQSRSFDTAPLGGRLNLTVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIAADP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVIDGAVFDKYRILSRPNRRRLTVSGNTRLRYSFPQKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVIDGAVFDKYRILSRPNRRRLTVSGNTRLRYSFPQKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTLTAAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTLTAAQGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGK GK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGK GKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTT CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGCA CGGAAGCGGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCCGC GTAAACATT CCTCCAAA CACTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCGG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGGT CTATCTCGA CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCTGA CCTGACCGCC ATCCCGTCGT
851 TTTTCAGACG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTCTAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAG CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 CGCGCGCACG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGTATATCT GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTGCCGA CATTTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCCGTC GATTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CTTTCCCGG GATTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTTCG
1801 CTCGATTTCG CGCTCAAAGG TTCCGCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTCTGTGT GGGCGGAGCG GAGGTTGTCTG
1901 ATACCGCCGA CCTGATGCTG GACGGCACGG GCGTGACGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGG GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCTCTGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA
2151 GGCATGGGG GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAACACGCG CTTTCAAAAC GACCGTATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GCGGATTAAC CGCGGATTTC GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAATGACAC CGCTCGGCGG CAGGATTACC
2551 GCCTTCCCTC CCGACTTGGG CACATTGAAG CCCTTTCTGC CGCGCGCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAATC GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCCGTC ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTC ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CGGCGACAAA CTTATTACC GCAACCAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGGA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCCGTAT
3051 GGAACACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CGGCCCCAAC CGCGCCTGA CGGTTTCCGG CAACACCGC
3151 CTGCGCTATC CGCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTCCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGCTGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGTTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGC GGCGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATAAGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGC CGCTCAACG ACCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGGG GCGGTGAAA TATTGGGCA CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCTTGGCTC ATCTCAACC GCGCCGGCAG TGGCAGCAGC GGCACAAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAACC GCGAACTCA ACCCGCCCGA ACAGGTGCTG ACCGTCGGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGT CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCCGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCTG CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

a285-1.pep

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1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLRGG IRLSGKIDTE
351 KDILDNLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAAWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGAQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGNM ANAPLGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSLNAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVQK SRSFDTAPLG GRNLTVADA EVFRNFLPVG QTVKGSNLAA
951 VTLLGSIADP HLGGSSINGDK LYRNTQGI ILDNGLSRSH IAGRKWIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDVVVLG EVKKEAAAPL
1101 PVMNMTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDL ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 SKGK*

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a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a285-1.pep	IDLPAAVYLDREFETGKISMKGAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
m285-1	IDLPAAVYLDREFETGKISMKGAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
	250	260	270	280	290	300
a285-1.pep	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
m285-1	PFAESLDKTL EEVLVKGFNINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDNLNIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDNLNIGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGLSLAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGLSLAIASDPANGQRKL					
	370	380	390	400	410	420
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	SLTAQGYLELFKDRLLKLD	IRSFADPSRIDPQLPAGNINGS	INLAGE	
m285-1	VLDTVNIAAGQGS	SLTAQGYLELFKDRLLKLD	IRSFADPSRIDPQLPAGNINGS	INLAGE	
	430	440	450	460	470 480
a285-1.pep		490	500	510	520 530 540
a285-1.pep	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD				
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD				
	490	500	510	520	530 540
a285-1.pep		550	560	570	580 590 600
a285-1.pep	RLNLNITAPDLSRFGFLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS				
m285-1	RLNLNITAPDLSRFGFLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS				
	550	560	570	580	590 600
a285-1.pep		610	620	630	640 650 660
a285-1.pep	LDFTLKGSPTSRPIRADIKGSRLSLSGGAEVVDTADLMLDGTGVQHRIRTHAAMTLDGK				
m285-1	LDFTLKGSPTSRPIRADIKGSRLSLSGGAEVVDTADLMLDGTGVQHRIRTHAAMTLDGK				
	610	620	630	640	650 660
a285-1.pep		670	680	690	700 710 720
a285-1.pep	PFKFDLDASGGINRELTRWKGSIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG				
m285-1	PFKFDLDASGGINRELTRWKGSIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG				
	670	680	690	700	710 720
a285-1.pep		730	740	750	760 770 780
a285-1.pep	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
m285-1	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
	730	740	750	760	770 780
a285-1.pep		790	800	810	820 830 840
a285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
	790	800	810	820	830 840
a285-1.pep		850	860	870	880 890 900
a285-1.pep	ANAPLGGGRITASLPDLGTLKPFLPAAAQNTGSLNAAAQIGGRVGSPSVNAAVNGSSNYG				
m285-1	ANAPLGGGRITASLPDLGALKPFLPAAAQNTGSLNAAAQIGGRVGSPSVNAAVNGSSNYG				
	850	860	870	880	890 900
a285-1.pep		910	920	930	940 950 960
a285-1.pep	KINGNITVGQSRSFDTAPLGGRLNLTVAEVRNFLPVGQTVKGSLNAAVTLGGSIAADP				
m285-1	KINGNITVGQSRSFDTAPLGGRLNLTVAEVRNFLPVGQTVKGSLNAAVTLGGSIAADP				
	910	920	930	940	950 960
a285-1.pep		970	980	990	1000 1010 1020
a285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS				
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS				
	970	980	990	1000	1010 1020
a285-1.pep		1030	1040	1050	1060 1070 1080
a285-1.pep	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP				
m285-1	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP				
	1030	1040	1050	1060	1070 1080
a285-1.pep		1090	1100	1110	1120 1130 1140
a285-1.pep	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR				
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR				
	1090	1100	1110	1120	1130 1140
a285-1.pep		1150	1160	1170	1180 1190 1200
a285-1.pep	GVGTVRVIKGRYKAYGQDLITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS				
m285-1	GVGTVRVIKGRYKAYGQDLITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS				

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTANEP	MSEKDKLSW	LILNRAGSG	SSGDNAALSA	AAGALLAGQ	INDRIGLVDD
m285-1	PRITLTANEP	MSEKDKLSW	LILNRAGSG	SSGDNAALSA	AAGALLAGQ	INDRIGLVDD
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQT	GELNPAEQVL	TVGKQLTGK	LYIGYEYSIS	SAEQSVKLIY	RLTRAIQAVAR
m285-1	TSKRSRNAQT	GELNPAEQVL	TVGKQLTGK	LYIGYEYSIS	SAEQSVKLIY	RLTRAIQAVAR
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGEL	TYTIRFDRFS	GSDKKDSAG	NSKKGX		
m285-1	IGSRSSGGEL	TYTIRFDRFS	GSDKKDSAG	NSKKGX		
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

```

1   atgcagaaca ccggtaccat gatgatcaaa ccgaccgccc tgctcctgcc
51  ggctttatth ttctttccgc acgcatacgc gcctgccgccc gacctttccg
101 aaaacaaggc ggcgggtttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtc aattaaacc caaattcccc gtccgcatcg acacgcagga
201 cagtgaatc aaagatatgg tcgaagaaca cctgccgctc atcacgcagc
251 agcaggaaga ggttttgat aaggaacaga cgggattcct tgccgaagaa
301 gcaccggaca acgttaaaac aatgctccgc agcaaaaggct atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacggtg cacatcacac
401 cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
451 atcctttcag acggcaacct cgccgaatac taccgcaacg cgctggaaaa
501 ctggcagcag ccggtaggca gcgatttoga tcaggacagt tgggaaaaaca
551 gcaaaacttc cgtcctcggc gcggtaacgc gcaaaggcta cccgcttgcc
601 aagctcggca acaccggggc ggccgtcaac cccgataccg ccaccgccga
651 ttgaaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcacccg cacacagcgt taccgccaac aaaccgtctc cggcctggcg
751 cgcttccaac cgggcacgcc ctacgacctc gacctgctgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcattatth cggcgcgctc gtacaagccg
851 acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaag tcagcgtaac
901 cgagggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcggaat
951 acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gtcggtcgt ctgggatag gacaaatacg aaaccacgct
1051 tgccgccggc atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaacgcccc
1151 ttctccggcg gcatctggta tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggggc gaatttctcg cagaaggccg gaaaatcccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaaacgc
1301 cagctgctca acaactgtct gcaccccgaa aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaattc
1401 gcacctctgc ccgcgcaggt tatttcttca cgcccgaata caaaaaactc
1451 ggcacgttca tcatacgcgg acaagcgggt tacaccgttg cagcgacaaa
1501 tgccgatgct ccctcggggc tgatgttccg cagcggcggc gcgtcttccg
1551 tgcgcgggta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

```

1   MQNTGTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKSKSPDT
51  ESVKIKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAITV HITPGPRTKI ANVGVAIGLD
151 ILSDGNLAIE YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201 KLGNTAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQTVSGLA
251 RFQPGTPYDL DLLLDFQQAL EQNGHYS GAS VQADFRLPR GPRPRQSQRN
301 RGQTPQTRNR HPPRFGIRFG RQNRRLRLQP LQRLYRLGR LGYGQIRNHA
351 CRRHQPAQAL SGQLLDKQRF LQPFDPKPR KTRLLRRHLV CARPRGHRQC
401 AGGGISRRRP ENPRLGCRFG QQRHDAADRL LETPAAQQR APRKRPLPRR

```

451 QNRDDFGHIP VLHRANPHLC PRRFLHARK QKTRHVHTR TSGLHRCTRQ
501 CRCPLGADVP QRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq
1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51 GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GGCGGGTTTC GCATTGTTCA AAAACAAAAG CCCCGACACC
151 GAATCAGTCA AATTAACC CAAATTCCTT GTCCTCATCG ACACGCAGGA
201 CAGTGAAATC AAAGATATGG TCGAAGACA CCTGCCGCTC ATCAGCAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTACAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCCGC CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTCAG ACGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAACA
551 GCAAAACTTC CGTCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
601 AAGCTCGGCA ATACGCAGGC GGCCGTC AAC CCGGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GGCGACTTTG
701 AAATCACCGG CACACAGCGT TACCCGAAC AAATCGTCTC CGGCCTTGCG
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGTGTC TCGACTTCCA
801 ACAGCGCTC GAACAAACG GGCATTATTC CGGCGCTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAACT CGAAACCGGC ATCCGCCTCG ATTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT
1051 GCCGCCGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCAACCA AAACCTCGAA AAACGCGCTT
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGCAT CGATGCCAGG
1201 CTGGGGGCGG AATTCTCGC AGAAGCGCGG AAAATCCCG GCTCGGCTGT
1251 CGATTGTGGC AACAGCCACG CCACGATGCT GACCGCTCT TGGAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCGAAA ACGGCCATTA CCTCGACGGC
1351 AAAATCGGTA CGACTTTGGG CACATTCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGT ACACCGTTGC CCGCGACAAT
1501 GCCGACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGCGC CGTCTTCCGT
1551 GCGCGGTTAC GAACGCGACA GCATCGGACT TGCCGCGCCG AACGGATCGG
1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTCCGG CCGGTGTTC CACGATATGG GCGATGCCG
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTTCCGGA CTGGGCGTGC
1751 GCTGGTTTCA CCCGCTTGCG CCGTTTTCCT TCGACATCGC CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep
1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLPKFP VLIDTQDSEI KDMVEEHLPL ITQQEEVLD KEQTGFLAE
101 APDNVKTMLR SKGYFSSKVS LTKDGAYTV HITPGPRTKI ANVGVAIGD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENKTSVLG AVTRKAYPLA
201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGMPYDL DLLLDFQAL EQNGHYS GAS VQADFRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYIGSVV WMDMKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNL KRAFSGGVWY VRDRAGIDAR
401 LGAEFLAAGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGTFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRLTSGAVF HMDGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

668

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP					
g286	MQNTGTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
g286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEEYRNALENWQQPVGSDFDQDS					
g286	LTEKDGAYTVHITPGPRTKIANVGVAILGDILSDGNLAEEYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDTATADLNVVVDSGRPIAFGDFEITGTQR					
g286	WENSKTSVLGAVTRKGYPLAKLGNTAAVNPDTATADLNVVVDSGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
	250	260	270	280	290	299
m286.pep	YPEQIVSGLARFQPGMPYDLDLLLDFQQALEQNGHYSVASVQADFDRQLQGDRVPVKVSV					
g286	YPEQTVSGLARFQPGTPYDLDLLLDFQQALEQNGHYSVASVQADFDRQLPRGPRPRQSQRN					
	250	260	270	280	290	300
	300	310	320	330	340	359
m286.pep	TEVKRHKLETGIRLDSEYGLGGKIAYDYNNLFNKGYIGSVVWMDKYETTLAAGISQPRN					
g286	RGQTPQTRNRHPPRFGRQNRLLQLQRLYRLGRLGYGQIRNHACRRHQPAQQL					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1197>:

a286.seq	
1	ATGCACGACA CCCGTACCAT GATGATTAAA CCGACCGCCC TGCTCCTGCC
51	GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101	AAAACAAGGC GGCGGTTTC GCATTGTTCA AAAACAAAAG CCCCACACCC
151	GAATCAGTTA AATTAAAACC CAAATTCCCC GTCCGCATCG ACACGCAGGA
201	TAGTGAAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCACGCAGC
251	AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301	GCACCGGACA ACGTTAAAAC AATGCTCCGC AGCAAAGGCT ATTTACAGCAG
351	CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401	CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451	ATCCTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501	CTGGCAGCAG CCGGTAGGCA GTGATTTCGA TCAGGACAGT TGGGAAAACA
551	GCAAACTTC CGTCCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
601	AAGCTCGGCA ACACCCGGGC GGCCGTCAAC CCCGATACCG CCACCGCCGA
651	TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GGCGACTTTG
701	AAATTACCGG CACGCAGCGT TACCCCGAAC AAATCGTCTC CGGCTTGGCG
751	CGCTCCAAC CGGGCACGCC CTACGACCTC GACCTGCTGC TCGACTTCCA
801	ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCGTCC GTACAAGCCG
851	ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901	GAGGTCAAAC GCCACAAGCT CGAAACCGGC ATCCGCCTCG ATTCGGAATA
951	CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001	GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT
1051	GCCCGCGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
1101	CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT
1151	TCTCCGGCGG CATCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201	CTGGGGCGG AGTTTCTCGC AGAAGGCCG AAAATCCCCG GCTCGGATAT
1251	CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCCTCT TGGAAACGCC
1301	AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC

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1351 AAAATCGGTA CGACTTTGGG CGCATTCTTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAAACTCG
1451 GCACGTTTAT CACACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACGCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCG ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTC CACGATATGG GCGACGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTGCGGA CTGGGCGTGC
1751 GCTGGTTTCA CCCGCTCGCG CCGTTTTCTT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```
a286.pep
  1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
 51 ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLLAE
101 APDNVKTMLR SKGYFSSKVS LTKDYGAYTV HITPGPRTKI ANVGVAIGLD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTAAVNP PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLDFQQAAL EQNGHYS GASVQADFDRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYIGSVV WMDMKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTTQNL KRAFSGGIWY VRDRAGIDAR
401 LGAEFLAAGR KIPGSDIDLG NSHATMLTAS WKRLNNNLV HPENGHYLDG
451 KIGTTLGAFL SSTALIRTSR RAGYFFTPEN KKLGTFFIIR QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NSVLPERAL LVGSLEYQLP
551 FTRTSLGAVF HDMGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*
```

m286/a286 98.7% identity in 615 aa overlap

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      10      20      30      40      50      60
m286.pep MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPKFP
|||||
a286      MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPKFP
      10      20      30      40      50      60

      70      80      90     100     110     120
m286.pep VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLLAEAPDNVKTMLRSKGYFSSKVS
|||||
a286      VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLLAEAPDNVKTMLRSKGYFSSKVS
      70      80      90     100     110     120

      130     140     150     160     170     180
m286.pep LTKDYGAYTVHITPGPRTKIANVGVAIGLDILSDGNLAAYRNALENWQQPVGSDFDQDS
|||||
a286      LTKDYGAYTVHITPGPRTKIANVGVAIGLDILSDGNLAAYRNALENWQQPVGSDFDQDS
      130     140     150     160     170     180

      190     200     210     220     230     240
m286.pep WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDTATADLNVVDSGRPIAFGDFEITGTQR
|||||
a286      WENSKTSVLGAVTRKAYPLAKLGNTAAVNPDTATADLNVVDSGRPIAFGDFEITGTQR
      190     200     210     220     230     240

      250     260     270     280     290     300
m286.pep YPEQIVSGLARFQPGMPYDLDLLDFQQALEQNGHYS GASVQADFDRLQGDRVPVKVSVT
|||||
a286      YPEQIVSGLARFQPGTPYDLDLLDFQQALEQNGHYS GASVQADFDRLQGDRVPVKVSVT
      250     260     270     280     290     300

      310     320     330     340     350     360
m286.pep EVKRHKLETGIRLDSEYGLGGKIAYDYNNLFNKGYIGSVVWMDMKYETTLAAGISQPRNY
|||||
a286      EVKRHKLETGIRLDSEYGLGGKIAYDYNNLFNKGYIGSVVWMDMKYETTLAAGISQPRNY
      310     320     330     340     350     360

      370     380     390     400     410     420
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670

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m286.pep  RGNYWTSNVSYNRSTTQNLEKRAFSGGVWYVRDRAGIDARLGAEFLAEGRKIPGSAVDLG
a286      RGNYWTSNVSYNRSTTQNLEKRAFSGGIWYVRDRAGIDARLGAEFLAEGRKIPGSDIDLG
           370      380      390      400      410      420

           430      440      450      460      470      480
m286.pep  NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286      NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
           430      440      450      460      470      480

           490      500      510      520      530      540
m286.pep  KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
a286      KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
           490      500      510      520      530      540

           550      560      570      580      590      600
m286.pep  LVGSLEYQLPFTRTSLGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPPLAPFSFDIAYGH
a286      LVGSLEYQLPFTRTSLGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPPLAPFSFDIAYGH
           550      560      570      580      590      600

           610
m286.pep  SDKKIRWHISLGRFX
a286      SDKKIRWHISLGRFX
           610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

```

g287.seq
1  atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51  ctgtgggggc ggcggtggcg gatcgcccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggccgcccc gttgttgctg aaaatgccgg ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgccgcaagc
201 cgatacgtag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 tttcggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaa atgccgccga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 cccccgcgtc aaaccctgcc cctgcgaatg gcggtagcga ttttgaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 gttgaccac tgtaaaggcg attcttgtaa tgggtgataat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaaagcat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaaacc acctactcgt tctgcacggc cgaggaggtc gcttccggcc
751 gagattccgc tgattcccgt caatcaggcc gatacgtgta ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcggtatc
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttgg
951 cacggccgtg tacaacggcg aagtgtcgca tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatggaaa cggctttaag gggacttggg
1151 cggaaaatgg cggcggggat gtttccggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattccgc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

```

g287.pep
1  MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV
51  LPKEKKDEEA AGGAPQADTQ DATAGEGSQD MAAVSAENTG NGGAATDNP
101 KNEDAGAQN DMPQNAESAN QTGNQNPAGS SDSAPASNPA PANGGSDFGR

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671

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151  TNVGNVSVVID  GPSQNITLTH  CKGDSCNGDN  LLDEEAPSKS  EFEKLSDEEK
201  IKRYKKDEQR   ENFVGLVADR  VKKDGTNKYI  IFYTDKPPTR  SARSRRSLPA
251  EIPLIPVNQA   DTLIVDGEAV  SLTGHSGNIF  APEGNYRYLT  YGAEKLPGGS
301  YALRVQGEPA   KGEMLVGTAV  YNGEVLHFHM  ENGRPYPSGG  RFAAKVDFGS
351  KSVDGIIIDSG  DDLHMGTOKF  KAAIDGNFGK  GTWTENGGGD  VSGRFYGPAG
401  EEVAGKYSYR   PTDAEKGFG  VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
  1  ATGTTTAAAC  GCAGCGTAAT  CGCAATGGCT  TGTATTTTGT  CCCTTTCAGC
51  CTGCGGGGGC  GGCGGTGGCG  GATCGCCCGA  TGTCAAGTCG  GCGGACACGC
101 TGTCAAAACC  TGCCGCCCTT  GTTGTCTTCT  AAAAAGAGAC  AGAGGCAAAG
151 GAAGATGCGC  CACAGGCAGG  TTCTCAAGGA  CAGGGCGCGC  CATCCGCACA
201 AGGCAGTCAA  GATATGGCGG  CGGTTTCGGA  AGAAAATACA  GGCAATGGCG
251 GTGCGGTAAC  AGCGGATAAT  CCCAAAAATG  AAGACGAGGT  GGCACAAAAT
301 GATATGCCGC  AAAATGCCGC  CGGTACAGAT  AGTTCGACAC  CGAATCACAC
351 CCGGATCCG  AATATGCTTG  CCGGAAATAT  GGAAATCAA  GCAACGGATG
401 CCGGGGAATC  GTCTCAGCCG  GCAAACCAAC  CGGATATGGC  AAATGCGGCG
451 GACGGAATGC  AGGGGGACGA  TCCGTCGGCA  GGCGGGCAAA  ATGCCGGCAA
501 TACGGCTGCC  CAAGGTGCAA  ATCAAGCCGG  AAACAATCAA  GCCGCCGGTT
551 CTTCAGATCC  CATCCCCGCG  TCAAACCCTG  CACCTGCGAA  TGGCGGTAGC
601 AATTTTGGAA  GGGTTGATTT  GGCTAATGGC  GTTTTGATTG  ACGGGCCGTC
651 GCAAAATATA  ACGTTGACCC  ACTGTAAAGG  CGATTCTTGT  AGTGGCAATA
701 ATTTCTTGA  TGAAGAAGTA  CAGCTAAAT  CAGAATTTGA  AAAATTAAGT
751 GATGCAGACA  AAATAAGTAA  TTACAAGAAA  GATGGGAAGA  ATGATAAATT
801 TGTCGGTTTG  GTTGCCGATA  GTGTGCAGAT  GAAGGGAATC  AATCAATATA
851 TTATCTTTA  TAAACCTAAA  CCCACTTCAT  TTGCGCGATT  TAGGCGTTCT
901 GCACGGTCGA  GGCGGTGCGT  TCCGGCCGAG  ATGCCGCTGA  TTCCCGTCAA
951 TCAGGCGGAT  ACGCTGATTG  TCGATGGGGA  AGCGGTCAGC  CTGACGGGGC
1001 ATTCGCGCAA  TATCTTCGCG  CCCGAAGGGA  ATTACCGGTA  TCTGACTTAC
1051 GGGGCGGAAA  AATTGCCCCG  CGGATCGTAT  GCCCTTCGTG  TTCAAGGCGA
1101 ACCGGCAAAA  GGCGAAATGC  TTGCGGGCGC  GGCCGTGTAC  AACGGCGAAG
1151 TACTGCATTT  CCATACGGAA  AACGGCCGTC  CGTACCCGAC  CAGGGGCAGG
1201 TTTGCCGCAA  AAGTCGATTT  CGGCAGCAAA  TCTGTGGACG  GCATTATCGA
1251 CAGCGCGCAT  GATTTGCATA  TGGGTACGCA  AAAATTCAA  GCCGCCATCG
1301 ATGGAACCG  CTTTAAGGGG  ACTTGACGG  AAAATGGCAG  CGGGGATGTT
1351 TCCGGAAAGT  TTTACGGCCC  GGCCGGCGAG  GAAGTGCGG  GAAAATACAG
1401 CTATCGCCCG  ACAGATGCGG  AAAAGGGCG  ATTCGGCGTG  TTTGCCGGCA
1451 AAAAAGAGCA  GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
  1  MFKRSVIAMA  CIFALSACGG  GGGGSPDVKS  ADTLSPAP  VVSEKETEAK
51  EDAPQAGSQ  QGAPSAQGSQ  DMAAVSEENT  GNGGAVTADN  PKNEDEVAQN
101 DMPQNAAGTD  SSTPNHTPDF  NMLAGNMENQ  ATDAGESSQP  ANQPDMANAA
151 DGMQGDPSA  GGQNAGNTAA  QGANQAGNNQ  AAGSSDPIPA  SNPAPANGGS
201 NFRVLDLANG  VLIDGPSQNI  TLTHCKGDSC  SGNNFLDEEV  QLKSEFEKLS
251 DADKISNYKK  DGKNDKFVGL  VADSVQMKGI  NQYIIFYKPK  PTSFARFRRS
301 ARSRRLPAE  MPLIPVNQAD  TLIVDGEAVS  LTGHSGNIFA  PEGNYRYLTY
351 GAEKLPGGSY  ALRVQGEPAK  GEMLAGAAVY  NGEVLHFHTE  NGRPYPTRGR
401 FAAKVDFGSK  SVDGIIDSGD  DLHMGTOKF  AAIDGNFGK  TWTENGSGDV
451 SGKFYGPAGE  EVAGKYSYRP  TDAEKGFGV  FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

              10      20      30      40      49
m287.pep      MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAPVSE-----KETEA
               |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287           MFKRSVIAMACIFLSACGGGGGGSPDVKSADTPSKPAPVVAENAGEGVLPKEKKDEEA
               10      20      30      40      50      60

```

	50	60	70	80	90	100	109
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN	DMPQNAAGT					
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQN	DMPQNA--					
		70	80	90	100	110	
m287.pep	110 DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGD	120	130	140	150	160	169
g287	-----						
m287.pep	170 AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVDLANGVLIDGPSQ	180	190	200	210	220	229
g287	-ESANQTGNNQPAGSSDSAPASNPAPANGGSDFGRTNVGNSSVIDGPSQ	120	130	140	150	160	170
m287.pep	230 CSGNNFLDEEVQLKSEFEKLSADKISNYKKDGNKDFVGLVADSVQMK	240	250	260	270	280	289
g287	CNGDNLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKD	180	190	200	210	220	230
m287.pep	290 KPTSFAFRFRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNI	300	310	320	330	340	349
g287	KPPT----RSARSRRSLPAEIPVQADTLIVDGEAVSLTGHSGNI	240	250	260	270	280	290
m287.pep	350 YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPT	360	370	380	390	400	409
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPS	300	310	320	330	340	350
m287.pep	410 KSV DGIIDSGDDLHMG TQKFKA AIDGN GFKGTW TENGSGDVS GKFYGPAGEE	420	430	440	450	460	469
g287	KSV DGIIDSGDDLHMG TQKFKA AIDGN GFKGTW TENGSGDVS GGRFYGPAGEE	360	370	380	390	400	410
m287.pep	470 PTDAEKG GFGVFAGKKEQDX	480	489				
g287	PTDAEKG GFGVFAGKKDRDX	420	430				

a287.seq

1	ATGTTTAAAC	GCAGTGTGAT	TGCAATGGCT	TGTATTGTTG	CCCTTTCAGC
51	CTGTGGGGCG	GGCGGTGGCG	GATCGCCGCA	TGTTAAGTCG	GCGGACACGC
101	TGTCAAAAAC	TGCCGCCCTC	GTGTGTACTG	AAGATGTCGG	GGAAAGAGGTG
151	CTGCCGAAAG	AAAAAGAAAG	TGAGAGGCGC	TGTAGTGGTG	CGCGCAAGC
201	CGATACGCAG	GACGCAACCG	CCGGAAGAGG	CGGTCAAGAT	ATGGCGGCAG
251	TTTCGGCAGA	AAATACAGGC	AATGGCGGTG	CGGCAACAAC	GGATAATCCC
301	GAATAATAAG	ACGAGGGACC	GCAAATGAT	ATGCCCGAAA	ATGCCCGCCG
351	TACAGATAGT	TCGACACCGA	ATCACACCCC	TGACCGGAAT	ATGCCAACCA
401	GAGATATGGG	AAACCAAGCA	CCGGATGCCG	GGGAATCGGC	ACAACCGGCA
451	AACCAACCGG	ATATGCCAAA	TGCGGCGAGC	GGATGTCAGG	GGGACGATCC
501	GTCCGCACGG	GAATATCCGC	GCAATACGGC	AGATCAAGCT	GCAATCAAG
551	CTGAAAACAA	TCAAGTCGGC	GGCTCTCAAA	ATCTGCCTC	TTCACCAAT
601	CCTAACGCCA	CGAATGGCGG	CAGCGATTTT	GGAAGGATAA	ATGTAGCTAA
651	TGGCATCAAG	CTTGACAGCG	GTTTCGGAAA	TGTAACGTTG	ACACATTGTA
701	AAGACAAGT	ATGCGATAGA	GATTCTTAG	ATGAAGAAGC	ACCACAAAAG
751	TCAGAAATTG	AAAAATTAAG	TGATGAAGAA	AAAATTAAAT	AATATAAAAA

673

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801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CGCGATTGAG GCGTTCTGCA CGGTCGAGGC GGTTCGCTTCC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GGCGGATACG CTGATTGTCG
1001 ATGGGGAAGC GGTGAGCCTG ACGGGGCATT CCGCAATAT CTTCGCGCCC
1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCCGGCGG
1101 ATCGTATGCC CTCAGTGTGC AAGGCGAACC GGCAAAAGGC GAAATGCTTG
1151 CGGGCACGGC CGTGTACAAC GGCGAAGTGC TGCATTTCCA TATGAAAAAC
1201 GGCCGTCCGT CCGCGTCCGG AGGCAGGTTT GCCGCAAAAG TCGATTTCGG
1251 CAGCAAATCT GTGGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGGAAG ATGGCGGCGG GGATGTTTCC GGAAGGTTTT ACGGCCCGGC
1401 CGGCGAAGAA GTGGCGGGAA AATACAGCTA TCGCCCGACA GATGCGGAAA
1451 AGGGCGGATT CGGCGTGTTC GCCGCAAAA AAGAGCAGGA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1204; ORF 287.a>:

```

a287.pep
  1 MFKRSVIAMA CIVALSAACGG GGGGSPDVKS ADTLSPAAP VVTEDVGEEV
 51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATTDNP
101 ENKDEGPQND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA
151 NQPDMANAAD GMQGGDDPSAG ENAGNTADQA ANQAENNQVG GSQNPASSTN
201 PNATNGGSDF GRINVANGIK LDGSENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VIIYKDKSAS
301 SSSARFRRSA RSRRLPAEM PLIPVNQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMEN
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGDD LHMGTQKFKA VIDNGNGFKGT
451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEKGGFGVF AGKKEQD*

m287/a287 77.2% identity in 501 aa overlap

      10      20      30      40      49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVSE-----KETEA
||||| ||| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287      MFKRSVIAMACIVALSAACGGGGGGSPDVKSADTLSPAAPVVTEDEVGEEVLPKEKKDEEA
      10      20      30      40      50      60

      50      60      70      80      90     100     109
m287.pep KEDAPQAGSQGGQAPSAGSQSDMAAVSEENTGNGGAVTADNPKNEDVAQNMDPQNAAGT
|||| :| |:::||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287      VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNPNKDEGPQNDMPQNAADT
      70      80      90     100     110

      110     120     130     140     150     160     169
m287.pep DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDDPSAGGQNAGNTA
||||| ||| :| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287      DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGGDDPSAG-ENAGNTA
      120     130     140     150     160     170

      170     180     190     200     210     220     229
m287.pep AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNITLTHCKGDS
|:|||| |:|:|:|:|:| :||| :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a287      DQAANQAENNQVGGSQNPASSTNPATNGGSDFGRINVANGIKLDGSENVTLTHCKDKV
      180     190     200     210     220     230

      230     240     250     260     270     280     289
m287.pep CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP
|: :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a287      CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVIIYKD
      240     250     260     270     280     290

      290     300     310     320     330     340
m287.pep KP--TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNRY
| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287      KSASSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNRY
      300     310     320     330     340     350

```

674

	350	360	370	380	390	400
m287 . pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287 . pep	GSKSVVDGIIDSGDDLHMGTKQFKAAIDNGNGFKGTWTENGSGDVSQKGYGPAGEEVAGKYS					
a287	GSKSVVDGIIDSGDDLHMGTKQFKAVIDNGNGFKGTWTENGSGDVSQKGYGPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287 . pep	YRPTDAEKGFGVVFAGKKEQDX					
a287	YRPTDAEKGFGVVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288 . seq
1   atgcacaccg gacaggcggt aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgtcaag caacctacc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcgggtg cgcccttacc gcaccttttc
201 acccttgccct gtgctgccaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccggccg ttaaccggca ttctaccctg
301 cggagcccgg actttcctcc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgctg cgcggttat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacagggt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtcgccc tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288 . pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288 . seq
1   ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTCTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTG CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCCTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288 . pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
	: : : : : : : : : : :					
g288	PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCTT GTGCTGCCAA AGCAGCCATC GCGGTTTTTG CTTTCTGTTC
251 CACTTTCGGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCGTC CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
	: : : : : : : : :					

676

```

a288      PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFEVACAQVF
           130      140      150      160      170      180

m288.pep   DTX
           ::
a288      NAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

```

g290.seq
1  atggcaaaaa tgatgaaatg ggcggctggt ggcggcggtcg cggcggcagc
51  ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
151 ggcgagatth cgccgtccaa cctggatcgc gtcggcgcg caggcttcggg
201 gcagattaaa aagctttatg tcaaactcgg gcaacaggtc aaaaagggcg
251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
301 gaaaaatcca aattggaaac gtatcaggcg aagctgggtg ccgcacagat
351 tgcattgggc agcgcggaaa aaaaatataa gcgtcaggcg gcgttggtga
401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
451 gccgcgcgca aagccaatgt tgccgagttg aaggctttaa tcagacagag
501 caaaatttcc atcaataccg ccgagtcgga tttgggctac acgcgcatta
551 ccgcgcagcat ggacggcacg gtggtggcga ttcccgtgga agaggggcag
601 actgtgaacg cggcgcagtc tacgccgacg attgtccaat tggcgaatct
651 ggatatgatg ttgaacaaaa tgcagattgc cgagggcgat attaccaagg
701 tgaaggcggg gcaggatatt tcgtttacga ttttgtccga accggatacg
751 ccgattaagg cgaagctcga cagcgtcgac cccgggctga ccacgatgtc
801 gtcgggcggc tacaacagca gtacggatac ggcttccaat gcggtctatt
851 attatgcccg ttcgtttgtg ccgaatccgg acggcaaaact cgccacgggg
901 atgacgacgc agaatacggg tgaaatcgac ggtgtgaaaa atgtgttgc
951 tattccgctc ctgaccgtga aaaatcgcg cggcaaggcg ttcgtacgcg
1001 tgttgggtgc ggacggcaag gcagtggaa cgcgaaatcc gaccggtatg
1051 aaagacagta tgaataccga agtgaaaagc gggttgaaag agggggacaa
1101 agtggctatc tccgaaataa ccgcgcgcca gcagcaggaa agcggcgaa
1151 gcgccttagg cggccgcgcg cgcgataa

```

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

```

g290.pep
1  MAKMMKWA AV AAVAAAVWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STTQNTIDM
101 EKSKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATSK EDLESAQDAL
151 AAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPD
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYARSFV PNPDGKLTATG
301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
351 KDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

```

m290.seq (partial)
1  ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
51  ACTCGGGCAA CAGGTTAAAA AGGGCGATTT GATTGCGGAA ATCAATTCGA
101 CCTCGCAGAC CAATACGCTC AATACGAAA AATCCAAGTT GGAAACGTAT
151 CAGGCGAAGC TGGTGTCTGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
251 ATTTGGAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
301 GAGCTGAAGG CTTTAATCAG ACAGAGCAA ATTTCCATCA ATACCGCCGA
351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
401 TGGCGATTCT CGTGGAAGAG GGGCAGACTG TGAACGCGGC GCAGTCTACG
451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAAATGCA
501 GATTGCCGAG GGCGATATTA CCAAGGTGAA GGCGGGGCAG GATATTTTCG
551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GCGGTTTACA ACAGCAGTAC
651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTCT TTTGTGCCGA

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677

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701   ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751   ATCGACGGCG TGA AAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801   TCGCGGCGGC AAGGCGTTTG TGCGCGTGTT GGGTGCGGAC GGCAAGGCGG
851   CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901   AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951   CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001  GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
  1   ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
51   QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101  ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151  PTIVQLANLD MMLNKMQUIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201  VDPGLTTMSS GGYNSSTDTA SNAVYYYARS FVPNPDGKLA TGMTTQNTVE
251  IDGVKNVLLI PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301  KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep                                10      20      30
                                      VSVGAQASGQIKILYVKLGQVKKGDLIAE
                                      |||||
g290      PQAAYTEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQVKKGDLIAE
          30      40      50      60      70      80

m290.pep                                40      50      60      70      80      90
INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
|||||:|||||:|||||
g290      INSTTQTNTIDMEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATSKEDLESAQD
          90     100     110     120     130     140

m290.pep                                100     110     120     130     140     150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||
g290      ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPEEGQTVNAAQST
          150     160     170     180     190     200

m290.pep                                160     170     180     190     200     210
PTIVQLANLDMMLNKMQUIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||||
g290      PTIVQLANLDMMLNKMQUIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
          210     220     230     240     250     260

m290.pep                                220     230     240     250     260     270
GGYNSSTDASNAVYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
|||||
g290      GGYNSSTDASNAVYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
          270     280     290     300     310     320

m290.pep                                280     290     300     310     320     330
KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
|||||
g290      KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
          330     340     350     360     370     380

m290.pep      PPRRX
              ||||
g290          PPRRX
              390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
  1 ATGGCAAAAA TGATGAAATG GCGGGCTGTT GCGGCGGTCG CCGGCGGCAGC
 51 GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTCAGGCGC GGCGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTATG TCAAACTCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTGGA AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATTA
551 CCGAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTTGTG CCGAATCCGG ACGGCAAAC CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CGGCAGGGCG TTTGTGCGCG
1001 TGTGGGTGTC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
  1 MAKMMKWAIV AAVAAAAVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
 51 GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDIAEIN STSQTNTLNT
101 ESKLETYQA KLVSAQIALG SAEKKYKQQA ALWKDDATAK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYARSFV PNPDKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

m290/a290 98.2% identity in 334 aa overlap

                                10      20      30
m290.pep                                VSVQAQASGQIKILYVKLGQOVKKGDIAE
a290                                PQAAYITETVRRGDISRTVSATGEISPSNLVS
                                30      40      50      60      70      80
                                VSVQAQASGQIKKLYVKLGQOVKKGDIAE

                                40      50      60      70      80      90
m290.pep  INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKQQAALWKENATSKEDLESAQD
a290  INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKQQAALWKDDATAKEDLESAQD
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m290.pep  AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
a290  ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m290.pep  PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
a290  PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
                                210     220     230     240     250     260

                                220     230     240     250     260     270
```

679

```

m290.pep      GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
a290          GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
               :||||||||||||||||||||||||||||||||||||||||||||||||||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               ||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggccttg gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaaa agccatcaaa gaagtacgcy
401 gcaacggcaa gctgaaagtc gccgtcttct cgcaccccca ttgtccgttc
451 tgcaaacgct tggaaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atggtgtcag cccgaccgtg ccaaagcgtg gacggatttg
601 atgcgtaaag gcaaattccc ggtcggcggc agcatctgcg acaatcccgt
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tcccaacagg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLP LLAC GQTPVSNANA ESAVKAESAG KSAVASLKR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTD AEG GYMFV GELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQ PDA
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAaaaaa CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCCTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGACAAA AGCCATCAAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCCATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC

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680

751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```

m292.pep
  1 MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLTKAR
 51 LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILTPFTVLPLLACGQTPVSNANAEP	PAVKAESAGKSVAASLTKARLEKTYSAQDL				
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAES	AVKAESAGKSVAASLTKARLEKTYSAQDL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLVSSETPVKGIYEVVVSQ	RQIIYTDAEGGYMFVGELINIDTRKNL	TEERAADLNKIDF			
g292	KVLVSSETPVKGIYEVVVSQ	RQIIYTDAEGGYMFVGELINIDTRKNL	TEERAADLNKIDF			
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPF	CKRLEHEFEKMTDVT	VYSFMMPIAGLHPDA			
g292	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPF	CKRLEHEFEKMTDVT	VYSFMMPIAGLHPDA			
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGKFPVGG	SICDNPVAETTS	SLGEQFGFN	GTPTLVFPNG		
g292	ARKAQILWCQPDRAKAWTDWMRKGKFPVGG	SICDNPVAETTS	SLGEQFGFN	GTPTLRLPQR		
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSPMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHFPQKPAVNPQX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1 ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGCGCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCCAGTGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTTCC GGTCGCGCGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC
751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAGG GYMFVGGELIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLV AVFSDPDCPF
151  CKRLEHEFEK MTDVTYSEF MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251  QLEEIIRKNQ *

m292/a292    100.0% identity in 260 aa overlap

              10      20      30      40      50      60
m292.pep      MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAPVKAESAGKSVAAASLKARLEKTYSAQDL
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a292           MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAPVKAESAGKSVAAASLKARLEKTYSAQDL
              10      20      30      40      50      60

              70      80      90      100     110     120
m292.pep      KVLVSSETPVKGIYEVVVSQRQIIYTDAGGGMFVGGELINIDTRKNLTEERAADLNKIDF
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a292           KVLVSSETPVKGIYEVVVSQRQIIYTDAGGGMFVGGELINIDTRKNLTEERAADLNKIDF
              70      80      90      100     110     120

              130     140     150     160     170     180
m292.pep      ASLPLDKAIKEVRGNGKLVAVFSDPDCPFCKRLEHEFEKMTDVTYSEFMPIAGLHPDA
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a292           ASLPLDKAIKEVRGNGKLVAVFSDPDCPFCKRLEHEFEKMTDVTYSEFMPIAGLHPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m292.pep      ARKAQILWCQPDRAKAWTDWMRKGFVGGGICDNPVAETTSLSGEQFGFNGTPTLVFPNG
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a292           ARKAQILWCQPDRAKAWTDWMRKGFVGGGICDNPVAETTSLSGEQFGFNGTPTLVFPNG
              190     200     210     220     230     240

              250     260
m292.pep      RSQSGYSPMPQLEEIIRKNQX
              ||||||||||||||
a292           RSQSGYSPMPQLEEIIRKNQX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
 51  gggttcgggc gtcagaacat catcgaaccg ctttcctcgc gcgttacgac
101  gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151  tggcatcggg tgcggcgggt caagtcgaat cggcggacgc gtggcgtgaa
201  gccgttgaaa aaaccttata tggcgagggg ggcggaatgc agatgcaggc
251  gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301  ccgaggcggg gcgggaagcg gtatgcggac atcgggggcg atagtgtatc
351  aatccgtatc cgagttttcc ggttgaggca tcgtatgagt atttatgccg
401  tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcgtg
451  ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgtcgcg
501  cgaggcgcgg cgcaagtggg aaaaggcaat gtcttaccgc gccgtcaggg
551  tgatgccgtt tgcggtcgga ctgctgttcg ccagggaac tctagatcgc
601  actgcagcag catgcctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAAVWSVRA VRTSSNRFFA ALRRYSAFRP TIFPKPAGTP
 51  WHRVRRFKSN RRTRGVKPLK KPYLARGAEC RCRAWTALS HNIAERARES
101  PRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151  FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVPFAVG LLFARGTLES
201  TAAACP....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

m294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTCGGGTT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTCCCGAC
 101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
 151 TGGCATCGGG TCGGCGGGT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
 201 GCCGTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
 451 TTTTTTGAAG TGCTGGTTTT GTCCGTCTCG CACACGGGAC GGGTGTGCGG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTGAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCCG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
 701 TCGCATCGC CGTCGTCAA ATGGCGCGT CCACACTGAC GGTGCGTTGG
 751 TCGAAATACA TACAGCCCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTT ATACAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep
 1 MRITCAPMSL LSAAVWSIRV VRTSSNRFP AFRYSAFQ TIFPKPADTP
 51 WHRVRRFKSN RRMGGKPLK KPYRPRGGC RCRRRAWTALS HNIAERARES
 101 PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
 201 ANRYSILGE PFATSFMTL TLKILLAFSV LAHFAIAVK MARSTLTGVW
 251 SKYIHAVVFT HMLLIVFLAK AMFYISW*

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSA	AVWSVRV	RTSSNRFP	ALRRYS	AFRPTIF	PKPAGTP
m294	MRITCAPMSLLSA	AVWSIRV	RTSSNRFP	ALRRYS	AFRPTIF	PKPAGTP
	70	80	90	100	110	120
g294.pep	RRTRGVKPLK	PPYLARGA	ECRRRAW	TALSHN	IAERARE	SPRCGK
m294	RRTRGVKPLK	PPYLARGA	ECRRRAW	TALSHN	IAERARE	SPRCGK
	130	140	150	160	170	180
g294.pep	RVFRLEHRMS	IYAVAH	IHLICAT	AFVGGV	FFEVLS	VLHTGR
m294	RVFRLEHRMS	IYAVAH	IHLICAT	AFVGGV	FFEVLS	VLHTGR
	190	200	210	220	230	240
g294.pep	AVRVMF	FAVGLL	FARGTL	ESTAA	ACP	
m294	AVRVMF	FAVGLL	FARGTL	ESTAA	ACP	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTCGGGCT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTCCCGAC
 101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT
 151 TGGCATCGGG TCGGCGGGT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
 201 GCCGTGAAA AAACCTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC
 251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GGTGGAGTA CCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG
 451 TTTTTTGAAG TGCTGGTTTT GTCCGTCTCG CACACGGGAC GGGTGTGCGG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTGAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCCG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

683

701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRRYSAFRP TIFPKPAGTP
 51 WHRVRRFKSN RRTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMPEFVVG LLFASGIVMA
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFIAVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRV	VRTSSNRFPAAFRRYSAF	QPTIFPKPADTPWHRVRR	FKSN		
a294	MRITCAPMSLLSAAVWSIR	AVRTSSNRFPAAFRRYSA	FRPTIFPKPAGTPWHRVRR	FKSN		
	10	20	30	40	50	60
	70	80	90	100	110	120
m294.pep	RRMRGGKPLKPYRPRGGG	CRRAWTALSHNIAERARE	SPRRCKRYADIGGDS	DTIRI		
a294	RRTRGGKPLKTYRPRRAE	CRRTALSHNIAERARE	SPRRYGKRYADIGGDS	DTIRI		
	70	80	90	100	110	120
	130	140	150	160	170	180
m294.pep	RVFRLEHRMSIYAVAHIV	HLHYCAIAFVGGVFFEVL	VLSVLHTGRVSR	EARREVEKAMSYR		
a294	RVFRLEYRMSIYAVAHIV	HLHYCAIAFVGGVFFEVL	VLSVLHTGRVSC	EARREVEKAMSYR		
	130	140	150	160	170	180
	190	200	210	220	230	240
m294.pep	AVRVMPEFVVGLLFASGIV	MAANRYLSILGEPFATS	FGTMLTLKILLAFSV	LAHFIAVVK		
a294	AVRVMPEFVVGLLFASGIV	MAANRYLSILGEPFATS	FGTMLTLKILLAFSV	LAHFIAVVK		
	190	200	210	220	230	240
	250	260	270			
m294.pep	MARSTLTVGWSKYIHAVV	FTHMLLIVFLAKAMFYI	SWX			
a294	MARSTLTVGWSKYIHTVV	FTHMLLIVFLAKAMFYI	SWX			
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq
 1 atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt
 51 gttgccacgc cgccagcagt ttttcgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaa
 151 ctgcccgcgc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccgca cacctgcacg gatgccgcgc ccaatttcgc caaccgcgc
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
 301 acgatcagg cgcggaactt tcagataacc gttcagcgat tttccgaca
 351 gccgcgcatt cgcaaaaac agcggcacac ccgctcgccg gcattccttc
 401 atcagatttg gccagatttc ggtttccatc aaaatgccga acatcgggcg
 451 gtgttcgcgc aaaaactgcc gtaccacagt tttttgtca tacggaagat
 501 agcggcattg cgcacggga aacagaactt gcgcggttcc cgtcccgtc
 551 ggggtcatct cgtcatcag cagcggcgca tcgggaaaac gccgccgcaa
 601 ctgcgctatc aagggttggg cggcacgcgt ttctccgacc gaaacggcgt
 651 gtatccaaac cgcccggtta acgggattcg gatgcggctt gccgaaacgc
 701 tcgtccctat gcgcccggtta tgcgggggca cttccggagc gtttgtccaa
 751 ataacgccgt atccatatcg gcgcaagcag ccacaatata tcataaagcc
 801 attggaacat ctttctattt cctgcaaaaac aaatgccgtc cgaacggttc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

g295.pep

```

1  MLGMARHDDGQ OGIAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK
51  LPRQRFHVF RHOVVFVFGIAA HLHGCRAQFR QPRRIRLRLR QTRQRSGCG
101 TDQAADFQIT VQRFRRQPRI RQKQRHTRSP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq

```

1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTCCGCCT CGTCTTACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCGCA CGGTATGATG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTGAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA
351 GCCGCGCATC CGCCAAAAAC AGCGGCACAC CGCGCGCGCG GCATTCCCTC
401 ATCAGGTTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTGCGGC AAAAAGTACC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATG CGCATCGGGA AACAGAACTT GCGCGGTTTC CCGCCCCGTC
551 GCGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAGAC GCCGCGGCAA
601 CTGCGGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGTCCCGAT GCGCCCGATA TGCCGGGGCA CTTCCGGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC TGAACGGTTC
851 AGACGGCATT TCGGCAACGG AATCAAATAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep

```

1  MLGMARHDDQ QRIAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK
51  LPRQRFHFLR RYDVVFVFGIAA HLHGCRAQFR QPRRIRLCLR QTPRQRSGGR
101 TDQAADFQIT VQRFRRQPRI RQKQRHTRAP AFPHQVGPDP GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PRRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV XTVQTAFRQR NQIS*

```

m295/g295 93.9% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
g295	10	20	30	40	50	60
m295.pep	70	80	90	100	110	120
g295	70	80	90	100	110	120
m295.pep	130	140	150	160	170	180
g295	130	140	150	160	170	180
m295.pep	190	200	210	220	230	240
g295	190	200	210	220	230	240
m295.pep	250	260	270	280	290	
g295	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTCAAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGCGAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTTCCATC AAAATGCCGA ACATCGGGCG
451 GTTTCGCGC AAAAACTGCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCGTC
551 GGGGTCTATCT GCGTCATCAG CAGCGGCGCA TCGGAAAAC GCTGCCGCA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TTCCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTCG GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCCGATA TGCAGGGGCA CTTCCGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDQ QGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRHFLFR RHQVVFQIAA HLHGCRAQFR QPRRIRLRLC QTARQRSGGR
101 TDQAADFQIT V*RRFRQPRI RQKQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPO
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
	MLGMARHDDQ	QRIAAILLPR	RQOFFRLVFT	PINARAAAHG	GNRPASDAFFK	LPRQRHFLFR
a295	10	20	30	40	50	60
	MLGMARHDDQ	QGIAAILLPR	RQOFFRLVFT	PINARAAAHG	NLPVSDAFFK	LPRQRHFLFR
m295.pep	70	80	90	100	110	120
	RYDVVFQIAA	HLHGCRAQFR	QPRRIRLRLC	QTARQRSGGR	TDQAADFQIT	VQRRFRQPRI
a295	70	80	90	100	110	120
	RHQVVFQIAA	HLHGCRAQFR	QPRRIRLRLC	QTARQRSGGR	TDQAADFQIT	VXRFRQPRI
m295.pep	130	140	150	160	170	180
	RQKQRHTRAP	AFPHQVGP	DFGFHQNAE	HRAVFAQK	LPYPRFFV	IRKIAALRIGKQNLRGF
a295	130	140	150	160	170	180
	RQKQRHTRAP	AFLHQIGP	DFGFHQNAE	HRAVFAQK	LPYPRFFV	IRKIAALCIRKQNLRGF
m295.pep	190	200	210	220	230	240
	PPRRGLRHQ	QRRIGKTP	PQLAYQGL	GGTRFSDR	NGVYPNR	RAGNGIRIRLAETLVPMRPI
a295	190	200	210	220	230	240
	PSRRGLRHQ	QRRIGKTP	PQLAYQGL	GGTRFSDR	NGVYPNR	RAGNGIRIRLAETLAPMRPI
m295.pep	250	260	270	280	290	
	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIKPLEH	LSISCKTNAV	XTVQTAFRQR	NQISX
a295	250	260	270	280	290	
	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIKPLEH	LSISCKTNAV	RTVRTAFRQR	NQISX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

```

51  GCTTGCCGTT TCGATTATTC TGGTGTcgcG GGCATACATT Gcttcgacag
101 agggggaccga gcgcgtcaga ccgcAGCGCG TggaacaaaA ACTGCCGCCG
151 CTGTCTTGGG gcggcaacgg CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tCGGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCAGTGCG CGCGAAGTGC AGTTTTttac CGACGAAGAC GGCGAGCGCA
401 aTctGGTcGC TTTGGAaaaa AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
701 CAACCCATCA GCGTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCgaG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 GAAGGCATG TGCCTGGCGG CGAGGTCATC GGTTTTGTG GTTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID.1236; ORF 297.ng>:

```

g297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PQRVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGG EAD
101 LRHLRADQSV HVLVGGDGSA REVQFTDED GERNLVALEK KGGIWRRSAS
151 DADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVAVRLLYD SLYFHGQQVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYVDEGGRV LQEKGGFNIE PLVYTRISSP FGVRMHPILH TWRLHTGIDY
301 AAPQGTFPVR SADGVITFKG RKGGYGNVAV IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPNVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

```

m297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTcgcG GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAACAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGCACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCAGCGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TCGGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCGAGCGCA
401 ATCTGGTcGC TTTGGAaaaG AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCAATG TGCGCGGCGG CGAGGTCATC GGTTTTGTG GTTCGACCGG
1101 GCGTTTCGACC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

```

m297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERVR PQRVEQNLPP
51  LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGG EAD
101 LRHLRADQSV HVLVGGDGGA REVQFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

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687

201 EGDVRLMYD SLYFHGQOVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
 251 GNYYDEDGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTTPVRA SADGVITFKG RGGYGNVAVM IRHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVSGTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIIILVSAAYIASTERTVRPQORVEQNLPPLSWGGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIIILVSAAYIASTEGTERVRPQORVEQKLPLPLSWGGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA					
g297	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTDEDGERNLVALEKKGGIWRRSASEADMKVLPRLSVVVKTSARGSLARAEPV					
g297	REVQFFTDEDGERNLVALEKKGGIWRRSASDADMKVLPRLSVVVKTSARGSLARAEPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRELSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQOVAAGDILAAEVVKGGRHQAFY					
g297	EIRELSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQOVAAGDILAAEVVKGTTTQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGNYYDEDGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGNYYDEDGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRASADGVITFKGRGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTTPVRASADGVITFKGRGGYGNVAVMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVSGTGRSTGPHLHYEARINGQPVNPVSVLPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVSGTGRSTGPHLHYEARINGQPVNPVSVLPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

```

1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
51  GCTTGCCGTT TCGATTATTT TGGTGTCTGGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA ACTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG TGTTCAAGAC GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCA GCGCACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA AATTGCCCGA ATAACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TCGTGCCGA CCACTCGGTT CATGTTTGG TCGGCGGCGA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GCGGAGCGCA
401 ATCTGGTCTG TTTGGAAGAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCT TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATTCGCG

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688

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551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTGAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TGC GCGGCGG CGAGGTCATC GGT TTTGTGCG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GGC GCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

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This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

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a297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV R PQRVEQKLPP
51  LSWGGSGVQT AYWVQEA VQP GD SLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGD GGA REVQFFTED GERNLVALEK KGGIWRRSAS
151 EADMKVLP TL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQQVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDEDGRV LQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY
301 AAPQGT PVRA SADGVITFKG RKGGYGNVAVM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

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m297/a297 99.3% identity in 430 aa overlap

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              10      20      30      40      50      60
m297.pep      MAVFPLSAKH RKYALRALAVSIILVSAAYIASTERTERV R PQRVEQNLPPLSWGGSGVQT
a297           MAVFPLSAKH RKYALRALAVSIILVSAAYIASTERTERV R PQRVEQKLPPPLSWGGSGVQT
              10      20      30      40      50      60

              70      80      90      100     110     120
m297.pep      AYWVQEA VQP GD SLADVLAR SGMARDEIAR ITEKYGGEADLRHLRADQSVHVLVGGD GGA
a297           AYWVQEA VQP GD SLADVLAR SGMARDEIAR ITEKYGGEADLRHLRADQSVHVLVGGD GGA
              70      80      90      100     110     120

              130     140     150     160     170     180
m297.pep      REVQFFTEDGERNLVALEKKGGIWRRSASEADMKVLP TLR SVVVKTSARGSLARAEVPV
a297           REVQFFTEDGERNLVALEKKGGIWRRSASEADMKVLP TLR SVVVKTSARGSLARAEVPV
              130     140     150     160     170     180

              190     200     210     220     230     240
m297.pep      EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSL YFHGQQVAAGDILAAEVV KGGTRHQAFY
a297           EIRESLSGIFAGRFSLDGLKEGDAVRLIYDSL YFHGQQVAAGDILAAEVV KGGTRHQAFY
              190     200     210     220     230     240

              250     260     270     280     290     300
m297.pep      YRSDKEGGGGNYYDEDGKVLQEKGGFNIEPLVYTRISSPFG YRMHPILHTWRLHTGIDY
a297           YRSDKEGGGGNYYDEDGRVLQEKGGFNIEPLVYTRISSPFG YRMHPILHTWRLHTGIDY
              250     260     270     280     290     300

              310     320     330     340     350     360
m297.pep      AAPQGT PVRASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
a297           AAPQGT PVRASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
              310     320     330     340     350     360

```

689

	370	380	390	400	410	420
m297 . pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297 . pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298 . seq

1	ATGAAAACT	TTCTTCCCT	TTTCGCTCC	ATACTGATGT	CTGCCCTGAT
51	TGCCGTGTGG	TTTACGCCAA	ACCCCATCAA	CGCCTACTGG	CAGCAGACCT
101	ACCACGCAA	CAGCCCGCTC	GAACCGCTTG	CCGCCTACGG	ATGGTGGCGG
151	AGCGGAGCGG	CGTTGCAAGA	AAACGCCTAC	GCCCTTTCAG	ACGGCATCAA
201	AACCTTCCTG	TCCGGCGAAA	cgccccccac	ggCTCAAGAC	GGCGGTTCCG
251	CAGATATGCC	GCCTGAAGCC	GCCGCATCCG	AAGCCGCCCC	GCCGGCCGGC
301	GGAAACAGAA	GGAAACAAGG	CACCGAAGCC	GCCGCCGTCC	GCAGCGGCGA
351	CAAAGTCTTT	TTCCGCCGAG	ATTCTGCTGAT	GCAGGGCGTT	GCGCCTTTCG
401	TGCAAAAAAG	CCTGAAACAG	CAATACGGCA	TCGAATCCGC	CAACCTCAGC
451	AAACAAAGCA	CGGGGCTTTC	CTATCCCTCA	TTCTTCGACT	GGCCGAAAAAC
501	GATTGAAGAA	ACCTTGAAAA	AACATCCCGA	AATCAGCGTA	CTCGCCGTCT
551	TCCTCGGCC	GAACGACCCG	TGGGATTTCC	CCGTCGGCAA	ACGCTACCTC
601	AAATTTCGCTT	CCGACGAATG	GGCGCAAGAA	TACCTGAAAC	GCGTCGACCG
651	CATCCTTGAA	GCCGCACACA	CGCACCGCGT	CCAAGTCGTC	TGGCTCGGCA
701	TCCCTACAT	GAAAAAAGTC	AAGCTCGACG	GTCAGATGCG	CTACCTCGAC
751	AAACTGCTTT	CGGAACACTT	GAAAGGCAAA	ATCATCCTGA	TTCCACCCGC
801	GCAAACTG	AGCGCGGGA	AAGgccGCTA	CACCGATTCC	GTCAACGTCA
851	ACGGCAAACC	CGTCCGCTAC	CGCAGTAAGG	ACGGCATAACA	CTTTACCGCC
901	GAAGGACAAA	AACTGCTGGC	GGAAAAATA	ATGAAAAAA	TCGTTTTTGA
951	ACCGAGTACG	CAACCATCAA	GTACACAGCC	ATGA	

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298 . pep

1	MKNFLSLFAS	ILMSALIAVW	FSQNPINAYW	QQTYHRNSPL	EPLAAYGWWR
51	SGAALQENAY	ALSDGIKTFI	SGETPPTAQD	GGSDAMPPEA	AASEAAPPAG
101	GTEWKQGTGA	AAVRSGDKVF	FAGDSLMOGV	APFVQKSLKQ	OYGIESANLS
151	KQSTGLSYPS	FFDWPKTIEE	TLKKHPEISV	LAVFLGPNDP	WDFPVGKRYL
201	KFASDEWAQE	YLKRVDRILE	AAHTRVQVW	WLGIPYMKKV	KLDGQMRYLD
251	KLLSEHLKGG	IILIPTAQT	SGGKGRYTD	VNVNGKPVRY	RSKDGIFHTA
301	EGQKLLAEKI	MEKIVFEPST	QPSSTQP*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298 . seq

1	ATGAAAACT	TTCTTCCCT	TTTCTCCTCC	ATACTGATGT	CTGCCCTGAT
51	TGCCGTGTGG	TTTACGCCAA	ACCCCATCAA	CGCCTACTGG	CAGCAGACCT
101	ACCACGCAA	CAGCCCGCTC	GAACCGCTTG	CCGCCTACGG	ATGGTGGCGG
151	AGCGGTGCGG	CGTTGCAAGA	AAACGCCTAC	GCCCTTTCAG	ACGGCATCAA
201	AGCCTTCCTG	TCCGGCGAAA	CGCCGCCGAC	GGCTCAAGAC	GGCGGTTCCG
251	CAGATATGCC	GTCTGAAGCC	GCCGCATCCG	AAGCCGTCCC	TCAAACCGGT
301	GAAACAGAA	GGAAACAAGA	CACCGAAGCC	GCCGCCGTCC	GCAGCGGCGA
351	CAAAGTCTTT	TTTGTCCGCG	ACTCGCTGAT	GCAGGGCGTT	GCCCCCTTCG
401	TGCAAAAAAG	CCTGAAACAG	CAATACGGCA	TCGAATCCGT	CAACCTCAGC
451	AAACAAAGCA	CGGGGCTGTC	CTACCCCTCA	TTCTTCGACT	GGCCGAAAAAC
501	GATTGAAGAA	ACCTTGCAAA	AACATCCCGA	AATCAGCGTA	CTCGCCGTCT
551	TCCTCGGACC	GAACGACCCG	TGGGATTTCC	CCGTCGGCAA	ACTCTATCTC
601	AAATTTCGCTT	CCGACGAATG	GGCGCAAGAA	TACCTGAAAC	GTGTCGACCG
651	CATCCTTGAA	GCCGCACACA	CGCACCGCGT	CCAAGTCGTC	TGGCTCGGCA
701	TCCCTACAT	GAAAAAAGCC	AAGCTCGACG	GACAGATGCG	CTACCTAGAC
751	AAACTGCTTT	CGGAACATTT	GAAAGGCAAA	ATCATCCTGA	TTCCACCCAC
801	GCAACCCCTG	AGCGCGGGA	AAGACCGCTA	CACCGACTCC	GTCAACGTCA
851	ACGGCAAACC	CGTCCGCTAC	CGCAGCAAGG	ACGGCATAACA	CTTTACCGCC
901	GAAGGACAAA	AACTGCTGGC	GGCAAAAATA	ATGAAAAAA	TCGTTTTTGA
951	ACCAAGTACG	CAACCATCAA	GTACACAGCC	ATGA	

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep
 1 MKNFLSLFSS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
 51 SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AASEAVPQTG
 101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
 151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
 201 KFASDEWAQE YLKRVDRIE AAHTRVQVV WLGI PYMKKA KLDGQMRYL
 251 KLLSEHLKGK IILPTHTL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
 301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGADMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	ALSDGIKTFISGETPPTAQDGGADMPPEAAASEAAPPAGGTEWKQDTEAAAVRSGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQYQIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQYQIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWFDPVGKLYLKFASDEWAQEYLKRVDRIEAAHTRVQVVWLGI PYMKKA					
g298	LAVFLGPNDPWFDPVGKRYLKFASDEWAQEYLKRVDRIEAAHTRVQVVWLGI PYMKKV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLKLLSEHLKGKIIILPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
g298	KLDGQMRYLKLLSEHLKGKIIILPTAQTLSGGKGRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq
 1 ATGAAAACT TTCTTTCCCT TTTGCGCTCC ATACTGATGT CTGCCCTGAT
 51 TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
 101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
 151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTTCA ACGGCATCAA
 201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCGGTTCGG
 251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAACCTGGC
 301 GAAACAGAAT GGAAACAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA
 351 CAAAGTCTTT TTCGCCGGCG ACTCGCTGAT GCAGGGCGTT GCACCCTTCG
 401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
 451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAAC
 501 GATTGAAGAA ACCCTGAAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
 551 TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC
 601 AAATTCGCTT CCGACGAATG GGCGCAAGAA TACCTGAAAC GCGTCGACCG
 651 CATCCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
 701 TCCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

691

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751  AAACTGCTTT CGGAATATTT GAAAGGCAAA ATCATCCTGA TTCCCACCGC
801  GCACACCCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851  ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901  GAAGGACAAA AACTGCTGGC GGCAGAAAATA ATGGAAAAAA TCGTTTTTGA
951  ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

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This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

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a298.pep
  1  MKNFLSLFAS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
 51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AAPETAPQTG
101  ETEWKQNTA AAVRTGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESVNLS
151  KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDF WDFPVGKRYL
201  KFASDEWAE YLKRVDRIE AAHthyVQVW WLGIpYMKKA KLDGQMRYLD
251  KLLSEYLGK IILIPtAHTL SGGKDRYtDS VNVNGKpVRY RSKDGIHfTA
301  EGQKLLAAKI MEKIVfEPST QPSStQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFLSGETPPTAQDGGADMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFLSGETPPTAQDGGADMPSEAAAPETAPQTGETEWKQNTAEEAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQYQIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLMOGVAPFVQKSLKQYQIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDFWDFPVGKLYLKFADEWAEYLKRVDRIEAAHthRVQVWVLGIpYMKKA					
a298	LAVFLGPNDFWDFPVGKRYLKFADEWAEYLKRVDRIEAAHthyVQVWVLGIpYMKKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLDKLLSEHLKGKIIILIPtHTLSGGKDRYtDSVNVNGKpVRYRSKDGIHfTA					
a298	KLDGQMRYLDKLLSEYLGKIIILIPtAHTLSGGKDRYtDSVNVNGKpVRYRSKDGIHfTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVfEPSTQPSStQPX					
a298	EGQKLLAAKIMEKIVfEPSTQPSStQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
  1  ATGAACCCCA AACACTTCAT CGCATTTTCC GCCCTGTTCC CCGCCACGCA
 51  GGCAGAAGCC CTGCCCCTCG CCTCCGTCAG CCCCGACACC GTTACCGTTT
101  CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151  AACGCCGCGC CCTCGCCTTG GATGAAAAAA CTCCGATCCG TCGCACAAGG
201  CAGCGGCGAG GCCTTCCGCA TCCTGCAAAT CGGCGACTCG CATACCGCCG
251  GCGACTTCTT TACCGACGCC CTGCGCAAAC GCCTGCAAAA AACATGGGGC
301  GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351  GGCGGCGGTC CGTCACAGCG GCAACTGGCA AAGCTTCACC AGCAGGAACA
401  ATACCGGAGA TTTCCCGCTC GGCGGCATCC TCGCCCAAAC CGGCAGCGGC
451  GGCGGCATGA CCCTGACCGC GTCTGACGGC AAAACCGGCA AACAGCGCGT

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g299.pep

1	<u>MNPKHFIAFS</u>	<u>ALFAATQAEA</u>	LPVASVSPDT	VTVSPSAPYT	DTNGLLLTDYG
51	NAAASPWMKK	LRSVAQGSSE	AFRILQIGDS	HTAGDFFDTA	LKRRLQKXTWG
101	DGGIGWVWPA	NVKGQRMAAV	RHSGNNQWST	SRNNTGDFFPL	GGILAQGTSG
151	GGMTLTASDG	KTKGRVSLF	AKPLLAEQTL	TVNGNTVTSAN	GGGWQVLDTG
201	AALPLAIQTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLAQGTGADL	VILSYGTNEA	FNNNIDIAQT	QKRWLDTQVQ	IRDSLPAAGI
301	LIIGAPESLK	NTLGVCGTRP	VLLTEVQQMQ	RRVARQGRQM	FWSQNWAMGG
351	ICSMKNWLNQ	GWAAKDGVHF	SAQGYRRAAE	MLADSLLEELV	RAAAIIRQ*

m299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTTC	GCCCTATTTCG	CCGCCACGCA
51	GGCAGAAGCC	CTACCTGTCG	CCTCCGTCAG	CCTCGACACC	GTTACCGTTT
101	CCCCGTCGCG	CCCCATACAC	GATACAAACG	GGTGCTGAC	CGCATACGGC
151	AACGCTCCCG	CCTCGCTTGT	GATGAAAAAA	TCCAATTCCG	TCGCACAAGG
201	CAGCGGCGAG	ACCTTCCGTA	TCTGCAAAT	CGGCGACTCG	CATACCGCGG
251	GCGACTTCTT	TACCGACAGC	CTGCGCAAAC	GCCTGCAAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCGGTC	GGGCACAACG	GTAACGTGCA	AAGCCTACC	ACGAGGAACA
401	ACACCGGAGA	CTTCCCGCTC	GGCGGCATCC	TCGCCACAC	CGGCAGCGGC
451	GGCAGCATGA	CCCTGACCGC	ATCGGACGGC	ATAGCAAGCA	AGCAGCGCGT
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCTTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAAAATCCC	CGCGCGGCAT	TACCGTTTTC	GCGATGGGCA
701	TCAACGCGCG	ACAATTAACC	CAGTGGTCGA	AATGGCTTGC	CGACCGTATG
751	AACGACCTCG	CCCAAACCGG	GGCGGATTTG	GTTATCTCTT	CTACCGGCAC
801	CAACGAAGCT	TTCAACAACA	ACATCGACAT	TGCCGACACC	GAACAAAAAT
851	GGCTGGGATC	CGTCCGCGCA	ATCCCGCACA	GCCTGCCTCG	CGCCGGCATC
901	CTCATCATCG	CGCACAACCG	ATCCCTGAAA	AACACGCTCG	GCGTATGCGC
951	CACACGCCCC	GTCGCGCTGA	CGCAAGTCCA	ACAGATGACG	CGCGCGTTCG
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAAACGC	CATGGGCGGC
1051	ATATGCAGCA	TGAAAAACGG	GCTCAACGCA	GGATGGGCGG	CCAAAGACGG
1101	CGTACACTTC	TCGCGCAAAG	CGTACCAGCG	CGCGGCGGAA	ATGCTGCCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

m299.pep

1	MNPKHIAFS	<u>ALFAATQAEA</u>	LPVASVSLDT	VTVSPSAPYT	DTNGLLLTDYG
51	NASASPWMKK	LQSAVQGSSE	TFRILQIGDS	HTAGDFPTDS	LKRRLQKQTH
101	DGGIGWVYPA	NVKGQRMVA	RHNGNQWSTL	SRNNTGDFPL	GGILAHTGSG
151	GSMTLTASDG	IASKQRVSLF	AKPLLAEQTL	TVNGNTVSAN	GGGWQVLDTG
201	AALPLTIHTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLAQTGADL	VILSYGTNEA	FNNNIDIATD	EQKWLDTVQR	IRDSLPAAGI
301	LIIGAPESLK	NTLGVCGTRP	VLRTVEQQMQ	RLVARQOQTM	FWSWQNMAGG
351	ICSMKNWLNQ	GWAAKDGVHF	SAKGYRRAAE	MLADSLEELV	RSAAITRQ*

m299/q299 95.5% identity in 397 aa overlap

m299.pep MNPKHLIAFSALFAATQAEALPVASVSLDTVTVPSPAPYTDNGLLTDYGNASASPWMKK

693

g299	MNPKHFIAFSALFAATQAEALPVASVSPDTVTVSPSAPYTDNGLLTDYGNAAASPWMKK
	10 20 30 40 50 60
m299.pep	LQSVAGSGSETFRILQIGDSHTAGDFFDLSLRKRLQKTWGDGGIGWVYPANVKGQORMAAV
g299	LRSVAGSGGEAFRILQIGDSHTAGDFFDLSLRKRLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
g299	RHSGNWQSFTRSNNTGDFPLGGILAHTGSGGSMTLTASDGTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
g299	TVNGNTVSANGGGWQVLDTGAAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKNLTGVCGTRPVRLTEVQQMQRVARQGQTMFWSWQAMGGICSMKNWLNQ
g299	LIIGAPESLKNLTGVCGTRPVLLTEVQQMQRVARQGQTMFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDGVHFSAGYRRAAEMLADSLEELVRSAAIRQX
g299	GWAAKDGVHFSAGYRRAAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTCC	GCCCTATTTCG	CCGCCACGCA
51	GGCAGAAGCC	CTACCTGTCG	CCTCAGTCAG	CCTCGACACC	GTTACCGTTT
101	CCCCGTCCGC	CCCCTACACC	GATACAAACG	GGCTGCTGAC	CGACTACGGC
151	AACGCTCCG	CCTCGCCTTG	GATGAAAAAA	CTCCAATCCG	TCGCACAAGG
201	CAGCGCGAG	ACCTTCCGTA	TCCTGCAAAT	CGGCGACTCG	CATACCGCCG
251	GCGACTTCTT	TACCGACAGC	CTGCGCAAAC	GCCTACAAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCCGTC	CGGCACAAACG	GTAAC TGCA	AAGCCTCACC	AGCAGGAACA
401	ACACCGGAGA	CTTCCCGCTC	GGCGGCATCC	TCGCCCACAC	CGGCAGCGGC
451	GGCAGCATGA	CCCTGACCGC	ATCGGACGGC	ATAGCAAGCA	AGCAGCGCGT
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAAAATCCC	CCGGCGGCAT	TACCGTTTCC	GCGATGGGCA
701	TCAACGCGCG	ACAATTAACC	CAGTGGTCGA	AATGGCGTGC	CGACCGTATG
751	AACGACCTTG	CCCAAACCGG	CGCCGATCTA	GTCATCCTTG	CCTACGGTAC
801	CAACGAAGCC	TTCGGCGACA	ACATCGACAT	TGCCGATACC	GAACAGAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTACCTGC	CGCCGGCATC
901	CTCATCATCG	GCGCGCCCGA	ATCCCTGAAA	AACACGCTCG	GCGTATGCGG
951	CACACGCCCC	GTCCGCTTGA	CCGAAGTCCA	ACAGATGCAG	CGGCGCATCG
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAAACGC	GATGGGCGGC
1051	GTTTGCAGCA	TGAAAAACTG	GCTCAACCAC	GGATGGGCCG	CCAAAGACGG
1101	CGTACACTTT	TCCGCCAAAG	GCTACCAACG	GTCGGCGGAA	ATGCTCGCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51  NASASPWMKK LQSV AQSGE TFRILQIGDS HTAGDFFTDS LKRRLQKTWG
101 DGGIGWVYPA NVKGQRM AAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151 GSMTLTASDG IASKQVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRO IRDSLPAAGI
301 LIIGAPESLK NTLGVCGTRP VRLTEVQQMQ RRIARQGQTM FWSWQNAMGG
351 VCSMKNWLNH GWA AKDGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

```

              10      20      30      40      50      60
m299.pep      MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK
a299           MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK
              10      20      30      40      50      60

              70      80      90      100     110     120
m299.pep      LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLQKTWGDGGIGWVYPANVKGQRM AAV
a299           LQSV AQSGETFRILQIGDSHTAGDFFTDSLRLQKTWGDGGIGWVYPANVKGQRM AAV
              70      80      90      100     110     120

              130     140     150     160     170     180
m299.pep      RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQVSLFAKPLLAEQTL
a299           RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQVSLFAKPLLAEQTL
              130     140     150     160     170     180

              190     200     210     220     230     240
m299.pep      TVNGNTVSANGGGWQVLDTG AALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
a299           TVNGNTVSANGGGWQVLDTG AALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
              190     200     210     220     230     240

              250     260     270     280     290     300
m299.pep      QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVROIRDSLPAAGI
a299           QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIDIADTEQKWLDTVROIRDSLPAAGI
              250     260     270     280     290     300

              310     320     330     340     350     360
m299.pep      LIIGAPESLKNTLGVCGTRPVRLTEVQQMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ
a299           LIIGAPESLKNTLGVCGTRPVRLTEVQQMQRRRIARQGQTMFWSWQNAMGGVCSMKNWLNH
              310     320     330     340     350     360

              370     380     390
m299.pep      GWA AKDGVHFS AKGYRRAEMLADSLEELVRSAAIRQX
a299           GWA AKDGVHFS AKGYQSAEMLADSLEELVRSAAIRQX
              370     380     390
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGTCC
201 TGTGGGGCG AAAGGACGTG CCGATGACGG TTTGATTAC GTTGTCAGCC
251 TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
```

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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCGTC ATCTTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACCTG TTTTATATGG
701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCGGACGG TATTTTGCGT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTTATT TCCTTGTGTG
1001 TTGCGCTGCG GGGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTTA TTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCTGCTCT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCG GGCTGATTAT GGCGACGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATTT GGGTATTTGT
1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1  MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLGISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGAVFLK
401 EVGLGGSVLF IGFIILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAAYRIGD SVTNIIIPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGTPTFY PVP*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTTCATT CCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTGCT
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGTATTG TTATTTTGTG ACTGAAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAAATCACG CCTTTGGAAT ATAAAGGATT AATTTGGGCT GGCGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGGA GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGTT TCCGTTTCGC CGTTTTTAAA
951 ATCGATTGTT GTTTTTATTT TCTTGTGTGT TGCATGyCG GGCmTTGTTT
1001 ATGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

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696

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1051 ATGCCGAAT CGATGAGTAC TCTGSGCTT TmTTTGswCA kcATCTTTTT
1101 TGCCGCACAG TTTGTCGCAT TTTTAAATTG GACGAATATT GGGCAATATA
1151 TTGCCGTTAA AGGGCGCAGC TTCTTAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTGTTTTC TCGGTTTTAT TTTAATTTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TCGCGCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCCG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GGCGTGGGTA
1451 CGCTGATTTT TATGATGTTG CCGTATTCCG CTTTCTTCTT GATTGCGTGG
1501 ATTGCCTTAT TCTGCATTTG GGTATTTGTT TTGGGCCTGC CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

m302.pep

```

1  MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHVPTL FIIFIVLLLI
51  ASAVGAYFGL SVPDRPVGA KGRADDGLIY IVSLLNADGF IKILHTVKN
101 FTGFAPLGTV LVSLGVGIA EKSGLISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFMVAFT FVIALIGYFV TEKIVEPQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVVFALSAL LAWSIVPADG
301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXIFFFAAQ FVAFFNWTNI GOYIAVKGAT FLKEVGLGGS
401 VLFIFILIC AFINLMIGSA SAQWAVTAPI FVPMMLAGY APEVIQAYR
451 IGDSVTNIIT PMMSYFGLIM ATVIKYKKDA GVGTLISMML PYSAFFLIAW
501 IALFCIWVVFV LGLPVGPGAP TFYPAP*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng) from *N. gonorrhoeae*:

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNMLPHVPTLFIIFIVLLLIASAVGAYFGL					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNMLPHVPTLFIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m302.pep	SVPDRPVGAKGRADDGLIYIVSLLNADGFIKILHTVKNFTGFAPLGTVLVSLGVGIA					
g302	SVPDRPVGAKGRADDGLIHVSLLDADGLIKILHTVKNFTGFAPLGTVLVSLGVGIA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLLTSPRKLTTFMVFTGILSNTASELGYVVLIPLSAIFHSLGRHPL					
g302	EKSGLISALMRLLLTSPRKLTTFMVFTGILSNTASELGYVVLIPLSAIFHSLGRHPL					
	130	140	150	160	170	180
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVAFTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVFALSALLAW					
g302	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVFALSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350

697

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m302.pep  SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SIVPADGILRHPETGLVAGSPFLKSIVVFIFLLFALPGIVYGRITRSLRGEREVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIFIGFILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      NLMIGSASAQWAVTAPIFVPMMLLAGYAPQVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKDAGVGT LISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFFYPAPX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g302      IKYKKDAGVGT LISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGPTPTFFYPVPX
          490      500      510      520      530

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251 TGCTCGATGC TGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCGGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAAT CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGCTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTATATGG
701 TAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCGT CATCCTGAAA CAGGATTGGT
951 TTCCGGTTCG CCGTTTTTAA AATCAATTGT TGTTTTTATT TTCTGTGTTG
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCCGAAG TTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTATAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTTT ATCGGTTTAA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTCG GGCTGATTAT GCGACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATTT GGGTATTTGT
1551 TTTGGGCTG CCCGTCGGTC CCGGCGCGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQTDTORQ GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTSPRK LTTFMVVFTG

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698

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIIITPM SYFGLIMATV IKYKKGAVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

```

m302/a302 96.1% identity in 533 aa overlap

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	TQRDGRFLRTVEWLGNM	LPHPVTLFII	FIVLLLIASAV	GAYFGL	
a302	MHSIYFFKEKQMSQTD	TQRDGRFLRTVEWLGNM	LPHPVTLFII	FIVLLLIASAAGAY	FGL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m302.pep	SVPDPRPVGAKGRADDGLI	YIVSLLNADGFIKIL	THTVKNFTGFAPL	GTVLVSL	LGVGIA	
a302	SVPDPRPVGAKGRADDGLI	HVVSLDADGLIKIL	THTVKNFTGFAPL	GTVLVSL	LGVGIA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLLTKSPR	KLTFMVVFTGILSNTASE	LGYYVLIPLSAIIFHSL	GRHPL		
a302	EKSGLISALMRLLLTKSPR	KLTFMVVFTGILSNTASE	LGYYVLIPLSAIIFHSL	GRHPL		
	130	140	150	160	170	180
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYSANL	FLSTIDPLLACITHQAA	-----VVGPEANW	FFMVASTFVI		
a302	AGLAAAFAGVSGGYSANL	FLGTIDPLLAGITQAAQ	IIHPDYVVGPEANW	FFMVASTFVI		
	190	200	210	220	230	240
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQLGPY	QSDLSQEEKDIRHSNEIT	PLEYKGLIWAGVV	FVALSALLAW		
a302	ALIGYFVTEKIVEPQLGPY	QSDLSQEEKDIRHSNEIT	PLEYKGLIWAGVV	FVALSALLAW		
	250	260	270	280	290	300
	300	310	320	330	340	350
m302.pep	SIVPADGILRHPETGLVSG	SPFLKSIVVFIFLLFALX	GXYGRVTRSLRGEQ	EVVNAMAE		
a302	SIVPADGILRHPETGLVSG	SPFLKSIVVFIFLLFALP	GIVYGRVTRSLRGEQ	EVVNAMAE		
	310	320	330	340	350	360
	360	370	380	390	400	410
m302.pep	SMSTLXLXLIFFFAAQFVA	FFNWTNIGQYIAVKGAT	FLKEVGLGGSVLF	IGFILICAFI		
a302	SMSTLGLYLVIIFFFAAQF	VAFFNWTNIGQYIAVKGAT	FLKEVGLGGSVLF	IGFILICAFI		
	370	380	390	400	410	420
	420	430	440	450	460	470
m302.pep	NLMIGSASAOAVTAPIFV	PMLMLAGYAPEVIQAAYR	IGDSVTNIIITPMMSY	FGLIMATV		
a302	NLMIGSASAOAVTAPIFV	PMLMLAGYAPEVIQAAYR	IGDSVTNIIITPMMSY	FGLIMATV		
	430	440	450	460	470	480
	480	490	500	510	520	
m302.pep	IKYKKGAVGTLISMMLPYS	AFFLIAWIALFCIWVFL	GGLPVGPGAPTFYPAPX			
a302	IKYKKGAVGTLISMMLPYS	AFFLIAWIALFCIWVFL	GGLPVGPGAPTFYPAPX			
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

699

g305.seq

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1  ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGTT GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
301 GACAAACAAA TCAAAGAGTA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GTGTGCCCA AGTGTGTTGCA CTGGTCCCG GTACGTCCCG
501 TTCGGGCAGT ACGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGGCCG TTCCGATGAT GGTGTCAGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTTCCT GGTGTTGGTAG
701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCGTTT
751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGTTGTC
801 GGGCTGGATA AGTTGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 DKQIKLEYLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)

```

1  AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CAGTTTGGC GGTAGTGTT GAATACCGGC AACGTTTCAG
201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
301 GGCAWACAAA TCAAAGAGyA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTyTG GrCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GCGTTGCCCA AGTGTGTTGCA CTGGTCCCG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA
551 CTGCGACAGA ATTCTCGTTT TTCTTGGCTG TGCCGATGAT GGTGCGCGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTCCTA GGCTTGGTAG
701 CGGTAAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFXILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

```

g305.pep      10      20      30      40      50      60
               MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m305          10      20      30      40      50      60
               MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF

```


700

	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVLNLAIAPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
m305	EYRQRFNSVLHGLGKDRKANRFVLNLAIAPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKRSRAEPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTMGGMLWGI					
m305	XGFXILWVEKRSRAEPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTMGGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHRYFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHRYFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1   ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCG
101 GCAATCTGAT TGATTTCAC AGCAATCACA AGGTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTTGGC GGTAGTGTG GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCAAACAAA TCAAAGAGTA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TTATTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATGTGTC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GCGTTGCCCA AGTGTGTGCA CTGGTTCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATT TTCTTGCCG TTCCGATGAT GGTTCAGACA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATG
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTTGTTC A GGCTTGGTGG
701 CGGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1   MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHRY FFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHKVFEITIQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVLNLAIAPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
a305	EYRQRFNSVLHGVGKDRKANRFVLNLAIAPAAVMGLLFGKQIKEYLFNPLSVAVMLVL					

701

	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKQRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
a305	GGFFILWVEKQRSRAEPKIVDLDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGLVAVKALLR					
	250	260	270			
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIILWLSGWISWEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCGGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCCTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGGCGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAAAC  GAGAAAAAAG  CTTCAAAAAG
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAGA  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAACTGGCA  ATCTTGGGCA  TATCTTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1  MFMNKFSQSG  KGLSGFFFL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREPEP  GQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1  ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCgMAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGAwCC  GGCCGATCAA  AACGCCTTGT  CCGAACCgGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAawGCT  GCCGACAAGC
251 AGCCCCTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGAGCGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451 TCAAAAAGAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCTCAACA  GCGGCAGCAT  CGAAAAGCG  CGCAGTCCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

702

```

601   ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
651   CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA
701   GGCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
751   ATGCGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

```

m306.pep (partial)
  1   ..GLFFGLILAT VIIAGILFYLNQSGQNAFKI PASSKQPAET EILKPXNQXK
 51   EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
101   EREPDGQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
151   SKEEKKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
201   IICKWARMPT VRARKGSPVN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
251   MR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

```

m306/g306
      10      20      30      40
m306.pep      GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX
                |:|||||:|||||:|||||:|||||:|||||:|||||:
g306      MFMNKFSQSGKLSGFFGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETEILKLK
            10      20      30      40      50      60

      50      60      70      80      90      100
m306.pep      NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP
                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
g306      NQPKEDIQPEPADQNALSEPDAEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP
            70      80      90      100      110      120

      110      120      130      140      150      160
m306.pep      GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
g306      GQAVRKKALTEEREQTVREKAQKKDAETVKKKAVKPSKETEKKASKEEKKAAKEKVAPKP
            130      140      150      160      170      180

      170      180      190      200      210      220
m306.pep      TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSPVNWQSWA
                |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
g306      TPEQILNSRSIEKARSAAAKEVQKMNFGQGSQRIICKWARMNPNGARKGSPVNWQSWA
            190      200      210      220      230      240

      230      240      250
m306.pep      YLPRWSVIRRDIKFTGCKAAICLPMRX
                |||:|:|||||:|||||:|||||
g306      YLPKWSAIRRDIKFTACKAAICPPMRX
            250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

```

a306.seq
  1   ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTTT
 51   CTTCCGTTTG ATACTGGCGA CGGTCAATTAT TGCCGGTATT TTGTTTTATC
101   TGAACCAGAG CGGTCAAAAT GCGTTCAAAA TCCCGGTTCC GTCGAAGCAG
151   CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT
201   CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGTCGCA
251   AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
301   GCCGACAAAG CCGACGAGGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGA
351   AAAGTCGGAC GGACAGGCAG TGCGCAAGAA AGCACTGACG GAAGAGCGTG
401   AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
451   AAACAAGCGG TAAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAAGA
501   AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCGGAAC
551   AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

```

703

```

601 GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTCGGTTAT CAGGCGGGAC
751 ATAAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
  1 MFMNKFSQSG KGLSGFFFGL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
 51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD GQAVRKKALT EEREQTVGEK AQKKDAETVK
151 KQAVKPSKET EKKASKEEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQMKMTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

                                10      20      30      40
m306.pep                      GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPK
                                |:|||||
a306                          MFMNKFSQSGKGLSGFFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
                                10      20      30      40      50      60

                                50      60      70      80      90      100
m306.pep                      NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP
                                || |||||
a306                          NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
                                70      80      90      100      110      120

                                110     120     130     140     150     160
m306.pep                      GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAEKVAPKP
                                |||||
a306                          GQAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKKAAEKVAPKP
                                130     140     150     160     170     180

                                170     180     190     200     210     220
m306.pep                      TPEQILNSGSIEKARSAAAKEVQMKMTPTRRKQRIICKWARMPTVRARKGSVPNWQSWAY
                                |||||
a306                          TPEQILNSGSIEKARSAAAKEVQMKMTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY
                                190     200     210     220     230     240

                                230     240     250
m306.pep                      LPRWSVIRRDIKRFTGCKAAICLPMRX
                                |||||
a306                          LPRWSVIRRDIKRFTGCKAAICLPMRX
                                250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
  1 atgaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
 51 cgcagcctgc ggcggtcaaa aagacagcgc gcccgagcc tctgccgccg
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
251 gcccgaaatc ggcatcggcg gagggcgagt tggacatcaa cgtcttccaa
301 cacaaccct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgcga ccgcgccttt gggactgtat ccgggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgccaac
451 gacccgtcca acttcgcacg cgccttggtg atgctgaacg aactgggttg
501 gatcaaatc aaagacggca tcaatccgct gaccgcatcc aaagccgaca
551 tcgcggaaaa cctgaaaaac atcaaaatcg tcgagcttga agccgcacaa
601 ctcgcgcgca gccgcgccga cgtggatttt gccgtcgtca acggcaacta
651 cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

```

704

```

701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaagacagc
751 caatggccta aagacgtaac cgaggcctat aactccgacg cgttcaaagc
801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg
851 aaggcgagc caaataa

```

This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:

```

g307.pep
  1 MKTFFKTLST ASLALILAAC GGQKDSAPAA SAAAPSADNG AAKKEIVFGT
 51 TVGDFGDMVK EQIQAELEKK GYTVKLVEFT DYVRPNLALA EGELDINVFO
101 HKPYLDDFKK EHNLDITEAF QVPTAPLGLY PGKLKSLEEV KDGSTVSAPN
151 DPSNFARALV MLNELGWIKL KDGINPLTAS KADIAENLKN IKIVELEAAQ
201 LPRSRAVDVF AVVNGNYAIS SGMKLTEALF QEPSFAYVNW SAVKTADKDS
251 QWLKDVTEAY NSDAFKAYAH KRFEGYKYP A WNEGAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1273>:

```

m307.seq (partial)
  1 ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
 51 CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCTGCC GCATGGAATG
101 AAGGCGCAGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1274; ORF 307>:

```

m307.pep (partial)
  1 ..QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA A WNEGAAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng) from *N. gonorrhoeae*:

```

m307/g307

                                10      20      30
m307.pep                                QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
g307      SGMKLTEALFQEPSFAYVNWNSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKYP
          230      240      250      260      270      280

          39
m307.pep      A WNEGAAKX
          |||||
g307      A WNEGAAKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1275>:

```

a307.seq
  1 ATGAAAACCT TCTTCAAAAC CCTTTCCGCC GCCGCACTCG CGCTCATCCT
 51 CGCCGCCTGC GCGGTCAAA AAGATAGCGC GCCCGCCGCA TCCGCTTCTG
101 CCGCGCCGCA CAACGCGCGG GCGAAAAAAG NAATCGTCTT CGGCACGACC
151 GTCGCGGACT TCGGCGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA
201 GAAAAAAGGC TACACCGTCA AACTGGTCGA GTTTACCGAC TATGTGCGCC
251 CGAATCTGGC ATTGGCTGAG GCGGAGTNGG ACATCAACGT CTTCCAACAC
301 AAACCCATATC TTGACGACTT CAAAAAAGAA CACAATCTGG ACATCACCGA
351 AGTCTTCCAA GTGCCGACCG CGCCTTTGGG ACTGTACCCG GGCAAGCTGA
401 AATCGCTGGA AGAAGTCAAA GACGGCAGCA CCGTATCCGC GCCCAACGAC
451 CCGTCCAAC TCGCCGCGCT CTTGGTGATG CTCGACGAAC TGGGTTGGAT
501 CAAACTCAAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGACATTG
551 CCGAAAACCT GAAAAACATC AAAATCGTCG AGCTTGAAGC CGCGCAACTG
601 CCGCGTAGCC GCGCCGACGT GGATTTTGNC GTCGTCAACG GCAANTACGC
651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT
701 TTGCTTATGT CAACTGGTCT GCCGTCAAAA CCGCCGACAA AGACAGCCAA
751 TGGCTTAAAG ACGTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA
801 CGCGCACAAA CGCTTCGAGG GCTACAAATC CCCTGCCGCA TGAATGAAG
851 GCGCAGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:

```

a307.pep
  1 MKTFFKTLA AALALILAAC GGQKDSAPAA SASAAADNGA AKKXIVFGTT

```

705

```

51  VGDGFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFOH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLNKI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                      QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

          39
m307.pep      AWNEGAAX
          |||||
a307      AWNEGAAX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTTCT  GTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCT  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCTC  TGTGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAG
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCT  CGATGTACCG  CAAGCCGCGA
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVFYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RMMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTLRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPQ
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTTCT  GTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCT  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTC  TGTGCGCAC  GGCTTCGGCG  ACAATCTGcT  GACGCGtTGGC
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GwAACGGAAG
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCT  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGT  GCACACGcT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCARGGAATG  gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

706

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNLMKR  XTEMGGVVFP  PVPAMYRKPQ
201 TADDIVAHSV  AHALSFLGID  TPDSA EWQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPCLSDFCFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPVAMYRKPQTADDIVAHSAHALSLFGIDTPDSA EWQGM A					
g308	VTEMGGVVFPVPVAMYRKPQTADDIVAHSAHTLSLFGIDTPDLA EWQGM ADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCCCT  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNLMXR  VTEMGGVVFP  PVPAMYRKPQ
201 TADDIVAHSV  AHALSFLGID  TPDSA EWQGM  AD*

```

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCF	FTIIAGLPLQAVLWERRMMVRR	LIIGISGASGFQY			
a308	MLNRIFYRILGVADNLYPYLSDFCF	FTIIAGLPLQAVLWERRMMVRR	LIIGISGASGFQY			
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALAD	FVHPIGNIGACIASGTF			
a308	GVKALXLLRAQDIETHLVVSKGAEMARASE	XYARDXVYALAD	XVHPIGNIGACIASGTF			
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMR	TLASVAHGFGD	NLLTRAADVVLKERRRLVLMVRETPL	NLAHL	DNM	KR
a308	KTDGMLVAPCSMR	TLASVHGF	GDNLLTRAADVVLKERRRLVLMVRETPL	NLAHL	DNM	KR
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVP	PAMYRK	PQTADDIVAH	SVAHSLFGID	TPD	SAEWQGM
a308	VTEMGGVVFPVP	PAMYRK	PQTADDIVAH	SVAHSLFGID	TPD	SAEWQGM
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGCGG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GCGGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCGT CGATGTACCG CAAGCCGCG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RMMVRRLLI
51  IISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMCR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGCGG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GCGGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCGT CGATGTACCG CAAACCGCG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTIIA GLPLQAVLWE RMMVRRLLI

```


708

51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
 101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSFGID TPDSA EWQGM AD*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308-1	MLNRVFYRILGVADNLYPCLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASE TAYARDEVYALADFVHPIGNIGACIASGTF					
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASEDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308-1	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308-1.pep	VTEMGGVFPVPVPAMYRKPO TADDIVAHSV AHALSFGIDTPDSA EWQGMADX					
g308-1	VTEMGGVFPVPVPAMYRKPO TADDIVAHSLAHTLSLFGIDTPDLA EWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
 51 TCCGATTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
 101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTGATAATC
 151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTGGANCT
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
 301 TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
 351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
 401 CGCTTGCCTC GGTCTGTCAC GGCTTCGGCG ACAACCTCTT GACGCGTCCG
 451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
 501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
 551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTG CGATGTACCG CAAACCGCAG
 601 ACGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTCGCTGTT
 651 CGGAATCGAT ACGCCGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

1 MLNRIFYRIL GVADNLYPYL SDFCFFTTIIA GLPLQAVLWE RMMVRRLLI
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
 101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVH GFGDNLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLDNMXR VTEMGGVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSFGID TPDSA EWQGM AD*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRIFYRILGVADNLYPYLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
m308-1	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF					
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASE TAYARDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a308-1	KTDGMLVAPCSMRTLASVHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					

```

m308-1      KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGMADX
              |||
m308-1      VTEMGGVVFPPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

```

g311.seq
1   atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgctgcccg gcgcgctttg ggggtgtttgg
101 gtttggaacac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaaacagtc agggcgggcg gtaaaacggt
201 tgccgtggtc ggtatcggca tcaatttcgt gctgcccagg gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgtgtgt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgcttc
501 gcacttggaac acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tgctgttgga aggcgggaac agccggctca agtgggcgtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgcgc taccgcgatt
701 tgtcgccctt gggcgcgagg tgggcggaaa aggcggatgg aaatgtccgc
751 atcgtcggtt gcgccgtgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgccg caggcttttg
851 gcatacgcaa ccactaccgc caccgccgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgctgt
951 cagttgcggc acggcggtaa cggttgacgc gctcaccgat gacggacatt
1001 atctcggcgg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg caccggccgt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggccggcgcg cgaaagtctc
1251 cgaagccctg ccgcctgcat ttttgccgga aaataccgtg cgcgtggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

```

g311.pep
1   MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILIEIV RAGGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLETL LAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVLHLE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLEGGN SRLKAWVEN GTFATVGSAP YRDLSPGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFRS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRP AGKRYPFPTT TGNASVSGMM DAVCGSIMMM HGRLKEKNGA
401 GKPVVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

```

m311.seq (partial)
1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTGCGCCT GTTGCGGCAG TGGCGTGTCT GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCATTAAG TGGCCCAATG ATTTGGTTGT CCGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCAAa GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCCTGCGG TCCGACnACA GGCCGTTTTC CGTGnCGAAG CGGCGGGATT

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710

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401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAC ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTCGCCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TGGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCCGACC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAGTT GCGGCACGGC GGTAAACGTT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCC GG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTTGCGGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAACCG
1001 GGGCGGGCAA GCCTGTCGAT GTCATCATTA CCGCGCGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGG GCGGAAAATA CCGTGCCTGT
1101 GCGGACAAC CTCGTCATT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGAATA TGAACAT...

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
  1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
 51 KLGILITV RTGGKTAVV GIGINFLPX EVENAASVQS LFQTASRRGN
101 ADAAVLLXXX XXXXEISLR SDXRPVSVXK RRDSEFLLL DGGNSRLKWA
151 WENGTFATV GSAPYRDLSP LGAEWAEKAD GNVRIVGCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDGHL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTGNV ASGMDAVCG SVMMHGRLK EKTGAGKPD VIITGGGAAG
351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AAEGREYEH...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311
      10      20      30      40      50      60
m311.pep MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGILITV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      MFSFGWAFDRPQYELGSLSPVAAALACRRALGCLGLETQIKWPNDLVVGRDKLGILITV
          10      20      30      40      50      60

      70      80      90      100     110
m311.pep RTGGKTAVVVGIGINFLPXEVENAASVQSLFQTASRRGNADA AVL LXXX-----
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      RAGGKTAVVVGIGINFLPKEVENAASVQSLFQTASRRGNADA AVL LLETLLAELGAVLEQ
          70      80      90      100     110     120

m311.pep -----XXXXXXXXX
          :
g311      YAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDGRGVLHLETAEGEQTVVS
          130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep XEISLRSDXRPVSVXKRRDSEFLLLDGGNSRLKWAWENGTFATVGSAPYRDLSP LGAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      GEISLRPDNRSVSPKRPDSEFLLLEGGNSRLKWAWENGTFATVGSAPYRDLSP LGAE
          190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      WAEKADGNVRIVGCAVCGESKKAQVQEQLARKIEWLPSSAQAL -GIRNHYRHPEEHGSDR
          250     260     270     280     290

```

711

	240	250	260	270	280	290
m311.pep	WFNALGSRRF SRNACVVVSCGTAVTVDALTDG HYLGGTIMPGF HLMKESLAVRTANLNR					
g311	WFNALGSRRF SRNACVVVSCGTAVTVDALTDG HYLGGTIMPGF HLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMMHGRLKEKTGAGKPVDV IITGGGAAKVAEA					
g311	PAGKRYPFPTTTGNAVASGMMDAVCGS IMMHGRLKEKNGAGKPVDV IITGGGAAKVAEA					
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLAENTVRVADNLVIYGLLNMI AAE GREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNLI AAE GGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTTC
51  GCTGTCGCCT GTTGC GG CAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAAC GCAAATCAAG TGGCCAAACG ATTTGGTTCG CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTCGT GCTGCCCAAG GAAAGTGGAAA
251 ACGCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTTGCT GGAAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTTGCAA TATGCGCGGG ACGGATTTGC GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTTCT
501 GCACTTGGA ACGGCAGAGG GCAAACAGAC GGTCGTCAGC GCGGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTCCG TGCCGAAGCG GCGGATTTCG
601 GAACGTTTTT TGCTGTTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAAAC GGCACGTTCC CAACCGTCGG TAGCGCGCCG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGGTT GCGCCGTGTG CCGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAAATCG AGTGCGTGCC GTCTTCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCGGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGACGCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGGTAA CGGTTGACGC GCTCACCGAT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCCGAA CCGCCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGGAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAAA AACCGGGGCG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GCGGCGCGG CAAAAGTTGC
1251 CGAAGCCCTG CCGCTGCAT TTTTGGCGGA AAATACCGTG CGCGTGGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCGC CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1   MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGILIETV RTGGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLETL LAELDAVLLQ YARDGFAPFV AEYQAANRDH GKAVLLLRDG
151 ETVFEGTVKG VDGQGVHLHLE TAEGKQTVVS GEISLRSDDR PVSVPKRRDS
201 ERFLLLDGGN SRLKWAVVEN GTFATVGSAP YRDLSPGLAE WAEKVDGNVR
251 IVGCAVCGEF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGF HLMKESL
351 AVRTANLNRH AGKRYPFPTT TGNASVSGMM DAVCGSVMMH HGRLKEKTGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFDRLPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV					
a311	MFSFGWVFDRLPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTAVVVGIGINFVLPXEVENAASVQSLFQTASRRGNADAALLXXXXXX-----					
a311	RTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADAALLLETLLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGGQVLHLETAEGKQTVVS					
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDXRPVSXKRRDSEFLLLDGGNSRLKWAWVENGTFATVGSAPYRDLSPLGAE					
a311	GEISLRSDDRPVSPKRRDSEFLLLDGGNSRLKWAWVENGTFATVGSAPYRDLSPLGAE					
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQALFGIRNHYRHPEEHGSDR					
a311	WAEKVDGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR					
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHLGGTIMGFHLMKESLAVRTANLNR					
a311	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHLGGTIMGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGNVAVSGMMDAVCGSVMMMHGRLKEKTGAGKPDVVIITGGGAAKVAEA					
a311	HAGKRYPFPTTTGNVAVSGMMDAVCGSVMMMHGRLKEKTGAGKPDVVIITGGGAAKVAEA					
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH					
a311	LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGCGGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGACAA GGCACACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGCG GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCCG GATGTTTCA GTTCGGCTGG CGTTTGACCG GCCGCGAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGCGCA CTTGCGTGCC GCGCGCCTTT
501 GGGGTGTTTG GGTTTGGAAG CGCAAATCAA GTGGCCAAAC GATTTGGTGC
551 TCGGACGCGA CAAATTGGGC GGCAATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAACACGG TTGCGGTGGT CCGTATCGGC ATCAATTTCT TGCTGCCCAA
651 GGAAGTGGA AAGCCGCTT CCGTGACGTC GCTGTTTCAG ACGGCATGCG
701 GCGGGGGCAA TGCCGATGCC GCCGTATTGC TGGAAACATT GCTTGGCGAA
751 CTGGGCGCGG TGTGGAACA ATATGCGGAA GAAGGGTTCG CGCCATTTTT

```

```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TCGAAGGCA CGGTAAAGG CGTGGACGGA
901 CGAGGCGGTT TGCATTGGA AACGGCAGaa ggCGAACAGa cggtcGtcag
951 cggcGaaATC AGccTGGCGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgttg aagggcgga cagccggctc
1051 aAGTGGgCgt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGCgCC
1101 gtaCCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGGCGCGTGT GCGGAGAATC CAAAAGGGA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCGAGC GCGGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTACCGA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCTTT TCCCGACCAC AACGGGCAAC GCCGTCGCA GCGGCATGAT
1551 GGACGCGGTT TCGGCGCTCGA TAATGATGAT GCACGGCGCT TTGAAAGAAA
1601 AAACCGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTLVKPSHWR VLAELADGLP QHVSQALAREA DMKPOQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTKLKEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVVDG
301 RGVHLHLETAE GEQTVVSGEI SLRPDNRVS VPKRPDSERF LLEGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAAL GIRNHYRHPE EHGSDRWENA LGSRRFSRNA
451 CVVSCGTAV TVDALTDGHL YLGGTIMPGF HLMKESLAVR TANLNRPAKG
501 RYFPFTTTGN AVASGMMDAV CGSIMMHGR LKEKNGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CCGTTTGCCG CAACACGCTC CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTTCACT TTTGGCTGGG TGTTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTGCGC TGTGCGGCA GTGGCGTGTC GGCAGCCTT
501 GTCGCGTTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTGGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTGTTGCA ATATGCGCGG GACGGATTTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCATTGGA AACGGCAGAG GGCAACAGAG CGGTCGTCAG
951 CCGCGAAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GCGGGGATTC GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CCGCACGTTT GCAACCGTGC GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGGCTGTGT GCGGAGAATC CAAAAGGGA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCGGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCA GCGGCATGAT
1551 GGATGCGGTT TCGGCGCTCG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACGG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFDPRQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILIVTRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVVG
301 QGVLHLETAE GKQTVVSGEI SLRSDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAFYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQLARKI EWLPSAQAL GIRNHYRHPE EHGSDFWNA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDGHL YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYPFPTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

m311-1.pep	10	20	30	40	50	60
g311-1	10	20	30	40	50	60
m311-1.pep	70	80	90	100	110	120
g311-1	70	80	90	100	110	120
m311-1.pep	130	140	150	160	170	180
g311-1	130	140	150	160	170	180
m311-1.pep	190	200	210	220	230	240
g311-1	190	200	210	220	230	240
m311-1.pep	250	260	270	280	290	300
g311-1	250	260	270	280	290	300
m311-1.pep	310	320	330	340	350	360
g311-1	310	320	330	340	350	360
m311-1.pep	370	380	390	400	410	420
g311-1	370	380	390	400	410	420
m311-1.pep	430	440	450	460	470	480
g311-1	430	440	450	460	470	480
m311-1.pep	490	500	510	520	530	540
g311-1	490	500	510	520	530	540
	550	560	570	580	590	

```

m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
              |||||
g311-1      VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTTCACT TTTGGCTGGG TGTGTTGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTTGCGGCA GTGGCGTGCC GGCGCGCCTT
501 GTCGCGTTTG GGTGTAAGAA CGCAAATCAA GTGGCCAAAC GATTGCGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCGGTGGT CCGTATCGGC ATCAATTTTC TGCTGCCCAA
651 GGAAGTGGA AAGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GGCGGGGAAA TGCCGATGCC GCGGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGCGC GTATTGCTGT
851 TGCGGACGCG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGACGCGA
901 CAAGCGCTTC TGCACTTGA AAGCGCAGAG GGCAAACAGA CGGTGCTCAG
951 CGCGCAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCGGAAGC
1001 GGCGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGCGGAA AAGTGGATG
1151 GAAATGTCCG CATCTCGGT TGCGCGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGACGCC GCGGCTTCA GCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTGACG CGCTACCGA
1401 TGACGGACAT TATCTCGGG GAACCATCAT GCCCGGTTT CACCTGATGA
1451 AAGAAATCGT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGG GGGCAAGCCT GTCGATGTCA TCATTACCG CGGCGGCGCG
1651 CVVVSCTAV TVDALTDG HLMKESLAVR TANLNRHAGK
1701 GCGCGTGGCG GACAACCTCG TCATTACG GCTGTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTLVKPSHWR VLAELADGLP QHVSQARMAD DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECMF SFGWVDRPQY
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGRDKLG GILLETVRTG
201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVVG
301 QGVLLHLETA EKQTVVSGEI SLRSDRPSV VPKRRDSERF LLLDGGNSRL
351 KWAVWENGTF ATVGSAFYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAAL GIRNHYRHPE EHGSDRWFA LGSRRFSRNA
451 CVVVSCTAV TVDALTDG HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

```

a311-1/m311-1 98.5% identity in 591 aa overlap

```

a311-1.pep      10      20      30      40      50      60
MTLVKPSHWRVLAELADGLPQHVSQARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
|||||
m311-1          10      20      30      40      50      60
MTLVKLSHWRVLAELADGLPQHVSQARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR

a311-1.pep      70      80      90      100     110     120
LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
|||||
m311-1          70      80      90      100     110     120
LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK

```


a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECLMFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLKTQIKWPN					
m311-1	130	140	150	160	170	180
	GRGRQGRKWSHRLGECLMFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPN					
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILIEVTRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
m311-1	190	200	210	220	230	240
	DLVVGRDKLGGILIEVTRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
m311-1	250	260	270	280	290	300
	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAWVENGTF					
m311-1	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAWVENGTF					
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGLAEWAEEKVDGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
m311-1	370	380	390	400	410	420
	ATVGSAPYRDLSPGLAEWAEEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHPPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGF					
m311-1	430	440	450	460	470	480
	GIRNHYRHPPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGF					
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPFTTGNVAVSGMMDAVCGSVMMMHGRLKEKTGAGKP					
m311-1	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPFTTGNVAVSGMMDAVCGSVMMMHGRLKEKTGAGKP					
a311-1.pep	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHTX					
m311-1	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNMIAAEGREYEHIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1   atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTaccat cggcaTTgaT tgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggtcg gcaaagactT GGTGGCAacg Gcgaaacacc tTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTTCTGC AACGCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTGCGCGT
651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAATTCT GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGTG CGCTGGCACC GACCCCGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CCGTACGCAC

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

```

g312.pep
  1 MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
 51 TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGC AKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFNRRG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

```

m312.seq
  1 ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
 51 CCAGAAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAATT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTC
351 CGCGTTGGTG CAAAAGGGA TGTCGCcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACcGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAAATTGT CGTGTCTGCG AACGCGGTGG AAGACAACCC GTTTWTGGCG
601 GCGCGGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCG GCGTATCCGG
651 CCCAGGTGTC GTAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAACTG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTCGCCGA CCCCGCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCGGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CAcGGTCGAG TTCGGCGGCT TGTTGGgCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

```

m312.pep
  1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
 51 TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCXSIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGC AKIVVFC NAVEDNPFXA
201 GAFHGSGDAV INVGVSGPGV VKAALENSDA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCGTHGTTA
301 ALALLNDAVK KGGMMASSAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLLGYAPV MPVKEGSCEV FVNRGGRIPA PVQSMKN*

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718

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMOVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTGVGKDLVTT					
g312	MSIQSGEILETVKMOVADRNFDVRTITIGIDLHDCISTDIDVLNQNIYNKITTGVGKDLVAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m312.pep	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYSVSAQTLDKAAKAIGVSFIGGFSALV					
g312	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSAQTLDKAAKAIGVSFIGGFSALV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m312.pep	QKGMSPSDEVLIRSIPEAMKTTDIVCXNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
g312	QKGMSPSDEVLIRSVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG					
	130	140	150	160	170	180
	190	200	210	220	230	
m312.pep	FGCAKIVVFCNAVEDNPFVAGAFHSGS--DAVINVGVS GPGVVKAALENS DATTLTEVAE					
g312	FGCAKIVVFCNAVEDNPFMAGAFHSGSEADAVINVGVS GPGVVKAALENS DAVSLTEVAE					
	190	200	210	220	230	240
	240	250	260	270	280	290
m312.pep	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTAVGDSVARILEEMGLSVCGTH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDVAVKKGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	GTTAALALLNDVAVKKGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPVGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
g312	CSVGLDMIAPVGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRGGRI PAPVQSMKNX					
g312	YAPVMPAKEGSCEVFVNRGGRI PAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

1	ATGAGTATCC	AATCCGGCGA	AATTTTAGAA	ACCGTCAAAA	TGTTGCCGA
51	CCAGAATTTT	GATGTCCGCA	CCATTACCAT	CGGCATTGAT	TGTCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAAAATATTTA	CAACAAAATT
151	ACCACGGTCG	GCAAAGACTT	GGTGGCGACA	GCAAAATATC	TGTCTGCCAA
201	ATACGGCGTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCACG	CCGATTGCCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTCAGCGT	GGCGCAAAT

719

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301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTGCCTTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTTCTGC AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGCGCCG GGTGTCGTAA AAGCCGCGTT GGAAAATTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACCGCCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGCTCG CGGTACGCAC
901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGCGCG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTCCGGTCG GCTTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCCGCGCA CACCATTTC GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATTCCGG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCCTG TAATGCCGGT AAAAGAAGGC TCATGCCAAG
1301 TGTCGTCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
  1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
 51 TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP VVKAALENS DATTLEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFNRRG RIPAPVQSMK
451 N*

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m312/a312 96.7% identity in 451 aa overlap

```

          10      20      30      40      50      60
m312.pep  MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
          |||
a312       MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT
          10      20      30      40      50      60

          70      80      90     100     110     120
m312.pep  AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVVAQTLDKAAKAIGVSFIGGF
          |||
a312       AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVVAQTLDKAAKAIGVSFIGGF
          70      80      90     100     110     120

          130     140     150     160     170     180
m312.pep  QKGMSPSDEV LIRSIPEAMKTTDIVCX SINIGSTRAGINMDAVKLAGETVKRTAEITPEG
          |||
a312       QKGMSPSDEV LIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
          130     140     150     160     170     180

          190     200     210     220     230
m312.pep  FGCAKIVVFCNAVEDNPF XAGAFHGS G--DAVINVGVS GPVVKAALENS DATTLEVAE
          |||
a312       FGCAKIVVFCNAVEDNPF MAGAFHGS GEADAVINVGVS GPVVKAALENS DATTLEVAE
          190     200     210     220     230     240

          240     250     260     270     280     290
m312.pep  VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVC
          |||
a312       VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVC

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720

	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFNRRGGRIAPVQSMKNX					
a312	YAPVMPVKEGSCEVFNRRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

```

g313.seq
1  atggacgacc cgcgcaccta cggatcgggc aatcccgggc cgaccaatgt
51  tttagcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcgatg
101 cgcgcaaagg tttggttgcc gttttgcttg cacgcgtgct tcaagaaccg
151 ctcggtttat ccgacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcatatg tggccggtgt tttcggatt taaggcgggc aaaggcggtg
251 caacggcatt gggcgtgctt ctggcactct ctctgcaac tgccttggtc
301 tgcgcgttga tttggcttgt gatggcattc ggcttcaaag taccctccct
351 tgccgcgctg gtcgccacaa ccgcccgcgc ccttgccgca ctgttttta
401 tgccgcatac ttcttggtt ttcgcaaccc tcgcaatcgc catattggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaaag gcaaagaaaag
501 caaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

```

g313.pep
1  MDDPRTYGS NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMAF GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNI LN LIKGESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

```

m313.seq
1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTAGTTGCC GTTTGTCTTG CACGCGTGCT TCAAGAACCG
151 CTCGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGTCT CTGGCACTCT CTCCCGCAAC TGCCTTGGTC
301 TGCGCGTTGA TTTGGCTTGT TATGGCATTG GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTCCGCGCA TCCTTCTTTA
401 TGCCGCACGT CTCGTGGGTT TGGGCGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

```

m313.pep
1  MDDPRTYGS NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMAF GFKVSSLAAL TATIAAPVAA SFFMPHVSWS WATVAIALLV
151 LFRHKSNI VK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTL LGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
g313	MDDPRTYGSNPGATNVLRSGKKKAAALTL LGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS VWVATVAIALLV LFRHKSNI VKLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILV LLRHKSNI LNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

a313.seq

1	ATGGACGACC	CGCGCACCTA	CGGATCGGGC	AATCCGGGGG	CAACCAATGT
51	TTTACGCAGC	GGCAAAAAAA	AGGCGGCCGC	GCTGACGCTC	TTGGGCGATG
101	CCGCCAAAGG	TTTGGTTGCC	GTTTTGCTTG	CACGCGTGCT	TCAAGAACCG
151	CTCGGTTTAT	CCGACAGCGC	AATCGCGGCC	GTCGCACTCG	CCGCGCTGGT
201	CGGGCATATG	TGGCCGGTGT	TTTTTCGATT	TAAAGGCGGC	AAAGGCGTGG
251	CAACGGCATT	GGGCGTGCTT	CTGGCACTCT	CTCCACAAC	TGCCTTGCTC
301	TGCGCGTTGA	TTTGGCTTGT	GATGGCATTG	GGCTTCAAGG	TGTCCTCCCT
351	TGCCGCATTA	ACCGCCACAA	TCGCCGCCCC	CCTTGCCGCA	CTGTTTTTTA
401	TGCCGCATAC	TTCTTGGATT	TTGCAACCC	TCGCAATCGC	CATATTGGTG
451	TTGCTCCGCC	ATAAGAGCAA	CATCCTCAAC	CTGATTAAAG	GCAAAGAAAG
501	CAAAATCGGC	GAAAAACGCT	GA		

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

1	MDDPRTYGS	NGATNVLR	S	GKKKAAAL	TL	LGDAAKGL	VAVLLAR	VLQEP
51	LGLSDSAIA	A	VALAALV	GHM	WPVFFG	FKGG	KGVATAL	GV LALSPTT
101	CALIWLVM	A	AFGVSSLA	AL	TATIAAP	LAA	LLFFMPHT	SWI FATLAI
151	ILV	LLRHKS	NI LN	LIKGESK	IG	EKR*		

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTL LGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
a313	MDDPRTYGSNPGATNVLRSGKKKAAALTL LGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS VWVATVAIALLV LFRHKSNI VKLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILV LLRHKSNI LNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
  1  atgaaattac aacaattggc tgaagaaaaa atcggcggttc tgatttgtgtt
 51  cacgctgctt gtagtcagtg tcggtctgtt gattgaagtt gtgcccttgg
101  cctttaccaaa ggcggcaaca cagccggcgc cgggcgtgaa gccttacaat
151  gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201  ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcgttacg
251  gtcattactc tgttgccgga gagtcggtt acgaccatcc gttccaatgg
301  gggtccaaac gtaccgggcc tgatttggca cgtgtggcg gccgctattc
351  cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401  agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451  gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501  cagtgatgag gaaattgcga aagcgctga ggctttggca aacaaatccg
551  agctggatgc ttagtcgcc tatctgcaag gattgggtct ggctttgaaa
601  aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
  1  MKLQQLAEEK IGV LIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNM PAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201  NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
  1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
 51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101  CCTTTACCAA GCGGCAACA CAGCCGGCGC CGGGCGTGAA GCCTTACAAT
151  GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTACAA
201  CTGCCACTCG CAAATGATTG GTCCGTTCCG TCGGAAACC GAGCGTTACG
251  GTCATTACTC TGTTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301  GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTCGCTATTC
351  CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401  AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451  GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501  CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551  AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601  AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
  1  MKLQQLAEEK IGV LIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNM PAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201  NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

```
m401/g401

          10          20          30          40          50          60
m401.pep  MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
g401       MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          10          20          30          40          50          60

          70          80          90         100         110         120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQW GSKRTGPDLARVGGRYSEW
```

723

```

g401      |||||
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFWLNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
g401      HRIHLLNPRDVPESNMPAFWLNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
g401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC  AACAATTGGC  TGAAGAAAAA  ATCGGCGTTC  TGATTGTGTT
51 CACGCTGCTT  GTAGTCAGTG  TCGGTCTGTT  GATTGAAGTT  GTGCCCTTGG
101 CCTTTACCAA  GCGGCAACA  CAGCCGGCGT  CGGGCGTGAA  GCCTTACAA
151 GCCCTGCAGG  TTGCCGGACG  CGATATTAC  ATCCGTGAGG  GCTGTACAA
201 CTGCCACTCG  CAAATGATTC  GTCCGTTCCG  TCGGAAACC  GAGCGTTACG
251 GTCATTACTC  TGTTCGCGGA  GAGTCGGTTT  ACGACCATCC  GTTCCAATGG
301 GGTTCCAAAC  GTACCGGTCC  TGATTGGCA  CGTGTGGGCG  GTCGCTATTC
351 CGACGAATGG  CACCGTATCC  ACCTGCTGAA  TCCCGTGAT  GTCGTGCCTG
401 AGTCCAATAT  GCCGGCATT  CCGTGGCTTG  CACGCAATAA  AGTCGATGTC
451 GATGCAACCG  TTGCCAAT  GAAGGCTTTG  CGTAAAGTAG  GTACTCCTTA
501 CAGTGATGAG  GAAATTGCGA  AAGCGCCTGA  GGCTTTGGCA  AACAAATCCG
551 AGCTGGATGC  TGTAGTCGCC  TATCTGCAAG  GATTGGGTCT  GGCTTTGAAA
601 AACGTAAGGT  AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1  MKLQQLAEEK  IGVLIIVFTLL  VSVGLLIEV  VPLAFTKAAT  QPASGVKPYN
51 ALQVAGRDIY  IREGCYNCHS  QMIRPFRAET  ERYGHYSVAG  ESVYDHPFQW
101 GSKRTGPDLA  RVGGRYSEW  HRIHLLNPRD  VVPESNMPAF  PWLNKVDV
151 DATVANMKAL  RKVGTPYSDE  EIAKAPEALA  NKSELDAVVA  YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

m401.pep      10      20      30      40      50      60
              MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
              |||||
a401           10      20      30      40      50      60
              MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
              |||||

          70      80      90      100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          |||||
a401      IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVPESNMPAFWLNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
a401      HRIHLLNPRDVPESNMPAFWLNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
a401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

```
g402.seq
1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  ttttccttacc ggatTATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag tccgtgcctc aggCATTtTC atttattcctt
151 gcctGttttc tgACCGtat cgcgcgtcggc gCgTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTG ATATTCCctT TATCGGGCAG TgcttccttgT
251 GGGCGGGTAT TgccaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATT TCCCACTTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCGC CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTtCT GCTGctgtcc
551 cTTTGTtTTg tacaCTGtTC CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCCCTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
1101 TGCCTATTCC ACTAACCTGT TGAGTGCgGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgetTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTcctt AATAAAGAAC
1301 TGCTCaagca aCGCCTTtcc cGTTTGATTG GGCCGGAAAG CGGCAGgcac
1351 gtATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGtctctCG
1401 TATGCTGATT CGGATGACGG AacctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA
```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

```
g402.pep
1  MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPQAFSFIL
51  ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIAGRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRIFFVVL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVVSRLMI RMTEPSAGAE VITDDNMIVE YKYGRGI*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

```
m402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCnTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACCCCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCGG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAsA sGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCGC CAmCGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TwTGATTtCT GCTGCTGTCC
551 CTTTGTtTTG TACACTGTTC CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcYtAC TGCCGGATTC
```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

1	MDIVNTKPNT	SLIYMXSFLS	GLLSLGIEVL	WVRMFSFAAQ	SVPQAFSFTL
51	ACFLTGIavg	AYFGKRICRS	RFVDIPFIGQ	CFLWAGIADF	LILGAAWLLT
101	GFSGFVHHAG	IFITLSAVVX	XLIFPLVHHV	GTGDNKSGRQ	VSNVYFAXVA
151	GSALGPVLIG	FVILDFLSTQ	QIYLLICXIS	AAVPLFCTLF	QKSLRLNAVS
201	VAVSLMFGIL	MFLLPDSVFQ	NIADRPDRLI	ENKHGIVAVY	HRDGDKVVYG
251	ANVYDGAYNT	DVFNSVNGIE	RAYLLPSLKS	GIRRIFFVVL	STGSWARVLS
301	AIPEMQSMIV	AEINPAYRSL	IADEPQIAPL	LQDKRVEIVL	DDGRKWLRRL
351	PDEKFDLILM	NTTYWYRASL	TNLLSAEFLK	QVQSHLTPDG	IVMNTHTSP
401	HAFATAVHSI	PAYAYRGHMV	VGSATPVFPF	NKELLQRLS	RLIWPESGRH
451	FVDSSTVDA	AQKVVSRLMI	QMTEPSAGAE	VITDDNMIVE	YKYGRGI*

Homology with a predicted ORF from *N. gonorrhoeae*

m402/q402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPPQAFSFTLACFLTGIAGV					
	: : :					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSFAAQSVPPQAFSFILACFLTGIAGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTDGNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
	:					
g402	GLIFPLVHHVGTDGNKSGRQVSNVYFANVAGSALGPVLIGFVILLDLLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVVYGANVYDGAYN TDVFNSVNGIERAYLLPSLKSGIRRI FVVG LSTG SWARVLS					

726

```

g402      |||||:|||||
          HRDGDKVYGANVYDGAAYNTDIFNSVNGIERAYLLPSLKSGIRRIFFVVLSTGSWARVLS
          250      260      270      280      290      300

          310      320      330      340      350      360
m402.pep  AIPQMISMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHRPDEKFDLILM
          |||||
g402      AIPQMISMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHRPDEKFDLILM
          310      320      330      340      350      360

          370      380      390      400      410      420
m402.pep  NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          :|||
g402      NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          370      380      390      400      410      420

          430      440      450      460      470      480
m402.pep  VGSATPVVFPNKELLKQRLSRLIWPESEGRHVFDSSTVDAAAQKVVSRLMIQMTEPSAGAE
          |||||
g402      VGSATPVVFPNKELLKQRLSRLIWPESEGRHVFDSSTVDAAAQKVVSRLIRMTGPSAGAE
          430      440      450      460      470      480

          490
m402.pep  VITDDNMIVEYKYGRGIX
          |||||
g402      VITDDNMIVEYKYGRGI
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGCTTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTTGACG
301 GGTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTAGA GGGTTGATT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCAA CAGATTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTTG TACTGTTC CAAAAAGTC TCCGACTGAA TGCAGTTCG
601 GTAGCAGTT CCCTAATGT CGGCATCCTC ATGTTCTTAC TGCCGGATTG
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGCTT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATT GGCCGGAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402.pep
1  MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL

```

727

51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQRLS RLIWPESGRH
451 VFDSSSTDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGLIEVLWVRMFSFAAQSVPAFSFTLACFLTGIAVG					
a402	MDIVNTKPNTSLIYMLSFLSGLLSLGLIEVLWVRMFSFAAQSVPAFSFTLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICKIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					
a402	HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m402.pep	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
a402	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m402.pep	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSSTDAAAQKVSRMLIQMTEPSAGAE					
a402	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSSTDAAAQKVSRMLIQMTEPSAGAE					
	430	440	450	460	470	480
	490					
m402.pep	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGCGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTCTCTC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAGC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAANK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTGT LTTSLSTLNA PALSRQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSKEIK PTEGLMVDFF DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAAATGGT CGATTCTCTC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAGC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAANK

```

729

```

51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGGLTG LTTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGPX *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406 . pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406 . pep	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	:					
m406	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406 . pep	LTTSLSTLNAPALSRQSDGSGSRSSLGLNIGGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	: :					
m406	LTTSLSTLNAPALSRQSDGSGSKSSLGLNIGGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406 . pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	:					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406 . pep	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIQPYGNHTGNSAPSVEADN					
	: :					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406 . pep	SHEGYGYSDEAVRQHRQGPX					
	: :					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

```

a406 . seq
1   ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGCGGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

730

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
  1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
  51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
 101  DYTPRYETT AETTSGLTGT LTSLSTLNA PALSRQSDG SGSKSSLGLN
 151  IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVSP ANADTDVFIN
 201  IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
 251  AYKENYALWM GPYKVSCKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301  SHEGYGYSDE AVRRHRQGPX *

m406/a406  98.8% identity in 320 aa overlap

          10          20          30          40          50          60
m406.pep  MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKDMDLQALHGR
          |||
a406       MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKDMDLQALHGR
          10          20          30          40          50          60

          70          80          90          100         110         120
m406.pep  KVALYIATMGDQSGSGLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTGT
          |||
a406       KVALYIATMGDQSGSGLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTGT
          70          80          90          100         110         120

          130         140         150         160         170         180
m406.pep  LTSLSTLNPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF
          |||
a406       LTSLSTLNPALSRQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF
          130         140         150         160         170         180

          190         200         210         220         230         240
m406.pep  FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
          |||
a406       FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
          190         200         210         220         230         240

          250         260         270         280         290         300
m406.pep  IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTGLMVDFSIRPYGNHTGNSAPSVEADN
          |||
a406       IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTGLMVDFSIRPYGNHTGNSAPSVEADN
          250         260         270         280         290         300

          310         320
m406.pep  SHEGYGYSDEVVRQHRQGPX
          |||
a406       SHEGYGYSDEVVRQHRQGPX
          310         320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
  1  atggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
 51  ggcaggcgga gatggcaaga tgcagcatca ctttgacggc aggggttgcgt

```

```

101  tcgtcaaacg attcggacac caagccgctg tctcgggtcga ggccgaggggt
151  cagctggggtc atgtcggttc agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggt cagacccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgctgccgc
501  cgaccagggt ggcgatttcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggatgc gtaaccggcg atgcggcgga
651  taatttcgcg tttcagttcg tcgtcttggt tgtcaaattc caacaaggct
701  ttcgggtgga tgccgatttg gcggttgatg ataaattcca tacgcgcaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801  tgccgacggt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taatttgtag gtccagcagg ccggcataga taaagccggg
901  atcgcttcgc gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaataccagc ttcgcgcgcg
1001 atgatggcgg cgtggcagggt gcgtccgcgg cggttggtca cgatggcgga
1051 agcagctttc atcacgggtt cccaatccgg atcggtcatt tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cggagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgacaaa
1201 gacgggtttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttgggg tttgacgggt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggg cgtcgcgctc ccattcgata tccatcgggc ggccgtagtg
1351 ttttctgatg gtcagcgctg agtgtgccaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatggtc ttgcgcagga tggcggtttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgctc gggttgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggagggt aacaaagacg acttggtgtg agccggattc
1651 ggtgctgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLTADT DIFVLLAAGG DGKMQHHFDG RFAFVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAAADQV GVFGFVGVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVFKF QQGFVRVDAL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDFDGCFWH IVQGDIGNLY VQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDBG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHALALTD FLTDGTTFAQ
401 DFFFAVDGVA AQVAAFFLGD FDGFGAGLQD VEFVAVQAVAS PFDIHRAAVV
451 FFDGQRVVQC LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFVRVDRALY DVFAQTVRGG NKDDL VVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggctcgac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101  tcgtcaaacg attcggatca caagccgctg tcgcgggtcga gaccgaggggt
151  cagttgggtc atgtcggttc agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtctt
301  gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  caacgttggg caaccccatc tcatcgcgga cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgttgccgc
501  cgaccagggt ggcgatttcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651  taatttcgcg ttttaattcg tcgtcttggt tgtcaaattc caacaargct

```


732

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttggcgaa gctgaatgcg agttcgggat
801 tgccgacggt catcatgact tttacagggt ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttcg gcacaggata cggtaacttc ttgaccgttt ttcagcaatt
951 cggttgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggccgcgg cggttggtaa cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcgggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcgcc cttcgcataa
1201 tacggttttg tcgccgttga tggcgaagcg gcgcaggttg cggttgccct
1251 cttcttgagg ttttacggtt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgccaa ctcagtaatt tcttcgtcgg
1401 taatggagaa gcggttgcgg tcttcctcgg ggacatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtggtttga
1501 acccatggtt ttacgcagga tggcgggctt gcccgytttg agcgtgggtt
1551 tgaacacatr aaattcgtcc ggggtgaccg caccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
  1  MVGXALTADA DIFVLLAAGG DGKVVQHHFDG RFAFVKRFGY QAAVAVETEG
 51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101  DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151  TEAQHRVFFM RFVYVAADQV GVFGFVGVGH TDDGFTRINR CGQCRHAFGD
201  FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QXXFGVDTDL AVDDKFHTRQ
251  ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIGNLY VQQTGIDKAG
301  IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
351  STFHHGFPIR IGHVGNFYVA GFDGIHLGSI FNQAHLLTD FLTDGAAFAX
401  YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVAVAVAS PFDIHRAAVV
451  FFDGQCVMRQ LSNFFVGNGE AVAVFLGDID VGYGFTGFCF VGKNHFDVFX
501  THGFTQDGLL ARFERGFEHX KFVRVDRITLY DVFAQTVRGG NKDDLIVXGF
551  GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

```

m501/g501
      10      20      30      40      50      60
m501.pep  MVGXALTADADI FVLLAAGGDGKVVQHHFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG
          ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      MVGRTLTAADTDI FVLLAAGGDGKMVQHHFDGRFAFVKRFGHQAAVSVEAEGQLGHVVRADG
          10      20      30      40      50      60

      70      80      90     100     110     120
m501.pep  EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFNDNGFGFAQSADERNHDFNVG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||
g501      EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG
          70      80      90     100     110     120

      130     140     150     160     170     180
m501.pep  QPHFIADAFQGFQGETVFEVVGDITRRTEAQHRVFFMRFBVYVAADQVGVFGFVGVGH
          | |||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      QTHFVTNAFQGFQGETVFEALGNITRRTEAQHRVFFMRFBVYAAADQVGVFGFVGVGH
          130     140     150     160     170     180

      190     200     210     220     230     240
m501.pep  TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXXFGVDTDL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

733

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAA DNFRFQFVVL FVKFQQGFRVDADL
	190 200 210 220 230 240
m501.pep	250 260 270 280 290 300
	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDIGNLYVQQTGIDKAG
	:
g501	AVDDKFHTRQADAFAGQIGEAEC EFGIADVHHDFDGC FWHIVQGDIGNLYVQQAGIDKAG
	250 260 270 280 290 300
m501.pep	310 320 330 340 350 360
	IAFGTGYGNFLT V FQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR
	: : : :
g501	IAFGTGYGNFLT V FQEFGR IAAADDGRNTQFARDDGGVAGASAAVGH DGGSTFHHGFPIR
	310 320 330 340 350 360
m501.pep	370 380 390 400 410 420
	IGHVGN EYVAGFDGIHLGSI FNQ AHLALTDFLTDGA AFAXYGFVAVDGEAAQVAVALFLG
	: : : :
g501	IGHVGNQYVAGFDGIHLGSI FNQ AHLALTDFLTDGTTFAQDGF FAVDGVAAQVAAFFLG
	370 380 390 400 410 420
m501.pep	430 440 450 460 470 480
	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGGQCV MRQLSNFFVGNGEAVAVFLGDID
	: : : :
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDGGQRVVCQLGDF FVGNGEAVAVFFGD F
	430 440 450 460 470 480
m501.pep	490 500 510 520 530 540
	VGYGFTGF CFVGNHFDVFXTHGFTQDGG LARFERGF EHXKFVRVDR TLYDVFAQTVRGG
	: : : : :
g501	VGYRFAGFGFVGNHFDVFRTHGLAQDGGFACFERGF EHIKFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	550
	NKDDLIVXGFGVEGEHHT
	:
g501	NKDDL VVAGFGVEGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq	(partial)
1	ATGGTCGGAC GGGCCTTGAC CGCAGATGCC GACATATTTG TTCTGCTTGC
51	GGCAGGCGGA GATGGCAAGG TGCAGCATCA CTTTGACGGC AGGGTTGCGT
101	TCGTCAAACG ATTCGGATAC CAAGCCGCTG TCGCGGTCGA GACCGAGGGT
151	CAGTTGGGTC ATGTCGTTCG AGCCGATGGA GAAGCCGTCG AAGTATTGCA
201	GGAATTGTTC CGCCAATACC GCGTTGCTCG GCAGCTCGCA CATCATAATC
251	AGGCGCAGGC CGTTTTTGCC GCGTTCCAAG CCGTTTTCTT TCAGGGCTTT
301	GACAACGGCT TCGGCTTCGC CCAAAGTGCG GACGAACGGA ATCATGATTT
351	CAACGTTGGT CAACCCCAT TCAATCGCGGA CGCGTTTCAA GGCTTTGCAT
401	TCCAAGGCGA AACAGTCTTT GAAGTTGTCG GCGACATAAC GCGCCGCACC
451	ACGGAAGCCC AACATCGGGT TTTCTTCATG CGGTTCTGAT ACGTTGCCGC
501	CGACCAGGTT GGCGTATTCG TTGGATTTGA AGTCGGACAT ACGGACGATG
551	GTTTTACGCG GATAAACCGA TGCGGCCAAT GTCGCCACGC CTTGCGCGAT
601	TTTATCGACG TAGAAGTCGA CAGGGGACGC GTAACCGGCG ATACGGCGGG
651	TAATTTCCGC TTTTAATTCG TCGTCTTGTT TGTCAAATTC CAACAAGGCT
701	TTGGGGTGGA TACCGATTTG GCGGTTGATG ATAAATTCCA TACGCGCCAA
751	GCCGATGCCT TCGCTGGGCA GGTGGCGGAA GCTGAATGCG AGTTCGGGAT
801	TGCCGACGTT CATCATGACT TTTACAGGTG CTTTAGGCAT GTTGTCCAAA
851	GCAACATCGG TAATTGTAC GTCCAGCAGG CCGGAGTAGA TGAAGCCGGT
901	ATCGCCTTCG GCACAGGATA CGGTAAC TTCGACGTTT TTCAGCAATT
951	CGGTTGCATT GCCGCAGCCG ACAACGGCAG GAATACCCAG TTCGCGCGCG

a501.pcp

1	MVGRALTADA	DIFVLLAAGG	DGKVQHFFDG	RVAFVKRFGY	QAAVAVETEG
51	QLGHVVVRADG	EAVEVLQELF	RQYRVARQLA	HHNQAQAVFA	AFQAVFFQGF
101	DNGFGFAQSA	DERNHDFNVG	QPHFIADAFQ	GFAFQGETVF	EVVGDITRRT
151	TEAQHRVFFM	RFVYVAADQV	GVFVGFEVGH	TDDGFTTRINR	CGCQRAHAFDG
201	FIDVEVDVRG	VTGDTAGNER	F*FVVLFEVKF	QQGFGVDTDL	AVDDKFHTRQ
251	ADAFAGQVGE	AECEFGIADV	HHDFYRCFRH	VVQSNIGNLY	VQQAGVDEAG
301	IAFGTGYGNF	LTVFQQFGCI	AAADNGRNTQ	FARDDGGVAG	TSAPVGHDBG
351	SAFHHRFPIW	VGHVGNQYVA	GFDGIHLGSI	FNQAYLALTD	FLTDGAAFAQ
401	DGFFAVDRKA	AQVAAAFFLG	FDGFGTGLQD	VEFAVQAVAS	PFDVHRAAVV
451	FFDGQCVMRQ	LGDFVVGNGE	AVAVFFGDID	VGYRFAGFCF	VGKNHFDVF*
501	AHGFAQVDGRF	ACFQRGFEHI	EFVGIDCALY	DVFAQTVG*S	DKDDLVTGTG
551	GIEGEHH				

[illegible]

	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTDFLT DGAA FAXYGFVA VDGEAAQVA VALFLG					
a501	: : : : : : : : : : : :					
	370	380	390	400	410	420
	VGHVGNQYVAGFDGIHLGSI FNQAYLALTDFLT DGAAFAQDGF FAVDRKAAQVAAFFLG					
m501.pep	430	440	450	460	470	480
	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGCVMRQLSNFFVGNGEAVAVFLGDID					
a501	: : : : : : : : : : :					
	430	440	450	460	470	480
	FDGFGTGLQDVEFAVQAVASPFDVHRAAVVFFDGCVMRQLGDFVGNGEAVAVFFGDID					
m501.pep	490	500	510	520	530	540
	VGYGFTGFCFVGKNHFDVFXTHGFTQDGLARFERGFEHXXKFVRVDRTLYDVFAQTVRGG					
a501	: : : : : : : : : :					
	490	500	510	520	530	540
	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGFEHIEFVGIDCALYDVFAQTVGXS					
m501.pep	550	559				
	NKDDLIVXGFGVEGEHHTX					
a501	: : : : : :					
	DKDDLVTGFGIEGEHH					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

```

g502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcacctgac
51  cgtcgccgtc gcttccgcac aggcgggcgc ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca aaccgtccaa
151 agcaaaaaga aaaccctaac cgcgacggc acgttcaaaa tctgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacggtca aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcgcgggc agccccgcgc ccattcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgcggc
451 ctaccaatac atccgcacgc gttcaaagg cggcaacctc gccgccatgc
501 agcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

```

g502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51  SKKKQTQAHG TFKILRPGLF KWEYTLPLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RGNAQTQRRR
151 LPIHPHRLQR QPRRHAAX*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

```

m502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcacctgac
51  cgtcgccgtc gcttccgcac aggcgggcgc ggttagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaccca amccgtccaa
151 wgcaaaaaga aaaccctaac cgcgacggc acgttcaaaa tctgcgacc
201 gggccttttc aaatgggaat acaccaaact t.acaggcaa accatcgctcg
251 gcgacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgcgc ccattcctgtc
351 gaacaaarcc gccctcgaaa gcagctacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgcccggcta
451 ccaatacatc cgcacgcgct tcaaaggcgg caacctcgcc gccatgcagc
501 tyaa

```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

```

m502.pep
1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51  XXXKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQRRRL
151 PIHPHRLQRR QPRRHAAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502.seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATTC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTCT
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTTGGC	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCGC	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502.pep

1	MMKPHNLFQF	LAVCSLTVSV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKTQTAHG	TFKILRPGLF	KWEYTSPLYK	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQQRRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSPLYKQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

```
g502-1.seq
1  ATGatGAAAc  cgcaCaacct  gttccaaTtC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTGGACGCG  CTCAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGCCC
201 GGGCCTCTTC  AAATGGGAAT  ACACTTTGCC  CTACAGACAG  ACTATTGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATTTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATCGGCGGC  AGCCCCGCCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGTTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CGGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GGCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAAA
601 GCGGTGGACG  TGTTGAGCAA  CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

```
g502-1.pep
1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTQVQ
51  SKKKTQTAHG  TFKILRPGLF  KWEYTLPLYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIGG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  RATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTPQLS  RGAFTFTPPK
201 GVDVLSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

```
m502-1.seq
1  ATGATGAAAC  CGCACAACTT  GTTCCAATTC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTAGACGCG  CTTAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGACC
201 GGGCCTTTTC  AAATGGGAAT  ACACCAAACC  TTACAGGCAA  ACCATCGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATCTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATAGGCGGC  AGCCCCGCCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGCTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CTGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GGCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAAA
601 GCGGTGGACG  TGTTGAGCAA  CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

```
m502-1.pep
1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTQVQ
51  SKKKTQTAHG  TFKILRPGLF  KWEYTKPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIGG  SPAAILSNKT  ALESSYTLKE  DGSSNGIDYV  LATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTPQLS  RGAFTFTPPK
201 GVDVLSN*
```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVAS	ASQAGAVDALKQFNNDADG	ISGSFTQTQVQSKKKTQTAHG			
g502-1	MMKPHNLFQFLAVCSLTVAVAS	ASQAGAVDALKQFNNDADG	ISGSFTQTQVQSKKKTQTAHG			
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQT	IVGDGQTVWLYDVDLAQVTK	SQDQAIGGSPAAILSNKT			
g502-1	TFKILRPGLFKWEYTLPLYRQT	IVGDGQTVWLYDVDLAQVTK	SQDQAIGGSPAAILSNKT			
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPYRQT	IVGDGQTVWLYDVDLAQVTK	SQDQAIGGSPAAILSNKT			
g502-1	TFKILRPGLFKWEYTLPLYRQT	IVGDGQTVWLYDVDLAQVTK	SQDQAIGGSPAAILSNKT			
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYV	LATPKRNNAGYQYIRIGFKG	GNLAAMQLKDSFGNQTSISF			
g502-1	ALESSYTLKEDGSSNGIDYV	RATPKRNNAGYQYIRIGFKG	GNLAAMQLKDSFGNQTSISF			
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYV	LATPKRNNAGYQYIRIGFKG	GNLAAMQLKDSFGNQTSISF			
g502-1	ALESSYTLKEDGSSNGIDYV	RATPKRNNAGYQYIRIGFKG	GNLAAMQLKDSFGNQTSISF			
	130	140	150	160	170	180

```

                190      200
m502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
g502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCTG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GGCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVO
51  SKKKTQTAHG TFKILRPLGF KWEYTSFYKQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep    MMKPHNLFQFLAVCSLTVSVASAQAGAVDAL KQFNNDADGISGSFTQTVO SKKKTQTAHG
                |||||
m502-1        MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL KQFNNDADGISGSFTQTVO SKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep    TFKILRPLGFKWEYTSFYKQTIVGDGQTVWLYDVLDAQVT KSSQDQAIGGSPAAILSNKT
                |||||
m502-1        TFKILRPLGFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVT KSSQDQAIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep    ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                |||||
m502-1        ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                130     140     150     160     170     180

                190     200
a502-1.pep    GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
m502-1        GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgtcggcatc ggtaatcatt ttgttccatg ccgcttcgat
51  ttcggcatcg agctgttcgg ggaaggcggt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggttag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTNF
51  ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

```
m503.seq
1      atgtccgcac  cgccggcatt  ggcaaccatt  ttgttccatg  ccgcttcgat
51     ttcggcatcg  agctgttcgg  ggaaaggcgt  atccaaaatc  cattggcgga
101    ttctcttgcc  gacgcgtgcc  agttcggcaa  cgtcttcgac  atccaatttt
151    gccagtcggg  cggaaatgcg  ttcgctcaga  ccgttgtgtg  cgaggaatgc
201    gcggtag
```

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

```
m503.pep
1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
51 ASAAEMRSLR PLCARNAR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

m503/g503

```

              10      20      30      40      50      60
m503.pep    MSAPPASATILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLR
             ||||| : ||||||||||||||||||||||||| ||||||| ||||| : |
q503        MSAPSASVILFHAASISASSCSGKGVSKIHWRISLPTRASSETTSSTSNFARAAEMRSFR
              10      20      30      40      50      60

                69
m503.pep     PLCARNAR
             ||||| |
q503         PLCARNAR

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

```
a503.seq
  1  ATGTCCGCGC  CGCCGGCATC  GGCAACCATT  TTGTTCCATG  CCGCTTCGAT
51  TTCGGCATCG  AGCTGTTCCG  GGAAGGGCGT  GTCCAAAATC  CATTTGGCGGA
101 TTTCTTTGCC  GACGCGTGCC  AGTTCGGCAA  CGTCTTCGAC  ATCTAATTTT
151 GCCAGTGC GG  CGGAAATGCG  TTCGCTCAGA  CCGTTGTGTG  CGAGGAATGC
201 GCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

a503.pep
1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
51 ASAAEMRSLR PLCARNAR*

m503/a503 100.0% identity in 68 aa overlap

```

      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLR
          |||||
a503      MSAPPASATILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLR
          10      20      30      40      50      60

      69
m503.pep  PLCARNARX
          |||||
a503      PLCARNARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

g503-1.seq

1	ATGGCGCGGT	CGTTGTACAG	GGAGGCGAAA	ACGTGGCGCA	TCGCTTTTTT
51	AACGTTATCC	AAGCCATTGA	TATTACGGAA	GGTTTCCTGT	TGGCCGGCAA
101	ATGATGCGTC	GGGCAGGTCT	TCGGCGGTTG	CGGAAGAGCG	TACGGCAACG
151	GAAATGTCGG	CGCCGTCGGC	ATCGGTAATC	ATTTTGTCTC	ATGCCGCTTC
201	GATTTCGGCA	TCGAGCTGTT	CGGGGAAGGG	CGTGTCCTAA	ATCCATTGGC
251	GGATTTCCTT	GCCGACGCGT	GCCAGTTCGG	AAACGTCCTC	GACATCCAAT
301	TTTGCCAGAG	CGGCGGAAAT	GCGTTCGTTC	AGACCGTTGT	GTGCGAGAAA
351	TCGCGCGTAG				

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep

```

1  MARSLYREAK TWRIAFLLS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSETSSTSN
101 FARAAEMRSF RPLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq

```

1  ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
51 AACGTTATCC AAGCCGTTGA TGTTCAAGAA GGTTTCCTGT TGTCACGCGA
101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
251 GGATTCTTTT GCCGACGCGT GCCAGTTCGG CAACGCTCTC GACATCCAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep

```

1  MARSLYREAN TWCIALTSL KPLMFKKVSC CPANDASGRS SAVAEERTAT
51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRIAFLLSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPSASVI					
m503-1	MARSLYREANTWCIALTSLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKIHWRIISLPTRASSETSSSTSNFARAAEMRSFRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRIISLPTRASSETSSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq

```

1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGGCGCA TCGCTTCTTT
51 AACGTTTTC AAGCCGTTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC
251 GGATTCTTTT GCCGACGCGT GCCAGTTCGG CAACGCTCTC GACATCTAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPPASAT					
m503-1	MARSLYREANTWCIALTSLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRIISLPTRASSETSSSTSNFASAAEMRSLRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRIISLPTRASSETSSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

```

g504.seq
1  atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacggt catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgtaa
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgccggaatc cgtactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccacgtgta ccgcacccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattatTTTT
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataccg ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggtatga aaccatacgc
901 cgggtacggct tgcccgaatg gcagcaggat gaagcgcgga accgtttctt
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcttc aggtttgcag
1051 atgacccggt cgccgggtgc gcttttggtc tatctcggct cggtattgtt
1101 ggttttgggt acagtattta tgttttatgt gcccaaaaaa cgggctgggg
1151 tattgttttc aaacdgcata atccgttttg ctatgtcttc ggccgcgagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

```

g504.pep
1  MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQDDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLLSH MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFNSKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

```

m504.seq..
1  atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacggt catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgtaa
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgcccgccgt gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccggtttt gcaggaaacg gattatTTTT
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataccg ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggtatga aaccatacgc
901 cgggtacggct tgcccgaatg gcagcaggat gaagcgcgga atcgtttctt
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgctc gggtttgag

```

```

1051 atgacccggt ccccggggtgc gcttttgggtc tatctcggtc cgggtgctggt
1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgacgc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
1251 gctcggcaag gacttgaatc atga

```

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

```

m504 . pep . .
  1  ILVQDLPEFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51  HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVLK ATSIHQFPLE
101  IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
151  IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
201  IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251  TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
301  RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351  MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401  ERDLQKEFPK HVESLQRLGK DLNHD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

```

m504 / g504

      10      20      30      40      50      60
m504 . pep  ILVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERIRVNHPLTLHGITI
: |||||
g504        MLVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERIRVNHPLTLHGITI
      10      20      30      40      50      60

      70      80      90     100     110     120
m504 . pep  YQASFADGGSDLTFKAWNLDASREPVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
: |||||
g504        YQASFADGGSDLTFKAWNLRDASREPVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
      70      80      90     100     110     120

     130     140     150     160     170     180
m504 . pep  MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPVLQEQ
: |||||
g504        MSEGAREKSLKSTLNDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPILQDK
     130     140     150     160     170     180

     190     200     210     220     230     240
m504 . pep  DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
: |||||
g504        DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKDAPAEI
     190     200     210     220     230     240

     250     260     270     280     290     300
m504 . pep  REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
: |||||
g504        REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQQDKMQGYFYEMLYGVMNAALDETIR
     250     260     270     280     290     300

     310     320     330     340     350     360
m504 . pep  RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV
: |||||
g504        RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV
     310     320     330     340     350     360

     370     380     390     400     410     420
m504 . pep  YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
: |||||

```

743

g504 YLGSVLLVLGTVFMFYVPPKKRAWVLFNSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504.pep DLNHD
 |||||

g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq

1	ATATTGGTTC	AGGACTTGCC	TTTTGAAGTC	AAACTGAAAA	AATTCCATAT
51	CGATTTTTTAC	AATACGGGTA	TGCCGCGCGA	TTTTGCCAGT	GATATTGAAG
101	TAACGGATAA	GGCAACCGGT	GAGAACTCG	AGCGCACCAT	CCGCGTGAAC
151	CATCCTTTGA	CCTTGCACGG	CATCACGATT	TATCAGGCGA	GTTTTGCCGA
201	CGCGGTTTCG	GATTTGACAT	TCAAGGCGTG	GAATTGGGT	GATGCTTCGC
251	GCGAGCCTGT	CGTGTGAAG	GCAACATCCA	TACACCAGTT	TCCGTTGGAA
301	ATTGGCAAAC	ACAAATATCG	TCTTGAGTTC	GATCAGTTTA	CTTCTATGAA
351	TGTGGAGGAC	ATGAGCGAGG	GCGCGGAACG	GGAAAAAGC	CTGAAATCCA
401	CGTGAAACGA	TGTCCGCGCC	GTTACTCAGG	AAGGTAAAAA	ATACACCAAT
451	ATCGGCCCTT	CCATTGTTTA	CCGTATCCGT	GATGCGGCAG	GGCAGGCGGT
501	CGAATATAAA	AACTATATGC	TGCCGGTTTT	GCAGGAACAG	GATTATTTTT
551	GGATTACCGG	CACGCGCAGC	GGCTTGCAGC	AGCAATACCG	CTGGCTGCGT
601	ATCCCTTGG	ACAAGCAGTT	GAAAGCGGAC	ACCTTTATGG	CATTGCGTGA
651	GTTTTTGAAA	GATGGGGAAG	GGCGCAAACG	TCTGGTTGCC	GACGCAACCA
701	AAGGCGCACC	TGCCGAAATC	CGCGAACAAAT	TCATGCTGGC	TGCGGAAAAC
751	ACGTGAACA	TCTTGCACA	AAAAGGCTAT	TTGGGATTGG	ACGAATTTAT
801	TACGTCCAAT	ATCCCGAAAAG	AGCAGCAGGA	TAAGATGCAG	GGCTATTTCT
851	ACGAAATGCT	TTACGGCGTG	ATGAACGCTG	CTTTGGATGA	AACCATACGC
901	CGGTACGGCT	TGCCCGAATG	GCAGCAGGAT	GAAGCGCGGA	ATCGTTTCCT
951	GCTGCACAGT	ATGGATGCGT	ACACGGGTTT	GACCGAATAT	CCCGCGCCTA
1001	TGCTGCTGCA	ACTTGATGGG	TTTTCCGAGG	TGCGTTCGTC	GGGTTTGCAG
1051	ATGACCCGTT	CCCCGGGTGC	GCTTTTGGTC	TATCTCGGCT	CGGTGCTGTT
1101	GGTATTGGGT	ACGGTATTGA	TGTTTTATGT	GCGCGAAAAA	CGGGCGTGGG
1151	TATTGTTTTT	AGACGCAAAA	ATCCGTTTGT	CCATGTCTTC	GGCCCGCAGC
1201	GAACGGGATT	TGCAGAAGGA	ATTTCCAAAA	CACGTCGAGA	GTCTGCAACG
1251	GCTCGGCAAG	GACTGAATC	ATGACTGA		

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep

1	ILVQDLPFEV	KLKKFHIDFY	NTGMPRDFAS	DIEVTDKATG	EKLERTIRVN
51	HPLTLHGITI	YQASFADGGS	DLTFKAWNLG	DASREPVVLK	ATSIHQFPLE
101	IGKHKYRLEF	DQFTSMNVED	MSEGAEREKS	LKSTLNDVRA	VTQEGKKYTN
151	IGPSIVYRIR	DAAGQAVEYK	NYMLPVLQEQ	DYFWITGTRS	GLQQQYRWLR
201	IPLDKQLKAD	TFMALREFLK	DGEGRKRLVA	DATKGAPAEI	REQFMLAAEN
251	TLNIFAQKGY	LGLDEFITSN	IPKEQQDKMQ	GYFYEMLYGV	MNAALDETIR
301	RYGLPEWQOD	EARNRFLLS	MDAYTGLTEY	PAPMLLQLDG	FSEVRSSGLQ
351	MTRSPGALLV	YLGSVLLVLG	TVLMFYVREK	RAWVLFSDGK	IRFAMSSARS
401	ERDLQKEFPK	HVESLQRLGK	DLNHD*		

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLE	IRVNHPLTLHGITI				
a504	ILVQDLPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLE	IRVNHPLTLHGITI				
	10	20	30	40	50	60
m504.pep	YQASFADGGS	DLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED				
a504	YQASFADGGS	DLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED				
	70	80	90	100	110	120
m504.pep	YQASFADGGS	DLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED				
a504	YQASFADGGS	DLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED				
	70	80	90	100	110	120
m504.pep	MSEGAEREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK	NYMLPVLQEQ				
a504	MSEGAEREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK	NYMLPVLQEQ				
	130	140	150	160	170	180

```

a504      |||||
MSEGAEREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ
      130      140      150      160      170      180

m504.pep      190      200      210      220      230      240
DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLDGEGRKRLVADATKGAPAEI
a504      |||||
DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLDGEGRKRLVADATKGAPAEI
      190      200      210      220      230      240

m504.pep      250      260      270      280      290      300
REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDEIR
a504      |||||
REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDEIR
      250      260      270      280      290      300

m504.pep      310      320      330      340      350      360
RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV
a504      |||||
RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV
      310      320      330      340      350      360

m504.pep      370      380      390      400      410      420
YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
a504      |||||
YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
      370      380      390      400      410      420

m504.pep      DLNHDX
a504      |||||
DLNHDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

g505.seq

```

1  atgtttcggt tacaattcag gctgtttccc cctttgcgaa ccgccatgca
51  catcctgttg accgccctgc tcaaatgcct ctccctgtg tcgctttcct
101 gtctgcacac gctgggaaac cggctcggac atctggcgtt ttacctttta
151 aaggaagacc gcgcgcgcat cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacggtca aagccgtttt tgcggaaacg gcaaaatgcg
251 gtttggaaact tgcccccgcg tttttcaaaa aaccggaaga catcgaaaca
301 atgttcaaag cggtagacgg ctgggaacac gtgcagcagg ctttggacaa
351 gggcgaaggg ctgctgttca tcacgcgcga catcggcagc tacgatttgg
401 gcggacgcta catcagccag cagcttccgt tccacctgac cgccatgtac
451 aagccgccga aaatcaaagc gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cgcccaccgg catacaaggg gtcaaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaccac
601 gtcccttctc cgcaggaagg cggcggcgtg tgggcggatt ttttcggcaa
651 acctgcatac accatgacac tggcggcaaa attggcacac gtcaaaggcg
701 tgaaaaccct gtttttctgc tgcgaacgcc tgcccagcgg acaaggcttc
751 gtgttgacac tccgccccgt ccaaggggaa ttgaacggca acaaagccca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgccgttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

g505.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL SLSCLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPD TQVKAVFAET AKCGLELAPA FFKKPEDIET
101 MFKAVHGWEE VQALDKGEG LLFITPHIGS YDLGGYISQ QLPFHLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTGIQG VKQIIKALRA GEATIILPDH
201 VPSPQEGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDQGQF
251 VLHIRPVQGE LNGNKAHDAA VFNRNTEYWI RRFPTQYLFM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

m505.seq (partial)

```

1  GGCATGTTTC GTTACAATT CAGGCTGTTT CCCCCTTTC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTTGCGGAA ACGGCAAAAG
251 GCGGTTTGGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351 CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTGCGGCG AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCCACC
601 ACGTCCCCTC CCCTCAAGAA GCGGGGAAG GCGTATGGGT GGATTCTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAATATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAAG
751 GTTTCGATTT GCACATCCGC CCCGTCCAAG GGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTTCCGACG CATATC...
```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGHlafYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI DKIMQAGRV R GKTAPT SIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGG EG VVWDFFGK PA YTMTLAAX LA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ G ELNGDKA HDA AVFNRNAE YW IRRFPTHI...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHlafYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLSLSCLHTLGNRLGHlafYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPD PKTVKAVFAETAKGGLLELAPFAFFRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPD TQTVKAVFAETAKGGLLELAPFAFFKKPEDIETMFKAVHGW EHVQQALDKGEG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAI DKIMQAGRV R GKTAPT SIQG					
g505	LLFITPHIGSYDLGGYISQQLPFHLTAMYPKPPKIKAI DKIMQAGRV R GKTAPT GIQG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVVWDFFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEAT IILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKGVKTLFF					
	190	200	210	220	230	
	250	260	270	280	289	
m505.pep	CCERLPGGQGF DLHIRPVQ GELNGDKAHDA AVFNRNAE YW IRRFPTHI					
g505	CCERLPDGGGFV LHIRPVQ GELNGKHA DA AVFN RTEY WIRRFPTQYLFMYNRYKTP					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCCACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAGGCG
251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGBAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGCG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATAACAAGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTTC GGCGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGHLAFYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
101 MFKAVHGWHEH VQQALDKHEG LLFITPHIGS YDLGGRYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGVRGK GKAPTISIQQ VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHD AAVFNRAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWHEHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWHEHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWHEHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWHEHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIKIMQAGVRGKGKAPTISIQQ					
a505	LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIKIMQAGVRGKGKAPTISIQQ					
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIKIMQAGVRGKGKAPTISIQQ					
a505	LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIKIMQAGVRGKGKAPTISIQQ					
	130	140	150	160	170	180
m505.pep	VKQIIKALRSGEATIVLPDHVPSPEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKTLFF					
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKTLFF					
	190	200	210	220	230	240
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```

1  ATGTTTCGTT  TACAATTCAG  GCTGTTTCCC  CCTTTGCGAA  CCGCCATGCA
51  CATCCTGTTG  ACCGCCCTGC  TCAAATGCCT  CTCCCTGCTG  CCGCTTTCCT
101 GTCTGCACAC  GCTGGGAAAC  CGGCTCGGAC  ATCTGGCGTT  TTACCTTTTA
151 AAGGAAGACC  GCGCGCGCAT  CGTCGCCAAT  ATGCGGCAGG  CGGGTTTGAA
201 CCGCGACCCC  AAAACGGTCA  AAGCCGTTT  TGCAGAAACG  GCAAAAGGCG
251 GTTTGGAAct  TGCCCCCGCG  TTTTTCAGAA  AACCAGGAAG  CATAGAAACA
301 ATGTTCAAAG  CGGTACACGG  CTGGGAACAT  GTGCAGCAGG  CTTTGACAA
351 ACACGAAGGG  CTGCTATTCA  TCACGCCGCA  CATCGGCAGC  TACGATTGG
401 GCGGACGCTA  CATCAGCCAG  CAGCTTCCGT  TCCCGCTGAC  CGCCATGTAC
451 AAACCGCCGA  AAATCAAAGC  GATAGACAAA  ATCATGCAGG  CGGGCAGGGT
501 TCGCGCAAA  GGA AAAACCG  CGCCTACCAG  CATACAAGGG  GTCAAACAAA
551 TCATCAAAG  CCTGCGTTCG  GCGGAAGCAA  CCATCGTCCT  GCCCGACCAC
601 GTCCCTCCC  CTCAAGAAAG  CGGGGAAGGC  GTATGGGTGG  ATTTCTTCGG
651 CAAACCTGCC  TATACCATGA  CGCTGGCGGC  AAAATTGGCA  CACGTCAAAG
701 GCGTGA AAAC  CCTGTTTTTC  TGCTGCGAAC  GCCTGCCTGG  CGGACAAGGT
751 TTCGATTGTC  ACATCCGCCC  CGTCCAAGGG  GAATTGAACG  GCGACAAAGC
801 CCATGATGCC  GCCGTGTTCA  ACCGCAATGC  CGAATATTGG  ATACGCCGTT
851 TTCCGACGCA  GTATCTGTTT  ATGTACAACC  GCTACAAAAT  GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP  PLRTAMHILL  TALLKCLSL  LPLSCLHTL  GNRLGHLAF  YLLKEDRARI  VAN
51  KEDRARIVAN  MRQAGLNPD  P KTVKAVFA  ET AKGGLEL  APA FFRKPEDI  ET
101 MFKAVHGEH  VQALDKHEG  LLFITPHIG  S YDLGGYIS  Q QLPFPLTAM  Y
151 KPPKIKAIK  IMQAGRVRG  K GKTAPTSI  QG VKQIIKAL  RS GEATIVLP  DH
201 VPSPQEGGEG  VVVDFFGK  PA YMTLAAK  LA HVKGVKTL  FF CCERLPGG  QG
251 FDLHIRPVQ  G ELNGDKA  HDA AVFNRNA  EYW IRRFPTQ  YLF MYNRYK  MP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLLSLCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGLELAPAFFKKPEDIETMFKAVHGEHVQALDKGEG					
	70	80	90	100	110	120
m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGLELAPAFFKKPEDIETMFKAVHGEHVQALDKGEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFHLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQG					
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRSGEATIVLPDHPVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGKTLFF					
g505	VKQIIKALRAGEATIILPDHPVSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKGKTLFF					
	190	200	210	220	230	240
m505-1.pep	VKQIIKALRSGEATIVLPDHPVSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGKTLFF					
g505	VKQIIKALRAGEATIILPDHPVSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKGKTLFF					
	190	200	210	220	230	
m505-1.pep	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX					
g505	CCERLPGGQGFVLDHIRPVQGEELNGDKAHDAAVFNRNTEYWIRRFPTQYLFMYNRYKTPX					
	240	250	260	270	280	290

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	70	80	90	100	110	120

m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMPKAVHGWHEHVQQALDKHEG
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMPKAVHGWHEHVQQALDKHEG
	70 80 90 100 110 120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTSTIQG
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTSTIQG
	130 140 150 160 170 180
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLPFF
a505	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLPFF
	190 200 210 220 230 240
m505-1.pep	CCERLPGGQGFDLHIRPVQGEINLNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
a505	CCERLPGGQGFDLHIRPVQGEINLNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
	250 260 270 280 290 299

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

```

g506.seq
1  ATGGCGGTAT  TTGATGAAGT  CGGGCGCATC  GCCCATGGCT  GCGGCGGTGT
51  TGTCAAACAA  AGCCTGTTTC  TGC CGTCGT  TCATCAGGTT  GAACAAGGCG
101 CGCGGTGGC  TGAAGTAGTC  GTCATCGTCT  TGGCGGTAGT  CCCAGTGTGC
151 CGCGTCGCCG  TTGATTTTCA  AAGGCGGTTT  GCGGAAGTCG  GGTGTTTGCT
201 GCCATTGGCC  GAAGCTGTTG  GGTTCGTAGT  GCGGCAGGCT  GCCGTAGTTG
251 CCGTCGCGCG  GGCCTTGTCG  GTCGCGCTGG  TTGCTGTGAA  CAGGGCAACG
301 CGGACGATTG  ACGGGGATTT  GCGGGAAGTT  CACACCCAAG  CGGTAACGTT
351 GCGCGTCGGC  GTAATTGAAC  AAACGGGCTT  GCAACATTTT  ATCCGGGCTC
401 GCGCCGATAC  CGGGAACGAG  GTTGCTCGGT  GCGAAGGCGG  ATTGTTCCAC
451 ATCGGCGAAG  AAGTTTTTCG  GATTGCGGTT  CAACTCGAAT  TCGCCCACTT
501 CAATCAGCGG  ATAGTCTTTT  TTCGGCCAAA  CTTTGGTCAA  GTCAAACGGA
551 TGATAAGGCA  CTTTTTCGCG  ATCGGCTTCA  GGCATGACTT  GGATGTACAT
601 CGTCCATTTC  GGGAACTCGC  CGCGCTCGAT  GGCTTCGTAC  AGGTCGCGCT
651 GATGGCTTTC  GCGGTCGTCG  GCGATGATTT  TTGCAGCTTC  TTCGTTGGTC
701 AGGTTTTTAA  TCCCTTGCTG  GCTGCGGAAA  TGGAATTTCA  CCCAAAACG
751 TTCGCCCGCT  TCGTTCCAGA  AGCTGTAGGT  ATGCGAACCG  AAGCCGTGCA
801 TATGGCGGTA  GCTGGCGGGA  ATACCGCGGT  CGCTCATCAC  GATGGTAACT
851 TGGTGCAGGG  CTTGCGGCAG  CAGCGTCCAG  AAGTCCCAGT  TGTGTTGGC
901 GGAACGCATA  TTGGTGCGCG  GATCGCGTTT  GACGGCTTTG  TTCAGGTCGG
951 GGAATTTGCG  CGGGTCGCGC  AGGAAGAACA  CGGGCGTGTT  GTTGCCGACC
1001 ACATCCCAGT  TGCCTTCTTC  GGTATAGAAT  TTCAACGCAA  AACCGCGGAT
1051 GTCGCGTTCC  GCATCGGCTG  CGCCGCGCTC  GCCTGCCACG  GTGGTGAAAC
1101 GGGCGAACAT  CTCGGTTTTT  TTGCCGACTT  CGCTGAAAAT  TTTGGCGCGG
1151 TGTTATTTGG  TGATGTCGTG  TGTACGGTA  AACGTACCGA  ACGCGCCCGA
1201 ACCTTTTGCG  TGCATACGGC  GTTCGGGGAT  GACTTCGCGC  ACGAAGTCGG
1251 CGAGTTTTTC  ATTCAGCCAC  AAATCTTGCG  TCAGCAGGGG  GCCGCGCGGG
1301 CCGGCGGTCA  GGCTGTTTTG  ATTGTCGGCA  ACGGGCGCGC  CGTTGTTTCA
1351 GGTCAGATGG  GTTACGGGGC  ATTTGGAGGT  AGTCATCGCT  CTTGTTCTTT
1401 TTCTCAGGTT  GGTCAAATGG  GGGGCAAACG  GCTTACAGTA  CGATTTGGCG
1451 GAAAGCGTAT  TCGTAACCGG  TTTCTTGATT  GTAATAAATT  TCTTGAATCG
1501 ACATTTTATT  TTCCTTTTGC  AAAAATATG  GATGCGATTA  TACGCCAAGA
1551 TTTTCGTTAT  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

```

g506.pep
1  MAVFDEVGRI  AHGCGGVVKQ  SLFLRVVHQQ  EQGARLAEVV  VIVLAVVPVC
51  RYAVDFQRRF  GEVGLLLPLA  EAVGFVVRQA  AVVAVGAALS  VALVAVNRAT
101 RTIDGLAEV  HTQAVTLRVG  VIEQTGLQHF  IRARADTGNE  VARCEGGLFH
151 IGEFVGIAV  QLEFAHFNQR  IVFFRPNFGQ  VKRMIRHFFG  IGRHDLDVH

```

201 RPFRELAALD GFVQVALMAF AVVGDDFCSF FVGQVFNPLL AAEMEFHPKT
 251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVC
 301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQKRTAD
 351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGQAVL IVGNGRAVVH
 451 GQMGYGAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFAKTM DAIIRQDFRY *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

1 ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
 51 TGCCGAACAA TGCTGTTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG
 101 CGCGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
 151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GCGCAATCG GGTGTGTGCT
 201 GCCATTGGCC GAAGCTGTyG GGTTCGTAGT GCGGCAGGCT GCCGyAGTTG
 251 CCGTCGGCGC GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG
 301 CGGACGATTG ACGGGAATTT GCGGGAAGTT TACGCCCCAA CGGTAGCGTT
 351 GTGCGTCGGC GTAATTGAAC AAACGCGCTT GCAGCATTTT ATCTsGGCTG
 401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
 451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CTCAAACGGA TGATAAGGTA
 501 CTTTTTCCGC GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC
 551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC
 601 GCGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC AGGTTTTTAA
 651 TGCCTTGTTG GGTGCGGAAA TGGAAATTCA CCCAAAAACG CTCGCCTGCT
 701 TCGTTCACAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA
 751 GCCGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT TGGTGCAGTG
 801 CTTCCGGCAG CAGCGTCCAG AAGTCCCAGT TGTTTGTGGC AGAGCGCATA
 851 TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG GGAACTTACG
 901 CGGGTCGCGC AGGAAGAACA CGGGCGGTGT GTTGCCGACC ACATCCCAGT
 951 TGCCTTCTTC GGTATAAAAT TTCAAGGCAA AACCCGGAT GTCGCGTTCT
 1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT
 1051 CTCGTTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGCG
 1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT
 1151 CTTGTTCTCT TTCTCAGGTT GGTCAAATGG GGGTAAACGG CTTACAGTAC
 1201 GATTTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT
 1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAACTATGG ATGCGACTAT
 1301 ACGCCAAGAT TTTGCTATT AA

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHVQ EQGARLAEIV VIVLAVVPVC
 51 RVAVDQRRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT
 101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTNE VARCEGGLFH
 151 IGEEVFIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHDLDVH
 201 RPFRLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT
 251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFQ QRPEVPVVC
 301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQKRTAD
 351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQR AARTGGQAVL IVGNRRVVH
 451 GQMGYRAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFVKTM DATIRQDFRY *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQVEQGARLAEIVVIVLAVVPVCRAVDQRRF					
	:: ::					
g506	MAVFDEVGRVIAHCGGGVVKQSLFLRVVHVQVEQGARLAEVVIVLAVVPVCRAVDQRRF					
	10	20	30	40	50	60

750

	70	80	90	100	110	120
m506 . pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAAXVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506 . pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFIRARADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506 . pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAAFDGFXXVALMAFAVVGDDFGGFFVGVFNALL					
g506	VKRMIRHFFGIGFRHDLDVHRPFRCLAALDGFVQVALMAFAVVGDDFCSFFVGVFNPLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506 . pep	GAEMEFHPKTLACFVPEAVGMRTAEVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVCG					
g506	AAEMEFHPKTFARFVPEAVGMRTAEVHMAVAGGNTAVAHHDGNLVQCFGQQRPEVPVVCG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m506 . pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIKFQKGTADVAFCIGCAAF					
g506	GTHIGARIAFDGFVQVGEFARVAQEEHGRVVADHIPVAFFGIEFQRKTADVAFRIGCAAL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506 . pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVCYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506 . pep	IQPQILRQORAARTGGQAVLIVGNRAVVHGMGYRAFGGSHRSCSFSQVGMGGKRLTV					
g506	IQPQILRQQGAARAGGQAVLIVGNRAVVHGMGYGAFGGSHRSCSFSQVGMGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506 . pep	RFGGKRIRNRFLDCNKFLESTFYFPFKTMDATIRQDFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTMDAIIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

a506 . seq

```

1   ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATGCG GCGGCGGTGT
51  TGCCGAACAA TGCTGT TTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGCGC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTT GCGGAAGTCG GGCTGCTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GTCCTGTGCC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGGTTG ACAGGGATTT GGCGGAAGTT CACGCCCAAG CGGTAGCGTT
351 GCGCGTCGGC GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCAAAA CTTTGTGCAA GTCAAACGGA
551 TGATACGGCA CTTTTTCCGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTT GGAAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT

```

```

651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTTAA TGCCTTGTG GGTGCGGAAA TGGAAATTTCA CCAAAAAACG
751 CTCGCCTGCT TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGTG CTTGCGGCAG CAGCGTCCAG AAGTCCAGT TGTGTTGGC
901 AGAGCGCATA TTGGTGCAGG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTT GGTATAGAAC TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTACGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTTAT
1351 GGTCAGATGG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCCCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAACG GCTTACAGTA CGATTTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1   MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVR
51  RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
201 RPFRLAALD GFVQVALMAF TVVGDDFFGG FVGQVFNALL GAEMEFHFKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRAVVH
451 GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

```

              10      20      30      40      50      60
m506.pep     MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF
a506          MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF
              10      20      30      40      50      60

              70      80      90      100     110     120
m506.pep     GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG
a506          GEVGLLLPLAEAVGFVVRQAQAVVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG
              70      80      90      100     110     120

              130     140     150     160     170     180
m506.pep     VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNRIVFFRPNFGQ
a506          VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNRIVFFRPNFGQ
              130     140     150     160     170     180

              190     200     210     220     230     240
m506.pep     VKRMIRYFFRVCFRHDLVDHVPFRKLAALDGFXXVALMAFAVVGDDFFGGFFVGQVFNALL
a506          VKRMIRHFFRIGFRHDLVDHVPFRKLAALDGFVQVALMAFTVVGDDFFGGFFVGQVFNALL
              190     200     210     220     230     240

              250     260     270     280     290     300
m506.pep     GAEMEFHFKTLACFVPEAVGMRTAVHMAVAGGDAVAHHHDGNLVQCFGQQRPEVPVVC
a506          GAEMEFHFKTLACFVPEAVGMRTAVHMAVAGGDAVAHHHDGNLVQCFGQQRPEVPVVC
              250     260     270     280     290     300

```

752

	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVDHIPVAFFGKIFQGKTADVAFICGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVDHIPVAFFGKIFQGKTADVAFICGCAAF					
	310	320	330	340	350	360
m506.pep	370	380	390	400	410	420
	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
m506.pep	430	440	450	460	470	480
	IQPQILRQRAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFQVGMGGKRLTV					
a506	IQPQILRQRAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFQVGMGGKRLTV					
	430	440	450	460	470	480
m506.pep	490	500	510	520		
	RFGGKRIRNRFLDCNKFLESTFYFPFKTMDATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFKTMDATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTCCTCTG CTTACAGACGG
101 CCTTTGCGCT CTCGTGCTT GGCAACGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGAATTCCTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTT CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGGTTGGTG CAGGTTTTGC CGGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNGLFGMGKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFFDLQLVF LKLHADLLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTTAAGGCTT GGTTCCTCTG TTTACAGACGA
101 CCTTTGCGCT CTCGTGCTT GGCAATCGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTT TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTAATC GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCA TCGGTTGGTG CAGGTTTTGC TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTG CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTLOQGG CFLRGGGFGF VGQVXGLVFL FQTTFALFVL GNRLFGMGKL

```

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLLVFG NLHRPFRQLG
 101 LFFFDLQLVF FKLHADLLLL LMNALXRLRL CLLVAFDALV QVLLMADLFF
 151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng)

from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFNGMGLLLLQRQFAAD					
	: : : :					
g507	MLLPALQQGGGFLSGGGFGLVGVQGLVFLQTAFALFVLGNRLFNGMGLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL					
	: : : :					
g507	AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQGLLFFFDLQLVFLKLHADLLLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m507.pep	LMNALXRLRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG					
	: : : :					
g507	LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVYCLLLRLFGSLQG					
	130	140	150	160	170	180
m507.pep	VYFVV					
	:					
g507	VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

a507.seq
 1 ATGCTCTTGC TGGCTTTGCA ACAAGGCGGC AGCTTCCTGC GCGGCGGCGG
 51 TTTCCGCTTC GTCAGGCAGA TTCAGGGCTT GGTTTTCTCTG TTTCAGACGA
 101 CCTTTGCGCT CTCGTGCTT GGCAACGGTT TGTTCCGCAT GGGCAAGCTG
 151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTTGCT
 201 GGGTTTGGAA GCGCGCATTG AGTGTGGCTT GGGTTTCTTC CAATTCGGGC
 251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAATTCGGT
 301 TTGCTTTTCT TCCGCCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
 351 GCTGCTGCTC CTGATGGATG CGCTGCATCT GCGCCTGCGC CGCCTGCTTG
 401 TCGCGTTCGA TCGTTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC
 451 CAAACGGGCA ATCTGTTCGC GCAACACGCC GCGTTTGTG CCAATTCGT
 501 GCACCGCCTG CTGCTGCGAC TGTTCCGCAG TCTGCAAGGC GTGTACTTCG
 551 TCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep
 1 MLLLALQQGG SFLRGGGFGF VRQIQGLVFL FQTTFALFVL GNGLFGMGKL
 51 LLLQRQFAAD AVCLVLLGLE GGIECGLGFF QFGQTLFVFG NLHRPFRQFG
 101 LLFFRLQLVF FKLHADLLLL LMDALHLRL RLLVAFDALV QVLLMADLFF
 151 QTGNLFAQHA AFVAQFVHRL LLRLFGSLQG VYFVV*

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFNGMGLLLLQRQFAAD					
	: : : :					
a507	MLLLALQQGGSFLRGGGFGFVRQIQGLVFLFQTTFALFVLGNRLFNGMGLLLLQRQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m507.pep  AVCLVLLGLEGGVERGLGFFQFGQTLFVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
          |||||
a507       AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
          70      80      90      100     110     120

          130     140     150     160     170     180
m507.pep  LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
          |||||
a507       LMDALHLRLRLRLLVAFDALVQVLLMADLFFQTGNLFAQHAAFVAQFVHRLLLRLFGSLQG
          130     140     150     160     170     180

m507.pep  VYFVVX
          |||||
a507       VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51 TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGCAG GGTTTGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTTCTCTG
151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GGCGATTTGC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLREFFL
51 HGDVFFVQRV YGFGQLVELD VLLVVLELGF IGEGKLLPAF LPVQGLLFEP
101 GDLLPVVFLF RVEFVDGDFG KPVLA VG FQ GKLR L FQTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAAAGCGG
51 TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGCAG GGTTTGCACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTCTCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
301 GGCGATTTGC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAGGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLREFFL
51 HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLAF LPVEGLLFKL
101 GDLLPVVFLF LVEFVDGDFG KPVLA VG FQ GKLR L FQTAL LLLAAVRGGL
151 LLVFEFGGGF LQGNV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

755

	10	20	30	40	50	60
m508.pep	MVAFGVDQGF	LLQGGGLGG	LKLRLQLGL	QGLHFSVLL	PALFLNLRE	FLHNNIFFVQGL
g508	MVAFGVDQGL	LLQGGGLGG	LKLRLQLGL	QGLYAGVLL	PALFLNLRE	FLHGDVFFVQRV
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLD	VLLVLELGF	IGEGKLLLA	FLPVEGLLF	FKLGDLLPV	VLLVEFVDGDFG
g508	YGFQQLVELD	VLLVLELGF	IGEGKLLPA	FLPVQGLLF	EPGDLLPV	VLLFLRVEFVDGDFG
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQ	QKLRFLFQT	ALLLLAAVR	GGLLLVF	FEFGGFLQ	GNNDVV
g508	KPVLAVGFQ	QKLRFLFQT	ALLLLAAVR	GGLLLVF	FEFGGFLQ	SSDVV
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```

a508.seq
1   ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGCGCAGCT TGGTTGTCAG GGTTTGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTCTCTCTG
151 TACGACAATA TATTCTTCGT CCAAACCTCG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTGTGT GTTCAAGCTG
301 GGCAATTTGC TGTGTTAGT TTTGTTTGTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGTTGG CTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```

a508.pep
1   MVAFGVDQGF LLLQGGGLGG GLKLRLQLGL GLYAGVLFPT LLLNLREFLL
51  YDNIFFVQTL YGFAQLFELD VLLVLELGF IGEGKLLLAFL LPIEGLLFKL
101 GNLLLVVFL LVELVDGDFG KPVLAVGFQQ GKLRFLFQTTL LLLAAVRGGL
151 LLVFEFGGGF LQNGDVV*

```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGF	LLQGGGLGG	LKLRLQLGL	QGLHFSVLL	PALFLNLRE	FLHNNIFFVQGL
a508	MVAFGVDQGF	LLQGGGLGG	LKLRLQLGL	QGLYAGVLF	PFTLLNLRE	FLLYDNIFFVQTL
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLD	VLLVLELGF	IGEGKLLLA	FLPVEGLLF	FKLGDLLPV	VLLVEFVDGDFG
a508	YGFAQLFELD	VLLVLELGF	IGEGKLLLA	FLPIEGLLF	FKLGNLLV	VLLVLELVDGDFG
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLAVGFQ	QKLRFLFQT	ALLLLAAVR	GGLLLVF	FEFGGFLQ	GNNDVVX
a508	KPVLAVGFQ	QKLRFLFQT	ALLLLAAVR	GGLLLVF	FEFGGFLQ	NGDVVX
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq


```

1  atgggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgttgtag
101 tcttccaagc ctgctgtgtg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgcaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgctga taagggaacg ttgcaatttt ttcaaatacat cgagaaattt
301 ttgggcccga gcataaggct cgagaaagcc gaatttgacg cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgcataat gtaggcaatg
401 gcgcggcggg aagggtcttc ggtgcggcg atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttagcgcgg cggtggaaa
501 gcggcagttc gcggtaaaag ttgtcgagtt cgctgcggta aaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaa cgcagggttt cgccagaaac
601 aaacggattg ccgtcgcggc cgccgcgat ccagccgcg attttaagga
651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cagcccggtt tgatttcgt cgttgacgtg gattttgtgg cggcgcgttt
801 cgctggcttg ccacaagccc agaagcacgg tgtcgatttc gcggcgacg
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttgcg gcagcagcgc
901 gcggatgcgg cggttgaaat tcaaaacggg ttggcgttgc acttcggctc
951 ggtgcgcggg caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttcgtgg atttggcggc
1101 ggcgcttcgt gtgcacgtct tcggcgatat tcagaatctg ggcgaaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtc ggaaaggac aagagtttga
1251 ccgttttcga aaccaacggc gaggcttctt cgtcaggag gtgaaacagg
1301 gactgtttca aaaattccgc gtccgccgcc aaagcccggt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcattgccg taaataatgt
1401 aaatgtacct caaatgccgc atccgtgcca aaccgttcac actttaacca
1451 ctcatgtccc gaaatgccgt ctgaagtga acgccgccg acggcggcgt
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatac
1651 tttggtcgtc ggctgcggcg gattgggcgc cgcgcgccct gcctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAFALRQQR
301 ADAAVEIQNG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVAVG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLR
451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVPKCR LKLNAAARRR
501 YNRPQLFFSE HHHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFFRAY
551 FGRLRRIGR RRPCPISPPR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTTGCT CTTCTTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTG
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCGTTGTGCA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGCGGTT AGGGTTCTTC GCGCGGGCG ATTTCTTCGT CGGCGGATTT
451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGT CCGCGCGATA GAAGCGGAAC

```

551	ACGGCATCGG	CGTGGCGGCG	GAAGGCAAAG	CGCAGGGTTT	CGGCAGAAAC
601	AAACGGATTG	CCGTCGCGGT	CGCCGCGCAT	CCAGCCGCGC	ATTTTGAGGA
651	TGTCGGGAAC	GCGGACGCGG	GGATAGGCCG	TCTGAAAGTC	GTGTTCCATC
701	TTGCGGTAGA	GCTTGCGCAG	GGCTTGCAAA	AAGATCATCG	GGAAAGATGGA
751	CACGCCGTTG	TTGATTTCGT	CGTTGACGCT	GAGTTTGTGG	CGGC GCGTTT
801	CGCTGGTCTG	CCACAAGCCC	AGCAGGATAG	TGTCGATTtC	GcGCGCAGC
851	CGTGCCAGCG	CGTCGGCATT	GGTGACGCGT	TCyCGTTGCG	GCAACAGTGC
901	GCGGATGCGG	CGGTTGAAGC	TTAAGACGGT	TTGGCTGTGC	ACTTCGGTGC
951	GGTGCGCGGT	CAAAACGCGC	GTAACGACAG	TATTGTCCAA	CCTCGCGTGC
1001	ACCGATTTCG	CGTCGGCTTT	CCCCGCTTTG	AGCCTGCGGA	CGGTTTCCGT
1051	CAGGCTGCCT	TCCGCGCCGC	CGCGTCCGEC	TTCTTCGTGG	ATTTGGCGGC
1101	GGCGTTTCGT	GTGCACGTCT	TCGGCGATGT	TCAAAATCTG	GGCGAACAGG
1151	CCGCAGGCGA	AGGTTAAATC	GTGGGTTTGT	TGTTCTGCTCA	ATTGCGGCAA
1201	TACTTTTTCA	ATCAATCCGC	CGCTGTCTGT	GGAAGTGGAC	AAGAGTTTGA
1251	CTGTTTCGAC	AACCAACGGC	GAGGCTTCTT	CGTGCAGGAG	GTTGAACAGG
1301	GATTGTTTCA	GAAATTCGCG	GTCGCGCGCC	AAAGCCGCGT	CCTTTGGATT
1351	GTTCAAGATA	TGCAGTTGCA	TGATTTTCTT	CTCTCGCTGT	CCGTAATATAT
1401	TGTAAAGTA	CCCCAATATG	CGCATCCGTG	CCAAACCGTT	CACACTTTAA
1451	CGCCCCGTGT	CCCGAAATGC	CGCTGAAGT	TGAACCGCCG	CCGACGGCAG
1501	CGTTACAATC	GCCCCGAACT	GTTTTtTTCC	GAACATCATC	ATGACCACGA
1551	CGGAACACGA	CAACGACGAT	GCATTCTCTG	TGCGGTACAG	CCGCCACATC
1601	CTCTTGAGAC	AAATCGGCAT	GGAAGGGCAG	CAGAAACTTT	CCGCCCGCGA
1651	TATTTTGGTC	GTCCGGTCTCG	CGGGTTTGGG	TGCCGCGCGA	CT . GCCCTAC
1701	CTTGCCGCTT	CGGGTGTCTG	CACGCTGA		

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

m509.p	1	MVAVCDKRAH	QRTLMAQFAQ	QGGFLFLFVQ	AVVVFQACVL	EKLGNHIGVF
	51	ACLRCKQVERH	HVKAEHGYGT	DEVCQTAFGK	QTAADVVDKGT	LQFFQIIQKL
101		LCRSIRLEKA	EFAAHTQTER	ARFAHSARHN	VGDGAAVGGF	GAGDFFVGRF
151		VGQRRYIAVD	FDAADGERQF	AVEFVEFAAI	EAEHGIGVAA	EGKAQGFRN
201		KRIAVAVAAD	PAADFEDVRN	ADAGIGRLKV	VFHLAVELQG	GFKAHREDG
251		HAVVDFFVDA	EFVAARFAGL	PQAQQDSVDF	AAQPCQRVGI	GAAFALRQFC
301		ADAAVEAXDG	LALHFGFRVG	QNGNGRIVQ	LP LHRFAVGF	PRFEPADGFR
351		QAAAFRAAASG	FFLDLAAAFV	VHVFQDVQNL	GEQAAGQGXI	VGLLFFVQLRQ
401		YFFNQCRVAV	SGSQEFDCFD	NQRRGFFVQE	VEQGLFQKFR	VRRQSRVLWI
451		VQNMQLHDFS	LSSAVNIVNV	PQMPHPCQTV	HTLTARVPKC	RLKLNAAARRQ
501		RYNRPQLFFS	EHHHDHNRV	QRRCPAAVQ	PPHPLGRNRH	RRAAETFRRA
551		YFGRRLRRFG	CRXTXPTLPL	RVSAR*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m509 . pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH					
	: :					
g509	MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509 . pep	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER					
	: :					
g509	HVEAEHGHGTDEVCQTAFGKQAAAVVDKGTLQFFQII EKFLGRSIRLEKAEFAAHAQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509 . pep	ARFAHSARHNVGDGAAVGFFGAGDFFVGRFVGRQRRYIAVDFDAADGERQFAVEFVEFAAI					
	:					
g509	ARFAHSARHNVGNGAAVRFFGAGDFFVRREGCQCHYVVVDFDAADGKRQFAVKFVEFAAV					
	130	140	150	160	170	180

	190	200	210	220	230	240
m509 . pep	EAEHGIGVAAEGKAQGFGRNKR	IAVAVAADPAADFEDVRNADAG	IGRLKVVFHLAVELGQ			
g509	KTEHGIGVAAEGKAQGFARNKR	IAVAVAADPAADFKDIRNADIG	IGRLKVVFHLAVEFGQ			
	190	200	210	220	230	240
	250	260	270	280	290	300
m509 . pep	GFKAHREDGHAVVDFVVD	AEFVAARFAGLPQAQQDSV	DFAAQPCQRVGIGAA	FALRQQC		
g509	GFKAHREDGHAVVDFVVD	AEFVAARFAGLPQAQKHG	VDFAAQPCQRVGIGAA	FALRQQR		
	250	260	270	280	290	300
	310	320	330	340	350	360
m509 . pep	ADAAVEAXDGLALHFGR	VRGQNGNGRIVQLPLHR	FAVGFP	RFEPADGFRQAA	FRAAASG	
g509	ADAAVEIQNGLALHFGR	VRGQNGNGRIVQLPLHR	FAVGFP	RFEPADGFRQAA	FCCVVAG	
	310	320	330	340	350	360
	370	380	390	400	410	420
m509 . pep	FFVDLAAAFVVHVFGD	VQNLGEQAAGQGXIVGL	LFVQLRQYFFNQCR	AVVSGSQEFDCFD		
g509	IFVDLAAAFVVHVFGD	IQNLGEQPAQRQIVGL	PFVQLRQYFFNQCR	AVVSGSQEFDRFD		
	370	380	390	400	410	420
	430	440	450	460	470	480
m509 . pep	NQRRGFFVQVEVQGLF	QKFRVRQR	SRVLWIVQNMQLHDF	SLSSAVNIVNVPQ	MPHPCQTV	
g509	NQRRGFFVQVEVQGLF	QKFRVRQR	SRVLWIVQNMQLHDF	PLI-AVNTVNVPQ	MPHPCQTV	
	430	440	450	460	470	
	490	500	510	520	530	540
m509 . pep	HTLTARVPKCR	LKLNAARRQRYNR	PQLFFSEHHHD	DRTRQRRCI	PAAVQPPHPLGR	NRH
g509	HTLTTHVPKCR	LKLNAARRRRYNR	PQLFFSEHHHD	DRTRQRRRT	PAAVQPPHPLGR	NRH
	480	490	500	510	520	530
	550	560	570			
m509 . pep	RRAAETFR	RAYFGRRLRR	FGCRRTCPTL	PLRV	SAR	
g509	RRAAEAF	RAYFGRRLRR	IGRRRPCI	SPPRGS	SAR	
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

```

a509 . seq
1  ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGCT TGTTTTTGCT CTTCGTTGAG GCTGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTGTT
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGTCT GCCAAACGGC CTTCGGCAAG CAGGCGGCTG
251 CCGTTGTGCA TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGGTCTTTC GGCGCGGGCG GTTCTTTCGT CGGGCGATTT
451 GTCGGACAAC GCCATCACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTGAGATT CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 GAACGGATTG CCGTCGCGGT CGCCGCGGAT CCAGCCGCGG ATTTTGAGGA
651 TGTCCGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTTTCG CTGTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTTC GCGGCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

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901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTGC
951 GGTGCGGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCGGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTTCGTG GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCAA
1201 TACTTTTTC AATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCGC GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTGT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGGCAGCAG AAACCTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGGCG GTTTGGGTGC CGCCG.CCCT GCCCTATCTC
1701 GCCGTTCCG GCATCGGCAC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

```

a509.pep
1  MVAVCDERTV QWTLMAQFAQ QGGLFLLFVE AVVVFOACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGNGATVGFF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVAVAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKAHRKDG
251 HAVVDFVVD AEFVAARFAGL PQAQQDSVDF AAQPCQRVGI GTAFALRQQR
301 ADAAVEIQDG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRADV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNVP QMPHPCQTVH TLTARVPKCR LKLNAARRQR
501 YNRPQLFXSE HHHDHDRTRQ RRCIPAAVQP PHPLGRNWHR RAAETFERRAY
551 FGRRLRRFGC RXPCPISPLP ASAR*

```

m509/a509 93.0% identity in 575 aa overlap

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFOACVLEKLGNHIGVFACVLAQVERH					
a509	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVFOACVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAEGHYGTDEVCQTAFGKQTAAVVDKGTQFFQIIQKLLCRSIRLEKA EFAAHTQTER					
a509	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGM LQFFQIIEKFLCRSIRLEKA EFAAHTQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVDGAAVGGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
a509	ARFAHSARHNVGNGATVGFFGAGGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVVHFLAVELGQ					
a509	KTEHGIGVAAEGKTQGFGRNERIAVAVAADPAADFEDVRNADIGIGRLKVVVHFLAVELGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFKAHREDGHAVVDFVVD AEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGIAAFALRQQC					
a509	GFKAHREDGHAVVDFVVD AEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGTAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360

760

```

m509.pep  ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG
          |||||  |||||  |||||  |||||  |||||  |||||
a509      ADAAVEIQDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG
          310      320      330      340      350      360

          370      380      390      400      410      420
m509.pep  FFVDLAAAFVHVFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVSGQEFDCFD
          |||||  |||||  |||||  |||||  |||||  |||||
a509      FFVDLAAAFVHVFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVSGQEFDRFD
          370      380      390      400      410      420

          430      440      450      460      470      480
m509.pep  NQRRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSAVNIVNVPQMPHPCQTV
          |||||  |||||  |||||  |||||  |||||  |||||
a509      NQRRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFS LI-AVNTVNVNVPQMPHPCQTV
          430      440      450      460      470

          490      500      510      520      530      540
m509.pep  HTLTARVPKCRLKLNAARRQRYNRPQLFFSEHHHDH DTRQRRCIPA AVQPPHPLGRNRH
          |||||  |||||  |||||  |||||  |||||  |||||
a509      HTLTARVPKCRLKLNAARRQRYNRPQLFXSEHHHDH DTRQRRCIPA AVQPPHPLGRNWH
          480      490      500      510      520      530

          550      560      570
m509.pep  RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRVSARX
          |||||  |||||  |||||  |||||  |||||
a509      RRAAETFRRAYFGRRLRRFGCRXPCPISPLPASARX
          540      550      560      570

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1  atgccttcgc ggacaccgca gggaaaaaagg ggttattcct gccccaaagcg
51 ggatagtgcc ttttggcagg cgttggtccat atcgggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggagggttt caataggctcg
151 tggacgacgt tgagcgcggc cataatgacg attttttcgc tgtccgcgac
201 gcgccgcct tcgcgcatgg cttcggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcggtgatg acttcgatgt agacttggtc gatgttcac ctttaatcct
351 tattgctgcg tttcctgccg ttgggggagg cgcgctgccg gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1  MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFD VDLF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTCTTCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCTG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCGCGGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAGC GGTCAGCCGG
301 GGCGTGCAWG ACTTCsAtGT GGACTTGTTT GATGTTTCATC CTTTAATCCT
351 TATTGCTGCG TTTCTGCGCA TTGGGGGAGG CCGCTGCGCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FQWALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
g510	MPSRTPQGKRGYSCPKRDSA FQWALSISVILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

1	ATGCCTTCGC	GGACACCGCA	GGGAAAAGG	GGTTATTCCT	GCGCCAAGCG
51	GGATAGTGCT	TTTTGGCAGG	CGTTGTCCAT	ATCGGCTATT	TTACGCGCAA
101	AATCGCCGAT	TGCCAAATCG	CCGCCGTTCA	GGGAGGTTTT	CAACAGGTCG
151	TGGACGACGT	TGAGCGCGGC	CATAATGACG	ATTTTTTCGC	TGTCCGCGAC
201	GCGTCCGCCT	TCGCGGATGG	CTTCGGCTTT	GCGTTGAGC	ATTCCGACTG
251	CCTGCAACAG	TGTGTCTTTT	TCTTCTGCCG	GCGTGTGAC	GGTCAGCCGG
301	G.CGTGCATG	ACTTCGATGT	GGACTTGTTT	GATGTTTCATC	CTTTAATCCT
351	TATTGCTGCG	TTTCTGCCG	TTGGGGGAGG	CGCGCTGCCA	GTGCGCTGA

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

1	MPSRTPQGKR	GYSCAKRDSA	FQWALSISAI	LRAKSPIAKS	PPFREVFNRS
51	WTTLSAAIMT	IFSLSATRPP	SRMASALPLS	IPACNSVSF	SSAGVLTVSR
101	XVHDFDVLDF	DVHPLILIAA	FPAVGGGALP	VR*	

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA FQWALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
a510	MPSRTPQGKRGYSCAKRDSA FQWALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

1	atgaaagtgc	ttgttttagg	tgcgggtggt	gccggcgat	cctccgtgtg
---	------------	------------	------------	-----------	------------

g512.pcp

m512.seq (partial)

m512.pep (partial)

m512/g512

```

                                10      20      30
m512.pep                      VLERYGVPYRRLKPEECAEFEPALARVTAK
                                |||||
g512      TDMNFEGRKKGTLQIFRQTEEVEAAKQDIAVLERYGVPPYRRLKPEECAEFEPALARVTAK
              130      140      150      160      170      180

                                40      50      60      70      80      90
m512.pep      IAGGLHLPPADATGDWRLF TENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGG LK
              |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g512      IVGGLHLPPADATGDCRLFTENLYKLCQEKGVRFYFNQTISRIDHNGLRIKAVETKQGG LK
              190      200      210      220      230      240

                                100      110      120
m512.pep      QMPLSARSVASAGRFWRSWISICPFIPSKAIP
              |||||:|||||
g512      QMPLSARSAASAGLCWRSWISICPFIPSKAIP

```

763

250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCGCGTG
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAAACCACT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGTCTGT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GCGGTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATGCGCAG AATTCGAGCC TCGCTGGCA CGCGTTACCG
551 CCAAATTGCG CGGCGGCCTG CACCTGCCCC CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAGGAAA AGGGCGTACG
651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAAACCGT TGAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
51  YTPWAAPGI PTKALKWLFK SHPLLFRPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMFR RFEAQTMNF EGRKKGTLQI FRQKEVEAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVEVK QGGLKQMPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVPYRRLKPEECAEFEPALARVTAK
a512                                |||
                                130      140      150      160      170      180

m512.pep                                40      50      60      70      80      90
                                IAGGLHLPADATGDWRFLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVEVKQGGLK
a512                                |||
                                IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVEVKQGGLK
                                190      200      210      220      230      240

m512.pep                                100      110      120
                                QMPLSARSVASAGRFWRKWSISICPFIPSKAIPX
a512                                |||
                                QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
                                250      260      270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
1  ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
51  TTCGCAAGGT ATGATTCAA TGCTGGGCGT GTTTGTGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGCG GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTC GGCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```


764

501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep
 1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKGK DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq
 1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTC GCGCGGTTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep
 1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKGK DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMXLRDYTAKLKMKGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHP					
	130	140	150	160	170	180
	190					
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

765

```

1  ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51  CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACACCGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTTG TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTTGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTTGTTTCG CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTCAGAT TTTTTCGGGC
751 CGGTTCAAAT TCGACGCGGC AGCAGGCGGC TACTCGGCG GTCTGATTTC
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGCGCG
851 GTATGGGTTC CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTGC ATACCATCAT
951 CGTTTGTCT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 CCGATTTGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCCGTC ATCCTGTTTA TGTTTGCCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CCTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```

a513.pep
1  MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLFFTVTG FVQFRLFGRS
51  IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGPGPA
101 VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGVFEEA VQNTNIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIPMI PDVFGQIFSG
251 AFKFDAAAGG LLGGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VFVDITIVCS CTAFIILYQ QPYGDLGSA LTQAAIVSQV
351 GQWGAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYTAKL
451 KMGKDPEFKL SEHPGLKRRRI KSDVW*

```

m513/a513 100.0% identity in 191 aa overlap

```

m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||
a513 260 270 280 290 300 310
DAAAGLLGLISQTM MMGIKRGlys NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
m513.pep TIIVCSCTAFIILYQ QPYGDLGSAAL TQAAIVSQV GQWGAGFLAV ILFMFAFSTVIGNY
|||||
a513 320 330 340 350 360 370
TIIVCSCTAFIILYQ QPYGDLGSAAL TQAAIVSQV GQWGAGFLAV ILFMFAFSTVIGNY

100 110 120 130 140 150
m513.pep AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANV PLVWDMADMA MGIMAWINLVAILL
|||||
a513 380 390 400 410 420 430
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANV PLVWDMADMA MGIMAWINLVAILL

160 170 180 190
m513.pep LSPLAFMLLRDYTAKL KMGKDPEFKL SEHPGLKRRRI KSDVW
|||||

```

a513 LSPLAFMLLRDYTAKLKMKGKDEPKLSEHPGLKRRRIKSDVWX
440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq
1 atggttcaaa tacaggttgt gcgcgcgcgc ggcgttgccc gtggtctgca
51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg
101 ccgtttttgaa tcacgaagcg cgcgcgcggtg gcaacacctt ccgcatacaa
151 atagctgctg cggaaagagc gggggatgtg cggttcttcg cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt
251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccga acggttggtat cgaagaggac ggggttagctg cctgtcggga
351 tgctgcggct gccgagtcgg cgcgaagtgc ggcgggcggc ggtttgaccg
401 atggtttcgg ggctgtccat atccggatgg cggcaggcgg aatcgtacca
451 gtagtcgcgc tgcattccgt tttcgtcggc ggcgacgacg ctgcaggaaa
501 tgctgtggtg cgtgctttgc cgtgtgcgg caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc ggtttgacc gccgcgcctt cggagttttc
601 gatgcggctg tccgtgtcca acgctgcctg ttcgcatgtt tttgccaaagc
651 cgacggcggc ttccgtatcc aaatcccatt cgtggtaaag gtcggggctg
701 ccgatgtgtt gcgccatcaa ctcggggtcg gcaagtccgg cgcaaccgtc
751 ttcggcgggtg tggcgggcga tgcggcggc ggcgcgacg gtgtcgcga
801 gggcttggtt ggagaagtcg gcggtgcgg cgcggcctt gcgtttgccg
851 acgtaaacgg taatgtccag cgatttgtcc tgctggaact cgatttgttc
901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt
951 cggttcggc ggcggtcgg cccgctgctt ttgccaagtc gagcgtgcgg
1001 cggcagaggt cgaggagttc ggaagcgggt tggttgaaca gcataacaat
1051 ctttcttggg ggagcgttgt ggcattttta

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep
1 MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGGNTFRIK
51 IAAAERAGDV RFFAQVEEIG QDFADAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAFA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)
1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCGAAAC
151 GGTGGTATCG AAGAGGACCG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGC CGGGCGGCGG TTTGACCGAT GGTTCGGGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCGGTA AACGTATTGG
401 TAATGGCCCG TTGCAACGCG CGCGCCTTCG GAGTTTTCGA TCGCTCATC
451 CTCGTTACAG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGGCGGCTk
501 CCGTATCCAA ATCCATTCTG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CGGCGGTGTG
601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGACAG GCTTTTTCGG
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTCG GTTTGCCGAC GTAAACGGTA
701 ATGTCCAGCG ACTTGTCTG CTGGAACCTG ATTTGTTsGA TTTsGCCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTG GCTGAAATCG GCTTCGGCGG
801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGC GGCG GCAGAGGTGCG
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTTGCGG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

Homology with a predicted ORF from *N. gonorrhoeae*

m515/q515

```

m515.pep                                     10      20      30
                                         GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                         ::|  |||||  |||||  |||||  |||||  |||||
g515    AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
          30      40      50      60      70      80

          40      50      60      70      80      90
m515.pep    VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515    VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
          90     100     110     120     130     140

          100     110     120     130     140     150
m515.pep    GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVVLVMAGLHRRAFGVFDALIL
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515    GGIVPVVALHSVFVGDDAAAGNAVVRALPVCCKTVGVAVNVVLVLSGLHRRAFGVFDAAVR
          150     160     170     180     190     200

          160     170     180     190     200     210
m515.pep    VQGGFLFALFCQADGGXRIQIPFVVKVGADVDFCHQTGIGKSGATVFGGVAGDVGDFGDFGV
          ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515    VQRCLFALFCQADGGFRIQIPFVVKVGADVLRHQLGVGKSGATVFGGVAGDVGGGADGV
          210     220     230     240     250     260

          220     230     240     250     260     270
m515.pep    LQGFFGEVGSTGAFAFADVNGNVQRLVLELDLXDQAQPHADALSQXFAEIGFGGGRAR
          ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515    AQGLFGEVGGAFAFAFADVNGNVQRFVLELDLFDFAQAHADALSERFAEVGFGGGRAR
          270     280     290     300     310     320

          280     290     300
m515.pep    RFCQVERAAAEEVEFGSGVVEQHRNLSXXCFAAF
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515    CFCQVERAAAEEVEFGSGVVEQHNNLSWWSVVAF
          330     340     350

```

a515.seq

1	ATGTTTCAAA	TAAAGTTGT	GCGCGCCGCC	GGCGTTGCCC	GTGGTCTGCA
51	TTCCGAGTTT	GCGCGCGCTG	TAAGTCTGA	GGAAATAGCC	TTCGACAATG
101	CCGTTTGTAA	TCACGAAGCG	CGGTGCGGTG	GCAACGCCTT	CCGATCAAAA
151	ATAGCTGCTG	CGGAAAGAGC	GGGGATGTG	CGGTCTCTCG	CGCAGGTTGA
201	GGAAATCGGG	CAGGACTTTT	TTGCCGATGC	TGTGCATCAG	GAAACTGCTT
251	TGGCGGTAGA	GCGCTCCGCC	GGAGAGTGCG	CCGACGAGGT	GTCCGATAAG
301	ACCGCCCGAA	ACGGTGGTAT	CGAAGAGGAC	GGGGTAGTTG	CCTGTCGGGA
351	TGCTGCGGCT	GCCGAGTCGG	CGCAAAGTGC	GGCGGGCGGC	GGTTTGACCG
401	ATGGTTTCGC	GGCTGTCCAT	ATCCGGATGC	CGGCAGGCGC	AATCGTAGCA
451	TGATGTCGCG	TGCATCCCGT	TTTCGTCGGC	GGCAACGACG	CTGCAGGAAA
501	TGCTGTGGTG	CGTGCTTTGC	CGGTTGTGGC	CAAAACCGTA	GGTGTGTCCG

768

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551 TAAACGTATT GGTAATGGCC GGTTCGACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCNNNGC GGC GCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CCGGCCTTT GCGTTGCGG
851 ACGTAAACGG TAATGTCCAG CCACTTGTC TGCTGAAACT CGATTGTGTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCAATGAT TCGCTGAAAT
951 CGGCTTCGGC GGC GGTGCG CCCGTCGCTT TTGCCAAGTC GAGCGTGGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGTTGAACA GCATAGAAAT
1051 CTTTCTTGAT GATGCTTTC GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1422; ORF 515.a>:

```

a515.pep
1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNVNLNHEA RCGGNAFRK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLMMA GLHRRAFGVF
201 DALILVQGL FALFCQADGG FRIQIPFVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVXX GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*FAEIGFG GGCARRFCQV ERAAAEVEEF GSGVVEQHRN
351 LS**CFAAF*

```

m515/a515 92.1% identity in 304 aa overlap

```

m515.pep                                     10      20      30
                                         GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                         ::| | | | | | | | | | | | | | | | | |
a515      AEEIAFDNAVNLNHEARCGGNAFRKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
           30      40      50      60      70      80

           40      50      60      70      80      90
m515.pep  VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGLTDGFGAVHIRMAA
           | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VERSAGECADEVSDKTARNGGIEEDGVVACRDAAAESAQSAAGGLTDGFGAVHIRMAA
           90      100     110     120     130     140

           100     110     120     130     140     150
m515.pep  GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
           150     160     170     180     190     200

           160     170     180     190     200     210
m515.pep  VQGGLFALFCQADGGXRIQIPFVKVGVADV FCHQTGIGKSGATVFGGVAGDV DGGFDGV
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VQGGLFALFCQADGGFRIQIPFVKVGVADVLRHQLGVGKSGATVFGGVAGDVXXGADGV
           210     220     230     240     250     260

           220     230     240     250     260     270
m515.pep  LQGFGEVVGSTGAFAFADVNGNVQRLVLLLELDLXDAQPHADALSQXFAEIGFGGGCAR
           | | : | | : | | | | | | | | | | | | | | | | | | | | | | | |
a515      AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLFDFAQPHADALSQXFAEIGFGGGCAR
           270     280     290     300     310     320

           280     290     300
m515.pep  RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
           | | | | | | | | | | | | | | | | | | | | | | | |
a515      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
           330     340     350     360

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1423>:

```

g515-1.seq
1  ATGGTTCAAA TACAGTTGT GCGCGCCGCC GCGCTGCCG GTGGTCTGCA

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769

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51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTTGA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CCGTCTCTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGTGTGCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCTGCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CCGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAGTGTC GGTTCGACC GCCGCGCCTT CGGAGTTTTT
601 GATGCGGCTG TCCGTGTCCA ACGCTGCTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCAT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTCGCGCA
801 GGCCTTGTTC GGAGAAAGTC GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTTGTCC TGCTGGAAC CGATTTGTTC
901 GATTTTCGCCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCCTGAAGT
951 CGGCTTCGGC GCGGTCGCG CCGCTGCTT TTGCCAAGTC GAGCGTGGC
1001 CCGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAA
1051 CTTTCTTGGT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFLVLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFQCV ERAAAEEVEF GSGVVEQHNN
351 LSWWSVVAFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGTTTGT GCGCGCCGCC GCGGTGCGCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTTGA TCACGAAGCG CCGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CCGTCTCTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGTGTGCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCTGCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CCGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAAATGGC GGTTCGACC GCCGCGCCTT CGGAGTTTTT
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCAT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGCTTGCA
801 GGCCTTTTTC GGAGAAAGTC GCAGTACTGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCC TGCTGGAAC CGATTTGTTC
901 GATTTTCGCCC AGCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEIEA FDNAVLNHEA RCGGNAFRK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGLL FALFCQADGG FRIQIPFVK VGVADVFC HQ TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGF GEVGSTGAFF AFADVNGNVQ RLVLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

	10	20	30	40	50	60
g515-1.pep	MVQIQVVRAAGVARGLHSEF	ARAVTAEIEAFDNAVLNHEA	ARRGGNTFRIKIAAAERAGDV			
m515-1	MVQIQVVRAAGVARGLHTEF	ARAVTAEIEAFDNAVLNHEA	RCGGNAFRIKIAAAERAGDV			
	10	20	30	40	50	60

770

	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVDVLRHQ					
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVDVFCCHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLLLELDLF					
m515-1	TGIGKSGATVFGGVAGDVGGFDGVLQGGFFGEVGGSTGAFAFADVNGNVQRLVLELDLF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVGFGGGRARCFQVERAAAEVEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGGTTGCCG GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTGTAA TCACGAAGCG CCGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGATGTGT CCGTCTCTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CCGTGTGCGG CAAAACCGTA GGTGTGCGG
551 TAAACGTATT GGTAAATGGC GGTTTGCACC GCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGCGGGCGGA TGTCGGCGGC GGCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CCGGCCTTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCG TGCTGAAACT CGATTTGTTC
901 GATTTCGCCG AGCCGCACGC TGACGCTTTG TCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEIEA FDNVLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAGNAVVR RALPVCCKTV GVAVNVLMVA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEIEAFDNVLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEIEAFDNVLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNNGGIEEDGVVACRDAAA					

771

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m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70      80      90      100     110     120

              130     140     150     160     170     180
a515-1.pep  AESAQSAAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              |||
m515-1      AESAQSAAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130     140     150     160     170     180

              190     200     210     220     230     240
a515-1.pep  GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVDVLRHQ
              |||
m515-1      GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVDVLRHQ
              190     200     210     220     230     240

              250     260     270     280     290     300
a515-1.pep  LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
              |||
m515-1      TGIGKSGATVFGGVAGDVGGGADGVLQGFGEVGGSTGAFAFADVNGNVQRLVLLKLDLF
              250     260     270     280     290     300

              310
a515-1.pep  DFAQPHADALSQX
              |||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

g516.seq

```

1  atgttgttcc gtaaaacgac cgccgccgtt ttggcggcaa ccttgatact
51 gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacgtt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccga agattcggcg aagctgacgg
251 gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccg gtcaaattcg aagcgcccgg
351 cagccagaat ttcagtaccg gaggtccttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcgggtcaaa
451 ctcgacaatc ggaccattta cagcgctgc gtatccgcca aaggcaataa
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaatg
551 tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttgttga tattggatgc
651 ggcggccgcg gtgctggtct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

g516.pep

```

1  MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51 VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAAA VLVLPMALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

m516.seq

```

1  ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51 GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGCGC CTTCCGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCGGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

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772

501 CTACGCCACA CCGCAAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
 551 TGCCTGCCGA TATTTATTAC ACGGTACTG AAGAACATAC CGACAAATCC
 601 AAGCTGTTTG CAAATATCTT ATATACGCCC CCCTTTTGA TACTGGATGC
 651 GCGGGGCGCG GTACTGGCCT TGCCTGCGGC GGCTCTGGGT GCGGTCGTGG
 701 ATGCCGCCCG CAAATGA

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep
 1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
 51 VAEDNAQLEK GSLVMMGGKY WFVNPEDSA KLTGILKAGL DKPFQIVEDT
 101 PSYARHQALP VKLESPGSQN FSTEGCLRLY DTDKPADIAK LKQLGFCAVK
 151 LDNRTIYTRC VSAKGYYAT PQKLNADYHF EQSVPADIYY TVTEEHTDKS
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

m516.pep	10	20	30	40	50	60
	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK					
	: : : : :					
g516	10	20	30	40	50	60
	MLFRKTTAAVLAATLILNGCTMLRGMNPNVSQTITRKHVDKDQIRAFGVVAEDNAQLEK					
	70	80	90	100	110	120
m516.pep	GSLVMMGGKYWFVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN					
	: : : : :					
g516	70	80	90	100	110	120
	GSLVMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN					
	130	140	150	160	170	180
m516.pep	FSTEGCLRLYDTDKPADIAKLKQLGFCAVKLDNRTIYTRCVSAKGYYATPQKLNADYHF					
	: : : : :					
g516	130	140	150	160	170	180
	FSTGGLCLRYDTGRPDIAKLKQLEFKAVKLDNRTIYTRCVSAKGYYATPQKLNADYHF					
	190	200	210	220	230	239
m516.pep	EQSVPADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
	: : : : :					
g516	190	200	210	220	230	
	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLLILDAAGAVLALPAAALGAVVDAARK					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

a516.seq
 1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT
 51 GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTGCGGTGTG
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
 201 CGGGAAATAC TGGTTCGTCT TCAATCCTGA AGATTCGGCG AAGCTGACGG
 251 GCATTTTGAA GGCCGGGTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
 301 CCGCGCTTTG CCTACCAAGC CCTGCCGCTC AAATCGAAT CGCCCGCCAG
 351 CCAGAATTTT AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTTGAAGC GGTCGAATCT
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAG GCAAATACTA
 501 CGCCACACCG CAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC
 551 CTGCCGATAT TTATTACACG GTTACGAAAA AACATACCGA CAAATCCAAG
 601 TTGTTTGAAG ATATTGCATA TACGCCACC ACGTTGATAC TGGATGCGGT
 651 GGGCGCGGTG CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
 701 CCTCAGACAA ATGA

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

773

```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51 VAEDNAQLEK GSLVMMGGKY WFWVNPEDSA KLTGILKAGL DKQFQMVEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIAKL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

              10      20      30      40      50      60
m516.pep      MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDDKDQIRAFGVVAEDNAQLEK
              |||||:||||:| ||| :|||||
a516           MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDDKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60

              70      80      90      100     110     120
m516.pep      GSLVMMGGKYWFWVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
              |||||:|||||:|||||:| ||| :||| :| :|||:|||||:|
a516           GSLVMMGGKYWFWVNPEDSAKLTGILKAGLDKQFQMVEPNRFA-YQALPVKLESPASQN
              70      80      90      100     110

              130     140     150     160     170     180
m516.pep      FSTEGLCLRYDTPDKPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
              |||||:|||||:|||||:| ||| :|||||:| ||| :||| :|
a516           FSTEGLCLRYDTPDRPADIAKLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
120           130     140     150     160     170

              190     200     210     220     230     239
m516.pep      EQSVADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
              |||||:|||||:|||||:| ||| :|||||:| ||| :||| :|
a516           EQSVADIYYTVTKKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIAATNSSDKX
180           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51  cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101  ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacg
151  tgcgtctttc aatcccgatt tgatgttttt gggcaggctg atttggtctg
201  tgtcgccggt aatgacggct ttcgcgccga agccgatgcg ggtcaggaac
251  attttcattt gttcgggctt ggtgttttgc gcttcgtcga ggatgatgta
301  tgcgccgttg agcgtcctgc cgcgcataata ggcgagcggg gcgatttcaa
351  tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401  tagaggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
451  gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501  ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT
51  CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101  CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDPLGQ
151  VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51  CGTAGGCTTC GACGATTTTT TGACCAAAG GATGCCGGAC AACGTCTTCG
101  CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
151  CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201  TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251  ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301  TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCGATTTCOA
351  TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401  TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

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774

451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

m517.pep	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
g517	10	20	30	40	50	60
	MHRVSDGIGSVVVFCRFVGFDDFLHQMPD NVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
m517.pep	70	80	90	100	110	120
	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFEEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
g517	70	80	90	100	110	120
	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFEEDDVCAVERPAAHIGERGDFNQAF					
m517.pep	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKR TKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : :					
g517	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKRTEVGVD FLGQVSGQEAQFLTGFDGRPN					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGACCAAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGCCGTGCA GTTCTCAGC
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCCGTTG AGCGTCTGCG CGCGCATATA GGCGAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTCGAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT
51 RIF*SRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGNLNQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQKTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

m517.pep	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
a517	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
m517.pep	70	80	90	100	110	120
	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFEEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
a517	70	80	90	100	110	120
	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFEEDDVCAVERPAAHIGERGNLNQTF					

775

	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKTQFLAGFDGRPHX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1   atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttggtgtct
51  ttcggcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac cattttttca gcataaatat tctgaccgga
151 agagcggcat ctccacgggc aaccgtgttc agactgcatac aggcggtacg
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctcct cggcgggcaa cgcttcatta taacagattg
301 ccccttaaaa aatcagaccc tgcttttgtg gcggagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1   MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RLHQAVRFHK MPKTISKMRN NYAVRITPPP RAATLHYNRL
101 PLKSDPAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1   ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTGCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCa GCATAAATAT TCTGACCCGA
151 AGAGCGGCAT CTCCACAGGC AACCGTGTC AGACGGCAGC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCG TAGAACTAC GCCGTCCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1   MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPOATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRERRR RCAVILSNR KKSDPAFVAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep      MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPOATVF
g518          MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR RAASPRATVF
               10      20      30      40      50      60

m518.pep      RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRERRRRCAVILSN
g518          RLHQAVRFHKMPKTISKMRNRYAVRITPPPPRAATLHYNRLPL-----
               70      80      90      100     110

m518.pep      120      130
g518          GRKKSDPAFVAESEI
               110

```

776

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCA GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCACGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....AAAAAAT CAGACCCTGC TTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF					
a518	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQA-RFARCRITINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSNG					
a518	RRHQAVRFRKMPTINKRRRNYAVRITPPSXAATRHYNRLPS-----					
	70	80	90	100		
	120	130				
m518.pep	RKSDPAFVAESEIX					
a518	-KKSDPAFVAESEIX					
		110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatcct gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcacccccc agcaggaagt ccacgttgct gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatatt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actggtgacg
251 gcatcatcta tttccaagta accgatccca aactcgcctc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgtgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgccgg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctacggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttggttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccgcct tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaacct
901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPOQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```

777

```

101 SNYIMAITQL AQTTLSRVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQOS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANAEAN
251 RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
301 NFRRHEKFSP EAKTAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

```

m519.seq (partial)
1   ..TCCGTTATCG GCGGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGTTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA
251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTGCGGAC ATCGGCAGCC
551 TGATTCTGTC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

```

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

```

m519.pep (partial)
1   ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGSQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLSAGMK IIDSSKTAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

```

m519/g519
                                     10      20      30
m519.pep                               SVIGRMELDKTFEERDEINSTVVAALDEAA
                                     |||:|||||:|||||:|||||:|||||
g519      YFQVTDPKLASYGSSNYIMAITQLAQTTLSRVIGRMELDKTFEERDEINSTVVSALDEAA
          90      100      110      120      130      140

          40      50      60      70      80      90
m519.pep      GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGSQREAE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g519      GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLAGSQREAE
          150      160      170      180      190      200

          100      110      120      130      140      150
m519.pep      IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAEAIRQIAAALQTQGGADAV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g519      IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAEANRQIAAALQTQSGADAV
          210      220      230      240      250      260

          160      170      180      190      200
m519.pep      NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g519      NLKIAEQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK
          270      280      290      300      310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

```

a519.seq
1   ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT

```

```

201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

a519.pep

```

1  MEFFIILLAA VVVFQKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLSYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGAEQAQVNA SNAEKIARIN RAKGEAESLR LVAEANAQEI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 99.5% identity in 199 aa overlap

```

                                     10      20      30
m519.pep                               SVIGRMELDKTFEERDEINSTVVAALDEAA
a519      YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
           90      100     110     120     130     140

                                     40      50      60      70      80      90
m519.pep      GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGKIEQINLASGQREAE
a519      GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGKIEQINLASGQREAE
           150     160     170     180     190     200

                                     100     110     120     130     140     150
m519.pep      IQQSEGEQAQAVNASNAEKIARINRAKGEAESLRLVAEANAQEI RQIAAALQTGGADAV
a519      IQQSEGEQAQAVNASNAEKIARINRAKGEAESLRLVAEANAQEI RQIAAALQTGGADAV
           210     220     230     240     250     260

                                     160     170     180     190     200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSTAKX
a519      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSTAKX
           270     280     290     300     310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

g519-1.seq

```

1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CTTTCGCGCA ATGCAGGCAC AAATTACGCG CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACAGGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCCAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA

```

801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAIAI
 251 RQIAAALQQT GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GGCCTTTCCA TCGCGCCCTG ACGGCGCGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
 451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCGG AGAAATCGC CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
 751 CGTCAAAATG CCGCGCCCT TCAAAACCAA GGCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAIAI
 251 RQIAAALQQT GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGKIEQINLASGQREAEIQSSEGEAQAANASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGKIEQINLASGQREAEIQSSEGEAQAANASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	KRARIAESEGKIEQINLASGQREAEIQSSEGEAQAANASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGKIEQINLASGQREAEIQSSEGEAQAANASNAEKIARINRAKGEAESLR					

780

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTGTTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAAATGC TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFGRKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVA YRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLSYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLR YEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 QREAEIQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFGRKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLSYGS SNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLSYGS SNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

```

```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in E.coli. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1   atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccc ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccc tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgcgaaacagt tcgaacggat cttttgacaa gggcgggcga cgggcccatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgccccaa gcggcgggaa atttcctctg cgttgtcccg caacacggga
501 gccgcaccgc cgccgaccgt acctaacctt aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1   MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDLILFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1   ATGCCTGCGC TTCTTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCC CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

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782

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301  GCAATGCCGG  TACCGCCGaa  CAATTCGACG  ACGACATCGA  CGTCTTCACG
351  TGCGACCACT  TCGAACGGAT  CTTTGACAAA  GGCTGc .CGG  ACGGGCAGGT
401  TTGTCGGGCT  TTTTCTTCAC  TCAAATCGCA  CACGGCAGAA  ATACGGATTT
451  CGCGCCCCAA  GCGACGGGAA  ATTTCTCCG  CGTTGTCCsCG  CAACACGGCA
501  GCCGTACCGC  CGCCGACCGT  ACCCAAACCT  AAAAGACCGA  TGTTTACTGG
551  CTTCATTGTG  TCTCCTTGTA  AGCCGACTGA  AATGTAAATA  TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1  MPALLSVHXA  NALPFSRISX  RMKLLVPLIM  PAMDILILFAA  KPSRRALMIG
 51  IPPATAASNW  TMTFCFSASG  KISLPYSASS  FLLAVTMCLP  FSMAFNTASL
101  AMPVPPNNST  TTSTSSRATS  SNGSLTKAXR  TGRFVGLFLH  SNRTRQKYGF
151  RAPSDGKFPF  RCXATRQPYR  RRPYPNLKDR  CLLASLCLLV  SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520

      10      20      30      40      50      60
m520.pep  MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW
          |||||::| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520       MPALLSIRANALPFSRISERMKLLVPLIMPAMDILILFAAKPSRTALMIGIPPATAASNW
          10      20      30      40      50      60

      70      80      90      100     110     120
m520.pep  TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520       TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS
          70      80      90      100     110     120

      130     140     150     160     170     180
m520.pep  SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPFRCXATRQPYRRRPYNLKDR
          ||||: ||::| :| ||||: ||||| ||||| ||||| ||||| ||||| |||||
g520       SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATRQPHRRRPYLSLKDR
          130     140     150     160     170     180

      190
m520.pep  CLLASLCLLVSRKCKY
          ||||| ||||| ||||| |||||
g520       CLLASLCLLVSRKCKY
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1  ATGCCTGCGC  TTCTTTCAGT  ACATCGG.CA  AACGCGCTGC  CTTTTTCGCG
 51  CATTCGGAG  AGGATGAAGT  TGCTGGTGCC  GTTAATAATG  CCGGCGATGG
101  ATTTAATCCT  GTTTGCCGCC  AAACCTTCGC  GCAGGGCTTT  GATGATTGGG
151  ATACCGCCCG  CTAAGTCCGC  TTCAAATTGG  ACGATGACGT  TTTGTTTTTC
201  CGCCAGCGGG  AAGATTTCTG  TGCCGTATTC  GGCGAGCAGT  TTTTGTGTTG
251  CGGTAACGAT  GTGTTTGCCG  TTTTCAATGG  CTTTCAACAC  CGCATCTTTG
301  GCAATGCCGG  TACCGCCGAA  CAATTCGACG  ACGACATCGA  CGTCTTCACG
351  TGCGACCACT  TCGAACGGAT  CTTTGACAAA  GGCTG. .CGG  ACGGGCAGGT
401  TTGTCGGGCT  TTTTCTTCAC  TCAAATCGCA  CACGGCAGAA  ATACGGATTT
451  CGCGCCCCAA  GCGACGGGAA  ATTTCTCCG  CGTTGTCCCG  CAACACGGCA
501  GCCGTACCGC  CGCCGACCGT  ACCCAAACCT  AAAAGACCGA  TGTTTACTGG
551  CTTCATTGTG  TCTCCTTGTA  AGCCGACTGA  AATGTAAATA  TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1  MPALLSVHRX  NALPFSRISE  RMKLLVPLIM  PAMDILILFAA  KPSRRALMIG
 51  IPPATAASNW  TMTFCFSASG  KISLPYSASS  FLLAVTMCLP  FSMAFNTASL
101  AMPVPPNNST  TTSTSSRATS  SNGSLTKAXR  TGRFVGLFLH  SNRTRQKYGF

```

783

151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTtCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTTGGC GGGCTTTTTT
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSILTAAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGCTGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TGCGGACGGG CAGGTTTGTC GGGCTTTTTT
351 TTCACCTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```

101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	NWTMTFCFSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	NWTMTFCFSASG	KISLPYSASSF	
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSLR	ATSSNGSLTKA	ADGQIWRAFSS	SLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPK	RREISSALS	RNTAAAPPPTV	PKPKRPMFTG	FIVSPCKPTEM	X
m520-1	SHTAEIRISRPK	RREISSALS	RNTAAAPPPTV	PKPKRPMFTG	FIVSPCKPTEM	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCGTTGC CGTATTCGCG GAGCAGTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTGC GACCAAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC
351 TTTCACTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCGCAACA CGGCAGCCGT ACCGCCGCGG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSF LLAVTMCLPF SMAENTASLA MPVPPNNSTT TSTSSRATSS
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	NWTMTFCFSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	NWTMTFCFSASG	KISLPYSASSF	
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPK	RREISSALS	RNTAAAPPPTV	PKPKRPMFTG	FIVSPCKPTEM	X
m520-1	SHTAEIRISRPK	RREISSALS	RNTAAAPPPTV	PKPKRPMFTG	FIVSPCKPTEM	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

```

1  ATGAAATCAA AACTCCCCTT AATCCTAATC AACCTTTCCC TGATTTC AAG
51  CCCATTGGGT GCGAATGCGG CCAAATCTA TACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG

```

q521n.pcp

1	MKSKLPLILI	NLSLISSPLG	ANAAKIYTCT	INGETVYTTK	PSKSCHSTDL
51	PPIGNYSSER	YILPQTPEPA	PSPSNGGQAV	KYKAPVKTVS	KPAKSNTPPQ
101	QAPVNNRRS	ILEAELSNER	KALTEAQKML	SQARLAKGGN	INHQKINAL*
151	SNVLDROONI	QALORELGRM	*		

m521.seq

MS117509

1	ATGAAATCAA	AACTCCTCTT	AATCCTAATC	AAC TTTTCCC	TGATTTCAAG
51	CCCATTGGGT	GCGAATGCGG	CCAAAATCTA	sACCTGCACA	ATCAACGGAG
101	AAACCGTTTA	CACCA _s CAAG	CCGTCCAAAA	GCTGCCACTC	AACCGATTTG
151	CCCCCAATCG	GCAACTACAG	CAGCGAACGC	TATATCCCGC	CCCAAACGCC
201	CGAACCGGTA	TCATCACCGT	CAAACGGCGG	ACwGGTTGTC	AAATATAAAG
251	CCCCGGTCAA	AACAGTATCC	AAGCCGGCAA	AATCCArTAC	GCCGCCGCCG
301	CAACAAGCAC	CCTCAAACAA	CAGCAGACGC	TCCATTCTCG	AAACAGAATT
351	GAGCAACGAA	CGCAAAGCAT	TGGTTGAAGC	CCAAAAAATG	TTATCACAAG
401	CACGTCTGGC	AAAGGCGCGC	AACATCAACC	ATCAAGAAAT	AAATGCATTA
451	CAAAGCAATG	TATTGGACAG	GCAGCAAAAT	ATTCAAGCCC	TGCAAAGGGA
501	ACTGGGGCGT	ATGTAA			

m521.pep

1 MKSKLLLLILI N¹FLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTDL
51 PPIGNYSSER YIPQTPEPV SSPSNGGXV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROON IOALORELGR M*

Homology with a predicted ORF from *N. gonorrhoeae*

m521/q521

	10	20	30	40	50	60
m521.pep	MKSKLLILINFLISSPLGANAAXIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSE					
	:					
g521	MKSKLPLIILINLSLISSPLGANAAXIYTCTINGETVYTTKPSKSCHSTDLPPIGNYSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQAPSNNRRSILETELSNE					
	: :					
g521	YILPQTPEPAPSPSNGGQAVKYKAPVKTVSKPAKSNTTP-QQAPVNNSRRSILEAEELSNE					
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDRQQNIQALQRELGRMX					
	:					
g521	RKALTEAQKMLSQARLAKGGNINHQKINALXSNVLDRQQNIQALQRELGRMX					
	120	130	140	150	160	170

a521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAAG

786

```

51 CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCCAAA GCTGCCTCTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCAAACATC
201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAAG
401 CACGTCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATCCAAGCAC TGCAAAGAGA
501 ATTGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI NFSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCLSTDL
51  PPIGNYSSER YIPPQTSEPT PSPSNGGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQQN IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

```

              10      20      30      40      50      60
m521.pep      MKSKLLLLILINFSLISSPLGANAAXIXTCTINGETVYTXKPSKSCSTDLPPIGNYSSER
              |||||  |||||  |||||  |||||  |||||  |||||
a521           MKSKLPLILINFSLISSPLGANAAXIYTCTINGETVYTTKPSKSCSTDLPPIGNYSSER
              10      20      30      40      50      60

              70      80      90      100     110     120
m521.pep      YIPPQTPEPVSSPSNGGXVVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE
              |||||  |||  |||||  :|||  |||||  |||||  |||||  |||||  |||||  |||||
a521           YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRSILETELSNE
              70      80      90      100     110     120

              130     140     150     160     170
m521.pep      RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDQQNIQALQRELGRMX
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a521           RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDQQNIQALQRELGRMX
              130     140     150     160     170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51  caaaaaagca aaagccaaaa tccgcacccat ccgcatttgg gcgtgggtca
101 ttttgcggtt gctcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcataa aaaatatcc
201 gtttgctgaa aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccg tctcgccgtc gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtc
351 acaagaacag cttgacctgc tcggcggcgc aaacgcgttt gaaactcgag
401 acaacaatg tgtcgcggat ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMs
51  KPQAKQKIVE SCMKNIPFAE KWQNDLKARG LDADNTRLAV DYCKMWEQP
101 LDGLSEKQIS SFGKLGAEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51  CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTGCG GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAA ACGATTGCGG GGCCCGCGGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

```

787

301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGKLGAQEQ					
	: :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKCMWEQPLDGLSEKQISSFGKLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
 51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
 201 GTTTGCCGAA AAATGGCAAA ACGATTGCG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCCG CCTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGKLGAQEQ					
	: :					
a522	SCVKNIPFAEKWQNDLRARGLDSDNNTRLTVDYCKCMWEQPLDRLSEKQISSFGKLGAQEQ					
	70	80	90	100	110	120

788

```

                130      140
m522.pep      LDLLGGANAFEARDKQCVADLKSEX
                |||||:|||||
a522          LDLLGGANAFETRDKQCVADLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
51 gacgggaacg gtttatcttt tggttgctag cgcggctttg gcgggttcgg
101 gactgccta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gactgcctt cgcgcctggg catttggttc gtacatgcca aaaccgccgt
201 gggaaaagtt gaaacggatt catatcagga tttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcatcgccc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKAEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
1  ..GCCGTCTTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GncGCTCTGC TTTCCGCGCT GGGTATTnG
151 TTCGTACACG CCAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTGGAT GCCGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTACGA AGTTTtTAT CGCGGTACGc ACTGGCAGGC TCAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCATTG TCCGAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLG AGQYVEILRH TGGNRYEVFY RGTHWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng) from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTXALLSALGIXF
                |||||:|||||
g523          MTVWFVAAVAVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLGAGQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g523          VHAKTAVGKVETDSYQDLDTGKAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
                |||||:|

```

g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

```
a523.seq
  1 ATGACTGTAT GGTGTGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT
 51 GACGGGAACG GTTTATCTTT TGGTGTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

```
a523.pep
  1 MTVWFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA
 51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*
```

m523/a523 94.4% identity in 126 aa overlap

```

              10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF
              |||
a523           MTVWFVAAVAVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF
              10      20      30      40      50      60

              60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
              |||
a523           VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
              70      80      90      100     110     120

              120
m523.pep      LIVRKEGNLLIITHPX
              |||
a523           LIVRKEGNLLIIAKPX
              130
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

```
g525.seq
  1 atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
 51 agcggcggct gccgaaatgg ttcaaatacga aggcggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcttgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 ccccaaatgg caaaaaggca ggatcggttc caaacaggca gaaccgcgtt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaattga aacagccggt taccaatatt tcctggtttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttcgcc acgcagaaaa aacggctcaa acgaaccggg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaagca ccgccgaac tactggggtg tttatgatat
551 gcacgggctg a
```

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

```
g525.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRT
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

m525 . pep

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

m525/q525

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

a525.seq

1	ATGAAGTTTA	CCCGGTTACT	CTTCTCTGT	GCGGCACTCG	CCGGCACTCA
51	AGCGGCAGCT	GCCGAAATGG	TTCAAATCGA	AGGCGGCAGC	TACCGCCCGC
101	TTTATCTGAA	AAAAGATACC	GGCCTGATTA	AAGTCAAACC	GTTCAAACTG
151	GATAAATATC	CCGTTACCAA	TGCCGAGTTT	GCCGAATTTG	TCAACAGCCA
201	CCCCCAATGG	CAAAAAGGCA	GGATCGGTTT	CAACAGGCA	GAACCCGGTT
251	ACCTGAAGCA	TTGGATGAAA	AACGGCAGCC	GCAGCTATGC	GCCGAAGGCG
301	GGCGATTTAA	AACAACCGGT	AACCAATGTT	TCCTGGTTCG	CCGCCAACGC
351	CTATTGCGCC	GCACAAGGCA	AACGCCTGCC	GACCATTGAC	GAATGGGAAT
401	TTGCCGGACT	TGCCTCGGCC	ACGCAG. AAA	AACGGTCAA	ACGAACCCGG
451	CTACAACCGC	ACTATTCTCG	ACTGGTATGC	GGATGGCGAC	CGGAAAGACC
501	TGCACGATGT	CGGCAAG. G	TCGCCCCAAC	TACTGGGGCG	TTTATGATAT
551	GCACGGTCTG	A			

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1 MKFTRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
||::||: | |||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      MKFTRLLFLCAALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
      10      20      30      40      50      60

      70      80      90     100     110     120
m525.pep AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVNTVSWXAANAYCA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA
      70      80      90     100     110     120

      130     140     150     160     170     180
m525.pep AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCQXVARTTGA
      130     140     150     160     170     180

m525.pep FMICTGX
|||||
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1 ATGAAGTACG TCCGGTTATT TTTCTCGGC ACGGCACTCG CCGGCACTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGCGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGACC GCCGAACTA CTGGGGTGT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAAC TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKDRPNYGV YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLFGRFAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1 ATGAAGTATG TCCGGTTATT TTTCTCGGC GCGGCACTCG CCGGCACTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGCGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

792

```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAACT TGGGCTTCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1  MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHWK NGSRSYAPKA
101 GELKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKGLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSSL
201 SNANAMQFCS SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLFGRCTS
251 R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLGAALAGTQAAA	AEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF				
g525-1	MKYVRLFFLGTALAGTQAAA	AEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF				
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHHWMKNGSRSYAPKAGELKQPVNTVSWFAANAYCA					
g525-1	AEFVNSHPQWQKGRIGSKQAEPAYLKHHWMKNGSRSYAPKAGELKQPVNTISWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGKGLHDVGKGRPNYWGV					
g525-1	AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGKGLHDVGKDRPNYWGV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSSLSSGNANAMQFCSGASIGSSDSNYYAAFLRYGIRTSLSQSKYV					
g525-1	YDMHGLIEWETEDFNSSLSSGNANAMQFCSGASVGSNYYAAFLRYGIRTSLSQSKYV					
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLFGRCTSRX					
g525-1	LHNLFGRCSRX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```

1  ATGAAGTTTA CCCGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCC GATGGCGACC GGAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAATATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAACT TGGGCTTCG TTGCACAAGC
751 CGATAA

```

1	MKFTRLFLFC	AALAGTQAAA	AEMVQIEGGS	YRPLYLKKDT	GLIKVKPFKL
51	DKYPVPTNAEF	AEFVNSHPQW	QKGRIGSKQA	EPAYLKHWMK	NGRSRYAPKA
101	GD LKQVTAHF	SWFANAYPA	AQGRKLSTID	EWEFAGLASA	TQKNGSNNEP
151	YNRTILDWYA	DGDRKDLHDV	GKGRPNYWG	YDMHGLIEW	TEDFNSLLS
201	SGNANAQMFC	SGASIGSSDS	SNYAAFLRYG	IRTSLSQSKY	LHNLGFRCTS
251	R*				

		10	20	30	40	50	60
m525-1.pep		MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVPFKLDKYPVTNAEF					
a525-1		MKFTRLLFLCAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVPFKLDKYPVTNAEF					
		10	20	30	40	50	60
		70	80	90	100	110	120
m525-1.pep		AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVNTVSWFAANAYCA					
a525-1		AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA					
		70	80	90	100	110	120
		130	140	150	160	170	180
m525-1.pep		AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVKGKRPNYWGV					
a525-1		AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVKGKRPNYWGV					
		130	140	150	160	170	180
		190	200	210	220	230	240
m525-1.pep		YDMHGLIWewTEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLQSKYV					
a525-1		YDMHGLIWewTEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLQSKYV					
		190	200	210	220	230	240
		250					
m525-1.pep		LHNLGFRCTSRX					
a525-1		LHNLGFRCTSRX					
		250					

1	atggttttac	cagtctcctt	ttttcagcct	gtccagtttg	cggcggtcgc
51	gcttggtcgg	tctgccgtcg	ggatgggcgg	aagtgatgcg	gctgaattgg
101	tcgagctgtt	tgcactcttc	cctcaatgct	gccgttttcg	cgtcttcttc
151	atacagaagc	cgcgcctcgg	gtgccgggcg	gcgttggttg	ttcaaacctt
201	taaccttgat	tttatgggga	aggggaattga	gcgtcaggtc	gataatatcg
251	ccgatgtcta	tggttttact	gtttttgact	ttcgagccgt	ttacttgaac
301	cctaccagct	tcgatatgct	tttgcgcaag	ggaacgggtc	ttgaaaaaac
351	gtgccgcca	aagccatttg	tccagccgca	tggcggaaga	atcgtgcttg
401	tccttcatac	gattttgttt	gaaataattg	aatttgtttc	gagtttagca
451	taa				

```

1  MVLPSVFFQP VQLAAVALGR SAVGMGGSDA AELVELFALF PQCCRFRVFF
51  IQKPRLCRA ALVVQTFNLD FMGKGIERQV DNIADVYGFT VFDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

1 ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGCGGTTCGC
51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTwTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCyTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

794

201 TAACCKTGAT TTTATAGGGA AGGG.AATTk AgCkTCaGty GrTwATaTCG
 251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA CTTGAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGTTC GAAATAATTG AATTGTGTTT GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep
 1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLV
 51 IQKPRXGCRA ALVVQTFNND FIGKXNXASV XXIADVYGFT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRXRVLV	FIQKPRXGCRA
g527	MVLPSVFFQP	VQLAAVALGR	SAVGMGGSDA	AELVELFALF	PQCCRFRVFF	FIQKPRLGCR
	10	20	30	40	50	60
	70	80	90	100	110	120
m527.pep	ALVVQTFNND	FIGKXNXASV	XXIADVYGFT	VFDLRAVYLN	PTQFDVLLRK	GTGLEKTCRP
g527	ALVVQTFNLD	FMGKGIERQV	DNIAADVYGFT	VFDLRAVYLN	PTQFDMLLRK	GTGLEKTCRP
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGR	IVLVFHTILF	EIIEFVSSLA			
g527	KPFVQPHGGR	IVLVFHTILF	EIIEFVSSLA			
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq
 1 ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
 51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
 101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
 151 ATACAGAAGC CGCGCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
 201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
 251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA CTTGAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGTTC GAAATAATTG AATTGTGTTT GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep
 1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLV
 51 IQKPRLGCR ALVVQTFNLD FIGKGIERQV DNIAADVYGFT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527.pep	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRXRVLV	FIQKPRXGCRA
a527	MVLPSVFFQP	VQLAAVALGR	SAVGIGGSDA	AELVELFALF	PQCCRFRVLV	FIQKPRLGCR
	10	20	30	40	50	60

795

```

              70      80      90      100      110      120
m527.pep      ALVVQTFNxdfiGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP
              ||||| ||||| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a527           ALVVQTFNldfiGKGIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP
              70      80      90      100      110      120

              130      140      150
m527.pep      KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a527           KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX
              130      140      150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaaattc gggtaataaa atatacggca acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggtg gtatgagtgt ttgtccttgt
101 ccggctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggcggcgaga gtccgctgtc tttagaggac tacgagatac cgctttcaga
201 cggaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatcct
251 acttttatag gaaaataggg aagtttgaag cctgcggggt ggattggcgt
301 acgcgtgacg gcaaaccttt ggttgagagg ttcaaacagg aaggtttcga
351 ctgtttggaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGTA
351 CTGCTTGGAA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QQSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

```

m528/g528

              10      20      30      40      50      60
m528.pep      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              |||:|||| |||:||||| |||:||||| |||:||||| |||:||||| |||
g528           MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
              10      20      30      40      50      60

              70      80      90      100      110      120
m528.pep      YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g528           YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
              70      80      90      100      110      120

```



```
a528.seq
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTTT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATGATTTT TTGGGATATT
151 GGCGGCGAGA GTCCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
351 TTGTTTGAAG AAGCAGGGGT TCGGCGCGAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA
```

```
a528.pep
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSIFYRKIG KFEACGLDWR
101 TRDGKPLIET FKOEGFDCCLK KOGLRRNGLS ERVRW*
```

```

      10      20      30      40      50      60
m528.pep  MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          |||||:|||||
a528      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLD
          10      20      30      40      50      60

      70      80      90     100     110     120
m528.pep  YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
          |||||:|||||
a528      YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
          70      80      90     100     110     120

```

```
m528.pep      K
               |
a528           KQGLRRNGLSERVRWX
               130
```

g528-1.seq

```
1  ATGGAATTC  GGGTAATAAA  ATATACGGCA  ACGGCTGCGT  TGTTCGATT
51  TACGGTTGCA  GGCTGCCGGC  TGGCGGGGTG  GTATGAGTGT  TGTCCCTGT
101 CCGGCTGGTG  TAAGCCGAGA  AAACCTGCCG  CCATCGATT  TGTGGATATT
151 GCGCGCGAGA  GTCCGCTGTC  TTTAGAGGAC  TACGAGATA  CGCTTTCAGA
201 CGGCAATCGT  TCCGTCAGGG  CAACCAATA  TGAATCCGC  CAAAAATCT
251 ACTTTTATAG  AAGAAATAGG  AAGTTTGAAG  CCTCGGGTGT  GGATTGCGGT
301 ACGCGTGACG  GCAAACTTT  GGTGAGAGG  TTCAACAGG  AAGGTTTCGA
351 CTGTTTGGAA  AAGCAGGGGT  TCGGCGCAA  CGGCTGTCC  GAGCGCGTCC
401  GATGGTAA
```

g528-1. pep

1	MEIRVIKYTA	TAAALFATVA	GCRLAGWYEC	SSLSGWCKPR	KPAAIDFWDI
51	GGESPLSLED	YEIPLSDGNR	SVRANEYESA	QKSYFYRKIG	KFEACGLDWR
101	TRDGKPLVER	FKOEGFDCLE	KOGLRRNGLS	ERVVR*	

m528-1.seq
1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT

797

```

51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GGCGGCCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGAA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51 GGESPPSLGD YEIPLSDGNNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

          10      20      30      40      50      60
g528-1.pep MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
          ||||:|||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90     100     110     120
g528-1.pep YEIPLSDGNNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m528-1      YEIPLSDGNNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90     100     110     120

          130
g528-1.pep KQGLRRNGLSERVRWX
          |||||:|||||
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGCGGCCGAGA GTCCGCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

          10      20      30      40      50      60
a528-1.pep MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90     100     110     120
a528-1.pep YEIPLSDGNNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m528-1      YEIPLSDGNNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90     100     110     120

          130
a528-1.pep KQGLRRNGLSERVRWX
          |||||:|||||
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

```
g529.seq (partial)
  1 atgacccata tcaaacccgt cattgccgcg ctgcactca tcgggcttgc
 51 cgcctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggctgcaccg cctgatcaaa ctggaagtcc cgctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc gggtcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcggatg
251 ccggaagtat tgaaaagcgt caaaggcgct cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgctgt tgacggcaaa tcccccgccg aaatctccgc
351 cgctttctg.
```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

```
g529.pep (partial)
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
 51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF..
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

```
m529.seq
  1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
 51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTCGCACCG CCTGATCAAA CTTGAAGTCC CACCTGATTG GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCTGA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAGACA GCTTGCCTCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GGCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAAGC AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGT GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTGCGCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

```
m529.pep
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNPN
 51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAELVLSV KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPAIGQME TEWAENRAKI
151 PQDSLRLRLFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDQTV WQSPSPDPNL EAAFLTRFMQ YLGVDGQQA NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELRL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

              10      20      30      40      50      60
g529.pep      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA
```

```
a529.seq
1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGACCG CCGTATCAAA CTCGAAGTCC CACCTGATTT GAACAAACCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAGGCGTC AAAGGTGTCT GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTGCA CGGCAAGTCT CATGCGCGAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAAATGGAA ACCGAGTGGG CGGAAAACCG TGCCAAAATC
451 CCCCAGACA GCTTGCGCCG CCTATTCGAC ACAGTCGGTT TGGGCGGCAT
501 CTACTCCACC GGCAGCGCGG ACAAAATCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAAGCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTTGGGCG
701 TTGACGACA GCAGGCGGAA AACGCATCGG CAAAAAAACC TACCCTTCCC
751 GCCGCCAAGC AAATGGCGCG TATCGAAGCG AAAAGCCTGA TTGTCTTTTG
801 CGACTACGGC AGAAATGGC GGCACACCGC GTCTGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAC CCGGCCTGTT
951 CAAACGCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CATGTGCGCCA ACGGCTCGCG CATCGTCTTG
1051 CTCACAAAGC ACGCGACGCG ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATCT CATTCCGAAC TGCGTTAA
```

a529.pep	1	MTHIKPVIAA	LALIGLAACS	GSKTEQPKLD	YQSRSHRLIK	LEVPPDLNNP
	51	DQGNLYRLPA	GSGLAVRASDL	EKRRTPAVQQ	PADAEVLKSV	KGVRLENDRGS
	101	QRWLVDVGKS	HAEIWPLLKA	FWQENGFDIK	SEEPaIGQME	TEWAENRRAKI
	151	PQDSLRLRLFD	TVGLGGIYST	GERDKFIVRI	EQGKNGVSDI	FFAHKAMKEV
	201	YGGKDKDTTV	WQPSPSDPNL	EAAFLTRFMQ	YLGVDGQQAE	NASAKKPTLP
	251	AANEMARIEG	KSLIVFGDYG	RNWRRTALAL	DRIGLTVVGQ	NTERHAFLVQ
	301	KPNKESNAVT	EQKPGLFKRL	LKGKKAEPKA	EQFELIVYAE	PVANGSRIVL
	351	LNKDGSAAYAG	KDASALLGKL	HSEL*		

	10	20	30	40	50	60
m529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA					
a529	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m529.pep	GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDGKSPAEIWPLLKA					
a529	GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDGKSHAEIWPLLKA					
	70	80	90	100	110	120
	130	140	150	160	170	180

800

```

m529.pep  FWQENGFDIKSEEP AIGQMETEWAENRAKIPQDSLRRFLDKVGLGGIYSTGERDKFIVRI
a529      FWQENGFDIKSEEP AIGQMETEWAENRAKIPQDSLRRFLDTVGLGGIYSTGERDKFIVRI
           130      140      150      160      170      180

           190      200      210      220      230      240
m529.pep  EQGKNGVSDIFFAHKAMKEVYGGKDKDTTVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
a529      EQGKNGVSDIFFAHKAMKEVYGGKDKDTTVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
           190      200      210      220      230      240

           250      260      270      280      290      300
m529.pep  NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGLTVVGQNTERHAFLVQ
a529      NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTALALDRIGLTVVGQNTERHAFLVQ
           250      260      270      280      290      300

           310      320      330      340      350      360
m529.pep  KAPNESNAVTEQKPGLFKRLLGKGKAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
a529      KAPNESNAVTEQKPGLFKRLLGKGKAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
           310      320      330      340      350      360

           370
m529.pep  KDASALLGKLHSELRX
a529      KDASALLGKLHSELRX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga ggcgggcaat gacgggtttg atatgggtca tcgtgtcatc
51 ctgtgtgatg gatattaaag tgtttgtcat gttatgccgt ccgaacgggt
101 cagacggcat ggctataatt aaagtgtgcc tgaggcttcc agggcgggcg
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgacag
201 tgcggtccgc atccgcccaa ggcggatacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgctgtaa at cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCVM DIKVFVMLCR PNGSDGMAIF KVVLRLSGRR
51  GLLPVRLPSA ERAAGARAVR IRPRRIPPIS VRRDWVRRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  WTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTTCATC
51  sTGTGTGATG GATATTAAAG TGTyTGTTC GwTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGGCGC
151 GGAkTtTGC WTGTCCGTTT yCCGTcAGCG GAACGAGCGG CAGGCGGACG
201 TGCgTTCGC ATCTGCCCAg GCGGATACC GCCATTTCG GTGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CCGTCTGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCVM DIKVXVAXCR PNGSDGMXIF KVVLRLSGRR
51  GLLXVRFPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

```

m530/g530

m530.pep  XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA
           |||

```

```
a530.seq
1  ATGAGTGC GA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCATC
51  CTGTGTGA TG GATATTAAG TGTTTGTTCG GTTATGCCGT CCGAACGGTT
101 CGGACGGCA T GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTC G CTGTCCGCC T TCCGTACAGC GAACGAGACG CAGGCGGACG
201 TGCGGTTC CG ATCTGCCCC G GCGGATACCC GCCCATTCGG GTGCGGCGGG
251 GCTGGGTT CG CAGAACATGG TGTCGTAAAT CGGAATCAGC CGTCTGTTGA
```

a530.pep
1 MSASAAMTGL IWVIVSSCVM DIKFVVALCR PNGSDGMAIF KVVLRSLGRR
51 GLLPVRLPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESAGR*

	10	20	30	40	50	60
m530.pep	XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA					
a530	MSASAAMTGLIWVIVSSCVMDIKVFVLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA					
	10	20	30	40	50	60
	70	80	90	100		
m530.pep	ERAAGGRAVRICPGRIPPISVRRGWVRTWCRKSESVGRX					
a530	ERAAGGRAVRICPGRIPPISVRRGWVRTWCRKSESAGR					
	70	80	90	100		

g531.seq

```
1  ATGACCGCCC TACTCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51  GGCAGGCATC GTCTATCCCG CCCTGCCCGG CTTGGCATTG ATGTTTGCCG
101 GAACATGGCT GCTTGCCTAT GCCGGCGGCT ATCAAATCTA CGGCGCAGGC
151 ATCTTGTTGA CGGTCGGACT CATCAGCCTT GGCGGCATAC TGGCGGACTA
201 TATGGCAGGC ATGTTGGGGG TAAAATACAC TGGGGCAGGC AAACCTGCCG
251 TCCGAGGTGC ATTGGCCGGC AGCATCATCG GCATATTTTT CTCCCTTCCC
301 GGACTAATA TCGGCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
351 TCGGGCAAT ATGCTTCAGG CAGGTAAGC GGCGCTGGGT ACGCTGTTGG
401 GGCTTGTCGT CGGCACGGCG TTCAAATCG GCTGCGCCGT ATCCATCTTG
451 TTTATCCTGT TGGTGAAATA CATCGCATAC CTGTTTTAA
```

g531.pep

1	<u>MTALLVILAL</u>	<u>ALIAVGTAGI</u>	<u>VYPALPGLAL</u>	<u>MFAGTWLLAY</u>	AGGYQIYGAG
51	<u>ILWTVGLISL</u>	<u>GGILADYMag</u>	<u>MLGVKYTgAG</u>	<u>KLAVRGALAG</u>	<u>SIIGIFFSLP</u>
101	<u>GLILGPFIGA</u>	<u>AAGELIDRRN</u>	<u>MLQAGKAGLG</u>	<u>TLLGLVVGTa</u>	<u>FKIGCAVSIL</u>
151	<u>FILLVKYIAY</u>	<u>LF</u>			

```
m531.seq
  1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
 51  GGCGGGCATC GTTTaCCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
101  GAACATGGCT GCTTGCCTAT GCCGGCGGCT ACCAAATCTA CGGCGCGGGC
151  GTTTTGTGGA CGGTGCGACT CATCAGCCTT GCCGGCATA C TGCGGACTA
201  TGTGGCAGG ATATGGGGGA CAAAATATAC CGGAGCGGGC AAGCTCGCCG
251  TTCGCGCGCG ATTGGCCGGC AGCATCATCG GCATATTTT CTCCCTTCCC
301  GGAATAATAC TCGGTCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
```

m531.pcp

1 MTVLTVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGKYTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

Homology with a predicted ORF from *N. gonorrhoeae*

m531/g531

		10	20	30	40	50	60							
m531.pep		MTVLT	VILAL	ALIAV	GTAGI	VYPAL	PGLAL	MFAGT	WLLAY	AGGYQ	IYGAG	VLWTV	GLISL	
		:										:		
g531		MTALL	VILAL	ALIAV	GTAGI	VYPAL	PGLAL	MFAGT	WLLAY	AGGYQ	IYGAG	ILWTV	GLISL	
			10	20	30	40	50	60						
		70	80	90	100	110	120							
m531.pep		AGILAD	YVAGI	WGTKY	TGAGK	LAVRG	ALAGS	IIGIFF	SLPGL	ILGPF	IGAA	AGELI	ERRN	
		:		:	:	:							:	
g531		GGILAD	YMAGM	LGVKY	TGAGK	LAVRG	ALAGS	IIGIFF	SLPGL	ILGPF	IGAA	AGELI	DRRN	
			70	80	90	100	110	120						
		130	140	150	160									
m531.pep		MLQAG	KAGLG	TLLGL	VVGTA	FKIGCA	VSILF	ILLVK	YIAYL	F				
g531		MLQAG	KAGLG	TLLGL	VVGTA	FKIGCA	VSILF	ILLVK	YIAYL	F				
			130	140	150	160								

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCCTGATAG	CGCGCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCGG	ATTGGCATTG	ATGTTTGCCG
101	GAACCTGGCT	GCTCGCCTAC	TCCGGCGGGT	ACCAATCTA	CGGCGCGGGC
151	GTTTTGTGGA	CGGTCCGAGT	CATCAGCCTT	CGCCGCATAC	TGGCGGACTA
201	TGTGGCAGGC	ATATGGGGGA	CAAAATATAC	CGGAGCGGGC	AAGTCGCCG
251	TTCGCGGCGC	ATTGGCCGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAC	TCGGTCCCTT	TATCGGCGCG	GCGGAGGCG	AACTGATCGA
351	ACGGCGCAAT	ATGCTTCAGG	CAGGTAAAGC	GGGCTGGGT	ACGCTGTTGG
401	GGCTTATCGT	CGGTACGGCG	TTCAAAATCG	GCTGCGCCGT	ATCCATCTTG
451	TTTATCTCTG	TGGTGAATA	CATCGCCTAC	CTGTTTTTAA	

a531.pcp

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFAGTWLLAY SGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTTYGTAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIERRN MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

```

      10      20      30      40      50      60
m531.pep  MTVLTVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGVLWTVGLISL
          ||:| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a531      MTALLVILALALIAAGTAGIVYPALPGLALMFAGTWLLAYSGGYQIYGAGVLWTVGLISL
          10      20      30      40      50      60

          70      80      90     100     110     120
m531.pep  AGILADYVAGIWGTKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAAGELIERN

```

803

```

a531      |||||
          AGILADYVAGIWGTYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERRN
          70      80      90      100      110      120

          130      140      150      160
m531.pep  MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          |||||
a531      MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acaggcggat tcgectgatt tgggtgtacgg
51  tttggaagac aggccgccgt tcggtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttcgtg ccgatgatta cgcgcgcgct gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctcg tgctgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTCG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CCGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTTCGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGCTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGCGATT ACCGATTTCG GCGGCGGGCT CGGCGCGAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAAGAA TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCGG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTGCGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTTAAATACG GTTTTGCTTT CGACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCCTG
901 CGCGGCGGCG TGTGCTGCTG CCGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTCAGA
1001 TGACCGCGCT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCCGTG TTGGGCGGCG CGATGGTTT GATGTTTCGGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCAG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CCGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTGT AAAAACCTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```


804

201 VLVFNCKMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLPPV
 251 FKYGFAPFDWH AFIVAGAIPL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
 301 RGGVLADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
 451 EAAVKFDTDH LEH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

g532/m532

	10	20	30	40	50	60
g532.pep	MAETMKKQADSPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	:	:				
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60

	70	80	90	100	110
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLS IQRYRHDCARRGDERGRFEX				
m532	AYLVSMAMVASGVGTYLQVNRFGVPVSGMLS IQSVNFSFVTVMIALGAGMKEGGLTKDAM				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTCG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CGGTGAATTT CTCGTTTCGT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTTCGACG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT TTCGGCGTGG CTCTGCGCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGGTACA
501 CGTCGGTATT ACCGATTTCG GCGGCGGCTT CGGCGCAAAG GCGGACGGCA
551 CGTTCGGCTC GATGAAAAAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGCAT GAAAAACCCG CTGCTGCGGA TGAGCGGCAT
651 TGCGGTCGGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCATGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTTAAATATG GTTTTGCTTT TGACTGGCAC GCATTTATTG TGGCGGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTG ACGGCGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCTTG
901 CGCGGCGGCG TGTTGGCGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGACA AAACAACGGC GTGATTACAG
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGA CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCCGC TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTGCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACCTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSMAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV

```

805

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFAFDWH AFIVAGAI FL LSVFEAVGDL TATAMVSDQP IEGEYTKRL
301 RGGVLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

m532.pep	MSGQLGKGADAPDLVYGLED	RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
a532	MSGQLGKGADAPDLVYGLED	RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
m532.pep	AYLVSMAMVASGVGYTLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM	
a532	AYLVSMAMVASGVGYTLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM	
m532.pep	ISTLLGVSVFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK	
a532	ISTLLGVSVFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK	
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLMSGIAVGLIAGYIVALFLGKVDFSALQ	
a532	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLMSGIAVGLIAGYIVALFLGKVDFSALQ	
m532.pep	NLPLVTLVPVFFKYGFAFDWHAFIVAGAI FL LSVFEAVGDLTATAMVSDQPIEGEYTKRL	
a532	NLPLVTLVPVFFKYGFAFDWHAFIVAGAI FL LSVFEAVGDLTATAMVSDQPIEGEYTKRL	
m532.pep	RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG	
a532	RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASRHHVGKYIAVILVLLGLFPVVG	
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF	
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREAVIAATSVGLGLGVAFEPEVF	
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX	
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

```

g535.seq
1  atgccctttc ccgttttcag acaantattt gcttngtcct tgctacggtt
51  ttttgccgta ggteggattc tcgaatccga catttccaac agcgggtttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatttaca tcgcttccaa ttctcgaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagtga tggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttcggc tgtttgaagt

```

806

```

351 catcgatgat tttgtcccgt tgtacggtgg tttggcgcgt gttgccgtag
401 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
451 gatttcttcg acgaagcggg atgcgatgcc gaattggggt tgctcgtgca
501 gcatgcgttg ctgtgccatg gtgatgtaga ggcgtttgcg ggcgcgggtg
551 atggcgacgt acatgaggcg gcgtttcttct tcgaggccgc cgcgctcggc
601 aaggctcatt tcgctgggga aacgcccctc ttccataacc gtgaggaaga
651 cggcggttga ttccaagcct ttggcggcgt ggacggtcat cagttggacg
701 gcttttttcg ctgcccctgc ttggttttcg ccggattcga gggcggcgtt
751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

```

g535.pep
  1 MPFPVFRQXF AXSLLRFFAV GRILESDISN SGFSETINAS NVFFVGYEYP
 51 ACISNLHRFQ FRKLGIOFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFEVIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

```

m535.seq
  1 aTGCCTTTtC CCGTTTTcAG ACGGCCTTTT GCTTTGTCCT TACTtACGTT
 51 TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTTCCAAC AGCGGTGTTT
101 CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTCCAATTT CGCAAACCTG GTGTCCAAct
201 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTcGCCT
251 TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTTGG CGTGCGGAC
301 GTTTTGTCG ATACGGAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GGCGCGTGTT GCCGTAActG
401 TCGTAGGCAG GCTTTTtGAC GGACAGGTAG TGCAATACTT CGGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
501 TGCGTTGTTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
551 GCGACGTACA TGAGCGGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
601 GCTCATTTcG CTGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
701 TTTTCGCCTG CGCTGCCTG GTTTTcACCG GATTCGAGGG CGGCATTGCT
751 TAGGAAGCGC AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

```

m535.pep
  1 MPFPVFRFPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
 51 YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAFICGIDN HAGAEFGVAD
101 VLSDTETCVG LGLFVVDDF IFGCGGLARV AVTVVGRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEENGEGGV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

```

m535/g535
      10      20      30      40      50      59
m535.pep MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ
|||||: || ||| ||||: || ||||| ||||: ||||| ||||| ||||| ||
g535      MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNVFFVGYEYPACISNLHRFQ
      10      20      30      40      50      60

      60      70      80      90     100     110     119
m535.pep FRKLGVLQFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSdTETCVGLGLFVVDD
|||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
g535      FRKLGIOFFHALFAEVDGQSGGFAFVCGIDNHAGAEFGVTDVLSDAEACVGLRLFEVIDD
      70      80      90     100     110     120

```



	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGR	LF	FDGQVVQYFGWDLF	DEAGD	DAELGLSVQHALLRH	GDVEAFA	
	:		:	:	:		
g535	FVPLYGGLARVAVAVEGG	FFD	GQVVQYFWRD	FFDEAGCDAELGLSVQHALLCH	GDVEAFA		
		130	140	150	160	170	180
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAA	AFGKAHFAGEAAFFHAGEED	GVK	FQAFGGVD	GH	LDGLFACAC	
			:	:	:		
g535	GAGDGDVHEAAFFFEAAALGKAHFAGET	PLF	HTGEEDGVEFQAFGGVD	GHQLD	GFFACPC		
		190	200	210	220	230	240
	240	250	260				
m535.pep	LVFTGFEGG	IA	XEGENGEGGVV				
	:	:	:	:			
g535	LVFAGFEGGVAQEGEDGEGG	I	V				
		250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

a535.seq	(partial)					
1	TTCAGACGGC	CTTTTGCCTT	GTCCTTGCTA	CAGTTTTTTG	CCATAGGTCG	
51	GATTCTCGAA	TCCGACATT	CCAACAGCGG	TTTTTCGGAA	ACGATAGACG	
101	CGTCAAATAT	TTTGTCCGA	TACGAGTATC	CAGCCTGCAT	TTCAAATTTA	
151	CATCGCTTCC	AATTTCCGAA	ACTTGGTGTC	CAACTCTTTC	ACGCCCTGTT	
201	TGCCGAAATT	GATGGTCAGT	CGGGCGGATT	CGCCTTTATC	TGCGGCATCG	
251	ATAATCACGC	CGGTGCCGAA	TTTGGCGTGG	CGGACGTTTT	GTCCGATACG	
301	GAACCTTCGC	TAGGTTTGGG	GCTGTTTGTA	GTGCTCATG	ATTTGTCTTT	
351	TGGGCGCGGC	GGTTTGCGCG	GTGTTGCCAT	AGCGGTCGTA	GGCGGGTTTT	
401	TTGACGGACA	GGTAGTGCAA	TACTTCGGGG	GGGATTTCTT	CGACGAAGCG	
451	GGAGACGATG	CCGAATTGGG	TTTGTCCGTG	CAGCATTCGT	TGTTTGCGCCA	
501	TGGTGATGTA	GAGGCGTTTG	CGGGCGCGGG	TGATGGCGAC	GTACATCAGG	
551	CGGCGTTCTT	CTTCGAGGCC	GCCGCGTTCG	GCAAGGCTCA	TTTCGCTGGG	
601	GAAGCGGCCT	TCTTCCATGC	CGGTGAGGAA	TACGGCGTTA	AATTTCAAGC	
651	CTTTGGCGGG	GTGCACGGTC	ATGAGTTGTA	CGGCTTTTTT	GCCCCGCGCCT	
701	GCTTTGGTTTT	CGCCGGAATC	GAGAGCAGCA	TTGCTTAGGA	AAGCGAGGAT	
751	GGGGAAGGCG	GGGTCGTCTG	A			

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep (partial)

1	FRRPFALSLL	QFFAIGRILE	SDISNSGFSE	TIDASNIFVG	YEYPACISNL
51	HRFQFRKLGV	QLFHALFAEI	DGQSGGFAFI	CGIDNHAGAE	FGVADVLSDT
101	ETCQVGLGLFV	VVDDEVFVGRG	GLARVAIAVV	GGFFDQGQVVQ	YFGRDFFDEA
151	GDDAELGLSV	QHALLRHGDV	EAFAGAGDGD	VHQAATFFFEA	AAFGKAHFAG
201	EAAFFHAGEE	YGVKFQAFGG	VHGHELYGFF	ARACLVFAGF	ESSIA*ESED
251	GEGGVV*				

m535/a535 88.7% identity in 256 aa overlap

	10	20	30	40	50	60
m535.pep	MPFPVFRPPFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGYEYPTYISNLHLFQF					
	:: ::					
a535	FRPPFALSLLQFFAIGRILESDISNSGFSETIDASNIFVGYEYPACISNLHRFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVQLFHAFALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
a535	RKLGVQLFHAFALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVAVTVVGRLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	: :: : : :					
a535	VFGRGGLARVAIAVVGGFDFGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

1	atgaaatccc	tttttatttg	gctgcttcta	tgggctcg	cggcaggcgt
51	tttctaccat	acccaaaacc	aatccctgcc	cgcgggcgaa	cttgtctatc
101	cgtccgcacc	gcaaatacag	gacggcggcg	atgcgtgca	ctacctcaac
151	cgcatacgc	cacaaatcgg	tttgacgcg	ctggcacacg	cgccgggttt
201	ggaaaattcc	gcccgcaggc	acgcacgcta	tctcacgctc	aatcccgaa
251	acggacatcg	cgaacaccat	ccgcacaatc	cgcactacac	cgcaaaaag
301	ctgaccgaac	gcacacgcct	tgcgggtat	ctctacaacg	cgctgcatga
351	aaacatcagc	acggaagagg	aagccgccga	atcgtccgac	agcgacatcc
401	gcacgcagca	acgccaagt	gacgctttga	tgagcgcaat	ctaccaccgc
451	ctttcgctgc	ttgaccgcca	taccgacgaa	gcaggtgcgg	catttgtgcg
501	cgaaaacggc	aaaaccgtcc	tcgtattcaa	tcagggcaac	ggcagcttcg
551	agcgcgcctg	tgcaaaagga	agggcgacga	cggaaagcag	acggaatatc
601	taccgcaacg	cttgccacaa	cggcgcgcc	gtttatgctg	cgaagccat
651	gcccgtaacg	gaattgcttt	ataccgccta	tccggttggc	ggcggcgcg
701	tgccttattt	ttacggggaa	cgtcccgacc	ccgtgccgga	atatgaaatc
751	acaggcaatc	ctgccagcat	tgatttttcc	gaggcggcag	gcaaaattgc
801	gatgaaaagt	ttcaagctgt	atcagggtaa	aaacgaaatc	cgccccgtca
851	gggttttaac	cgccggcaac	gaccctaagc	gcaggtcgac	cgcgcacca
901	ttcgcccttt	tcccgctcaa	acctttggaa	tacggcacgc	tttatacggc
951	ggtattcgac	tatgtccgca	acggacggca	cgcgcaggcg	aatggcagt
1001	ttagaaccgc	aaaaccgat	tacccttatt	ttgaggtaaa	cggcggcgag
1051	acacttgctg	ttagaaaagg	cgaaaaatat	ttcatccact	ggcgcgacg
1101	ctggtgtctg	gaagcgtgta	cccgttatac	ctaccggcgg	cagttcggca
1151	acagcctgtc	catactccgg	cacgaagcgg	gcggcattgt	cttcagcgtc
1201	agcggaatgc	cgggaagcgg	ctcagggctt	atccggaag	acagcccgga
1251	acgcggtgta	accctttatt	tgcaggattg	a	

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

1	MKSLFIWLLL	LGSAAGVFYH	TQNQSLPAGE	LVYPSAPQIR	DGGDALHYLN
51	RIRTQIGLHA	LAHAPVLENS	ARRHARYLTL	NPEDGHGEHH	PDNPHYTAQK
101	LTERTRLAGY	LYNGVHENIS	TEEEAAESSD	SDIRTQQRQV	DALMSAIYHR
151	LSLLDRHTDE	AGAAFVRENG	KTVLVFNQGN	GSFERACAKG	RRQPEAGRKY
201	YRNACHNGAA	VYADEAMPVT	ELLYTAYPVG	GGALPYFYGE	RPDPVPEYEI
251	TGNPASIDFS	EAAGKIAMKS	FKLYQGKNEI	RPVRVLTAGN	DPNGRLTAHQ
301	FALFPLKPLE	YGTLYTAVFD	YVRNGRHAQA	KWQFRTKRPD	YPYFEVNGGE
351	TLAVRKGEKY	FIHWRGRWCL	EACTRYTYRR	QFGNSLSILR	HEAGGIVFSV
401	SGMAGSRIRL	TPEDSPERGV	TLYLQD *		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

1	ATGAAATCCC	TTTTTATTCG	GCTGCTCCTG	TTGGGTTCCG	CGGCAGGCGT
51	TTTCTACCAT	ACCCAAAmCC	AATCCCTGCC	CGCGGGCGAA	CTTGCTATC
101	CGTCCGCACC	GCAAATCAGG	GACGGCGGGC	ATGCCTGCA	CTACCTCAAC
151	CGCATCCGAG	CCCCAATCGG	TTTGACAAG	CTGGCACACT	CGCCGGTTTT
201	GGAAAACTCC	CCCCGCAGGC	ACGCAAGCTA	CTCACGCTC	AATCCGAAG
251	ACGGACACGG	CGAACACCAT	CCCCACAATC	CGCATACAC	CGCACAAAAG

```

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

```

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

```

m537.pep (partial)
  1 MKSLFIRLLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
151 LSLDRHTDE SGAA...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

```

m537/g537

      10      20      30      40      50      60
m537.pep MKSLFIRLLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLNRIIRAQIGLHK
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g537      MKSLFIWLLLLLGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLNRIQTIGLHA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

      70      80      90     100     110     120
m537.pep LAHAPVLENSARRHASYLTLNPEDGHGEHHDPNPHYTAQKLTERTRLAGYLYNGVHENIS
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g537      LAHAPVLENSARRHARYLTLNPEDGHGEHHDPNPHYTAQKLTERTRLAGYLYNGVHENIS
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

      70      80      90     100     110     120

      130     140     150     160
m537.pep TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g537      TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

      130     140     150     160     170     180
g537      GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGLPYFYGE
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

      190     200     210     220     230     240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

```

a537.seq
  1 ATGAAATCCC TTTTATTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGCG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT
201 GGAAAATTCC GCCCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCG
501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
651 GCGCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
751 ACGGGCAATC CTGCCAGCAT TGATTTTTTC GAGGCGGCAG GCAAAATTAC
801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCCGTCA
851 GGGTTTTAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
951 GGTATTGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
1001 TTAGAACCCG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG
1051 ACACTTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGCGCGGACG
1101 CTGGTGTGTTG GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

```

810

```

1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTCAGCGTT
1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA
1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

```

a537.pep
1  MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
151 LSLDRHTDE AGAAVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPYEYEI
251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAYQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPSRLSIGR HKAGGIVFSV
401 DGMAGSRITL APEGETERGV TLYLQD*

```

m537/a537 98.2% identity in 164 aa overlap

```

              10      20      30      40      50      60
m537.pep      MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK
              |||||
a537           MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK
              10      20      30      40      50      60

              70      80      90      100     110     120
m537.pep      LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
              |||||
a537           LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
              70      80      90      100     110     120

              130     140     150     160
m537.pep      TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA
              |||||
a537           TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN
              130     140     150     160     170     180

a537           GRFERHCAQGRNQPEAGRKYRNRACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE
              190     200     210     220     230     240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

```

g538.seq
1  atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
51  cgtcatgctg gtgggcgtaa tgttgataa agatgatacg ggcagcaatg
101 ccgcccgtct gaacggtttt cagacggcat tggcggaaagc cgtcgagctg
151 gtcaaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaagcgca
201 ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcgagctgt
251 cggaagcagt tgccgcagac ggcattgatt tggtcgtatt caaccacgaa
301 cttactccca cgcaggaacg caatttgaa aaaatcctcc aatgccgcgt
351 attggacaga gtggggctga ttctggcgat ttctgcccgc cgcgcccgc
401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttggcg
451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggat
501 cggcatgaaa gggccgggcg aaaccaaact ggaaaccgac cgccgattaa
551 ccgcccacat gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
601 cagcgcgccc tgcgcgcgaa gtcccgcgag tcgggcagaa tcaaaacgtt
651 tgcgctggtc ggctatacca atgtcgcaa atccagcctg ttcaaccggc
701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
751 acgacggcgc ggcggctgta catcagtcgc gcatgcagca ttatcctgac
801 cgataccgtc ggattcgta cgcgctgccc gcacaaactg atttccgcct
851 tttccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcagctc
901 gtcgatgctg ccgcccggaa cagcgggcag cagattgaag acgtggaaaa
951 cgtactgcaa gaaatccatg cccacgatat tccgtgcatc aaggtgtaca
1001 acaaaaccga cctgctgccc tctgaagaac aaaacacggg catatggcgc
1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaatac

```

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

g538.pep

```

1  MSGRTGRNSA TQAQPERVML VGVMLDKDDT GSNAARLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHE
101 LTPTQERNLE KILQCRVLDR VGLILAI FAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLTAHRINA LKKQLANLKK
201 QRALRRKSRE SGRIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
251 TTARRLYISP ACSIIILDTV GFVSDLPKHL ISAFSATLEE TVQADVLLHV
301 VDAAARNNGSQ QIEDVENVLQ EIHADHIPC I KVYNKTDLLP SEEQNTGIWR
351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

m538.seq

```

1  ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGTAGTG
101 CCGCCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CAGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACACGAA
301 CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTsa AATGCCGCGT
351 ATTGGACAGG GTAGGGCTGA TTCTGGCGAT TTTCGCTCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CGCAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGCGGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAAC TGGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCCGCAA GTCnCGCGAA TCGGGCACAA TCAAAACGTT
651 TGCGCTGGTC GGCTATACAA ATGTCGGAAG ATCCAGCCTG TTCAACCGGC
701 TGACAAAGTC GGGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
751 ATTATCCTGA CCGATACCGT CGGATTCGTn AGCGATCTGC CGCAcAAACT
801 GATTTCCGCC TTTTCgCC.A CGCTGGAAGA AACCGCGCAA GCCGATGTGC
851 TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
901 GACGTGGAAG ACGTACTGCA AGAAATCCAT GCCGGCGATA TTCCGTGCAT
951 cAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
1001 GCATATGGCG CGACGCTGCG GGAAAAATTG CCGCCGTCCG CATTTCGTT
1051 GCTGAAAATA CCGGTATAGA CGCACTGCGC GAAGCcATTG CCGAGTCTTG
1101 TGCCGCCGCA CCAAACACAG ACGAAACCGA AATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

m538.pep

```

1  MTGRTGGNGS TQAQPERVML VGVMLDKDGT GSSAARLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHE
101 LTPTQERNLE KELKCRVLDR VGLILAI FAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LIKQLANLKK
201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDKLSPECS
251 IILTDTVGFV SDLPKHLISA FSXTLEETAQ ADVLLHV VDA AAPNSQQQIE
301 DVENVLQEIH AGDIPCIKVY NKTDLLPSEE QNTGIWRDAA GKIAAVRISV
351 AENTGIDALR EAIAESCAA PNTDETEMP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
	: : : :					
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPPTQERNLEKELKCRVLDR					
	: :					
g538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPPTQERNLEKILQCRVLDR					

812

	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQ EGR LQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQ EGR LQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQ RALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQ RALRRKSRESGRIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGFVSDLP HKLISAFSXTLEETAQADVLLHV					
g538	AKDQLFATLDTTARRLYISPACSIILTDTVGFVSDLP HKLISAFSATLEETVQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEI HAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQQIEDVENVLQEI HAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
g538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1  ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCCA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTTGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCGCCCCG CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGCGG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TGCGCCGCAA GTCCCGCGAA TCGGGCACAA TCAAAACGTT
651 TGCGCTGGTC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCTGCA GCGATCTGCC GCACAACTG ATTTCCGCCT
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA
951 CGTACTGCAA GAAATCCATG CCGGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGA CCGTCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1  MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLVVFNHE
101 LTPTQERNLE KILQCRVLDR VGLILAI FAR RTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

```

813

201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILTDTV GFVSDLPKLI SAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERV	MLGVMLDKDGTGSSAAR	LNGFQTALAEAVELVKA	AGGDSVR		
a538	MTGRTGRNGSTQAQPERV	MLGVMLDKDGTGSSATRL	NNGFQTALAEAVELVKA	AGGDSVR		
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTG	KAAELSEAVAADGIDL	VFNHELTPTQERNLEKEL	KCRVLD		
a538	VETAKRDRPHTALFVGTG	KAAELSEAVAADGIDL	VFNHELTPTQERNLEKIL	QCRVLD		
	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRL	QVELAQLSHLAGRLIRGY	HLQSQRGGIGMKGPGETK	LETD		
a538	VGLILAI FARRARTQEGRL	QVELAQLSHLAGRLIRGY	HLQSQRGGIGMKGPGETK	LETD		
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANL	KKQALRRKSRESGTIKTF	ALVGYTNVGKSSLFNRLT	KS		
a538	RRLIAHRINALIKQLANL	KKQALRRKSRESGTIKTF	ALVGYTNVGKSSLFNRLT	KS		
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSI	IILTDTVGFVSDLPKLI	SAFSXTLEETAQADVLLH	V		
a538	AKDQLFATLDTTARRLYI	SPECSIILTDTVGFVSDLP	KLISAFSATLEETAQADVLL	HV		
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQ QIEDVENVL	QEIHAGDIPCIKVYNKTD	LLPSEEQNTGIWRDAAGK	IAAVR		
a538	VDAAAPNSGQ QIEDVENVL	QEIHAGDIPCIKVYNKTD	LLPSEEQNTGIWRDAAGK	IAAVR		
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAE	SCAAAPNTDETEMPX				
a538	ISVAENTGIDALREAIAE	YCAAAPNTDETEMPX				
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

```

1  atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca taccagtcgc ggcaacggca
101 aggcggacga tgtattgttt gcgttccttt tggttggcgg cttcgatttt
151 ttgcgcgtca taggggtgcgg cgggtgtacc tgtctgccgg attttcaaca
201 gaatgtcggg gaggcggatt ttgccgtcgt cccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaaat ccgctgagca
351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggatttg
401 acttcgggca ggtcgtagag gcggatttgg tcgaggattt cttgaggcgg
451 cagttcgggt ttttcgcgtg cggcgggtgc tcgtttgtaa taactgccca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggg cttcgccttc gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtgga aacaggtttt tttcatggca tttcgggttc

```

814

```

651 gtctgtgttt ggtgcggcgg cacaatactc ggcaatggct tcgcgagctg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tgttcttcag acggcagcag
801 gtcggttttg ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgct gttccgggcg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgcacgg tttcttccaa
951 ggtggcggaa aaggcggaaa tcagtttgtg cggcagatcg ctgacgaatc
1001 cgacggtatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgcgctcg tgtcgagagt ggcgaaaagc tggctcttcg catatatgcc
1101 cgacttggtc agccggttga acaggctgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

```

g539.pep
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVQ ADLVEDFLGR
151 QGFFFRVGGG SFVITAGAGI DDALCDCLTA DAAGFAVFAF VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPFLRA
301 AASTCSSTS ACTVSSKVAE KAEISLCGRS LTNPTVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

```

m539.seq (partial)
1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTTCGATTTT
151 TTGCGCGTCA TAGGGTGC GG GTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAc GCGGCaGcGg
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAACACCGC CTCGCGCGTG CCGCGTGGG TTTCCACAAA GTCGGAGTGG
401 ACTTCGGGCA GGTCTGACAG CCGGATTGG TCGAGGATT CTTGGGGCGG
451 CAgCTCGGTT TTTTGCGCGT CGGCGGTGCG TTGTTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaAgG
551 GTTCGCGGTT CTTCTGTTTC GTAACGGACA GTCAGGTGGA GGTGTTTCGGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGCTATACCC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTTT
751 CCCGCGAGCGT CGCGCCATAT GCGCGTGTTC TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CGGCAGATCG CTnACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

```

m539.pep (partial)
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR
151 QLGLFRVGGG LFVITAQARV NNALCDRLTA GAQGFVAVFV VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTCSSTS ACAVSSSVAX KAEISLCGRS LTNPTVSVRI MLHSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

```

m539/g539
10 20 30 40 50 60
m539.pep MEDLQEIGFDVAAVKVGRQREHHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
|||||
g539 MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```

815

	10	20	30	40	50	60
m539 . pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDPFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
m539 . pep	130	140	150	160	170	180
	LARAAGVGHKVGGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGFHKVGGLDFGQVVQADLVEDFLGRQFGFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
m539 . pep	190	200	210	220	230	240
	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMVFVGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
m539 . pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHMVFVFCSSDGRSVLLYTLMHGISPAWISCSFTSTSSICCPFLGA					
g539	ATEMRTAAIFPAASRHMVFVFCSSDGRSVLLYTLMHGISWAWISCSFTSTSSICCPFLRA					
	250	260	270	280	290	300
m539 . pep	310	320	330	340		
	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVVSRVAKS					
	310	320	330	340	350	360
g539	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539 . seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGCGCGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGCGG CCGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTG TACGCAAAAG
301 CTGCTGTTCG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCGC CTGCGCGGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTTCGTACG GCGGATTTGG TCGAGGATT CTGGGGCGG
451 CAGTCGGTT TTTTGCGCGT CCGCGGTGCG TTGTTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTCGTTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGCG GGCAATTTT
751 CCCGACGCGT CGCGCCATAT GCCCGTGTTT TGTTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CGGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GGCGAAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539 . pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

```

816

```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFLRVGGA LFVITAQARV NNALCDCLTT GAAGFAVVFV VTDGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTCSSTS ACAVSSVAE KAEISLCGRS LTNPTVSVRI MLHSGLMYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

```

              10      20      30      40      50      60
m539.pep      MEDLQEIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLFAFFLVGGFDLRLVIGCGGVA
              |||||
a539           MEDLQEIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLFAFFLVGGFDLRLVIGCGGVA
              10      20      30      40      50      60

              70      80      90     100     110     120
m539.pep      YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
              |||||
a539           YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
              70      80      90     100     110     120

              130     140     150     160     170     180
m539.pep      LARAAGVGHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA
              |||||
a539           LARAAGVGHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDCLTT
              130     140     150     160     170     180

              190     200     210     220     230     240
m539.pep      GAQGFAVVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS
              || |||||:|:|:| ||||| ||||| ||||| |||||
a539           GAAGFAVVFVFTDGMQVFGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS
              190     200     210     220     230     240

              250     260     270     280     290     300
m539.pep      ATEMRTAAIFPAASRHMPVFCSSDGRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA
              |||||
a539           ATEMRTAAIFPAASRHMPVFCSSDGRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA
              250     260     270     280     290     300

              310     320     330     340
m539.pep      AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG
              |||||
a539           AASTCSSTSACAVSSSVAEAEISLCGRSLTNPTVSVRIMLHSGMLYSRRRAVVSSVAKS
              310     320     330     340     350     360

a539           WSFAYMPDLVSRLNRDLPTLVX
              370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq

```

1  atgccgcct cccgacgcg caacgggggtg ttttatcaaa acggcaaaact
51 tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101 tgccggtgcc gaaccgatg ccgtctgaac cttcagacgg catcggtgtg
151 ttattgtcc actcggacgg gtgcagggtc gtattgtgtc gattcgtcgc
201 cgtaatacag cacgccgagt ttgacgggga tgcgtccctg cgatttgcg
251 tggcggttg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg
301 gtagaagttt tcgcggttgc tgatttcaat catacgcgcg ccgccgcgcg
351 ctttgcgcca gttgaagtcc caataggcca catcatcgta aggcgcggcg
401 gcacggtgtc cgcagtcgtt gatttgcgcc atatttttcc agcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

g540.pep

```

1  MPPSRNGV FYQNGKLANA VSACRLPNRQ TFPVPVNPMP PSEPSDGIGC

```

```
m540.seq (partial)
1 ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTTGT
51 CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCTGC GCCGTAATAC
101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTGC GGTGGGCATT
151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCTCTG TGGTAGAAGT
201 TTTACGCTTT GCTGATTTC ATCATGCGCG CGCTGCCGCC GCCTTTGCGC
251 CAGTTGAAAT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
301 TCCGCAGTCG TTGATTTGCG CCATATTTTT CCAGCGTGA
```

```
m540.ppe      (partial)
      1      ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
     51      GIPQGIGTTA IFLLEVETFT ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
    101      SAVVDLRHIF PA*
```

```
m540/g540
```

.

```
m540.pep      10      20      30  
PNPMPSEPSDGIGCLFVHHPDGGRFVLCRFV  
g540          10      20      30      40      50      60  
GNGVFYQNGKLANAVSACRLPNRQTFFVPVPPNPMPSEPSDGIGCLFVHSDGCRFVLCRFV
```

40 50 60 70 80 90

```
m540.pep  
AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNFHAAAAAFAPVEIPIH  
g540          70      80      90     100     110     120  
AVIQHAEFDGDA SLRFAVGVGIAQGIRAAAVFLLEVFVAFADFNFHTRAAAAFAFVEVPIG
```

100 110

```
m540.pep  
HIIVRRGGAVSAVVDLRHIFPAX  
g540        130     140  
HIIVRRGGTVSAVVDLRHIFPAX
```

a540.seq	1	51	101	151	201	251	301	351	401
	ATGCCGTCCT	TGCCAATGCG	TGCCGATGCC	TTATTGTGCC	CGTAATACAG	TGGGCGTTGG	GTAGAAGTTT	CTTTGCGCCA	CGCGGCGCG
	CCCGACGCGG	GTTTCGCGATT	GAACCCGATG	ACCCGGATGG	CACGCCGAGT	AATCCCTCAG	TCACGTTTGC	GTTGAAATCC	GCGAGTCGTT
	CAACGGGGTG	GCAGATTGCC	CCGTCTGAAC	GTCCAGGTTT	TTGATGGGGA	GGAATAGGCA	TGATTTCAAT	CAATACACCA	AATCTGGTTC
	TTTTATCAAA	AAACCGGCAA	CTTCAGACGA	GTATTGTGTC	TTCTGCCCTG	CAACCGCAAT	CATACGCGCG	CATCATCGTA	ATGTTTTTCC
	ACGGCAAAC	ACCTTTCCCG	CATCGGGTGT	GATTCGTCGC	TGATTTGCGG	ATTCTGCTG	CTGCCGCCGC	AGGCGGGCG	A

a540.pep (partial)

1	MPSSRRGNGV	FYQNGKLANA	VSDCRLPNRQ	TFVPMPNPM	PSEPSDGIGC
51	LFVHPDGCRF	VLCRFVAVIQ	HAEFDGDSAL	*FAVGVGIPQ	GIGTTAIFLL
101	VEFTFADFN	HTRAAAFAP	VEIPIHHIIV	RRGGAAAADV	NLVHVEP

818

m540/a540 92.8% identity in 111 aa overlap

```

                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                |||||
a540      GNGVIFYQNGKLANAVSDCRLPNRQTFVPMPNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHARAAAFAPVEIPIH
                                |||||
a540      AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHTRAAAFAPVEIPIH
                                70      80      90      100     110     120

                                100     110
m540.pep      HIIVRRGGAVSAVVDLRHIFPAX
                                |||||
a540      HIIVRRGGAAAVNLVHVFP
                                130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

```

g542.seq
1  atgccgaaat ggtcgcgcat acggcggttc agcgtccttt cgctgatgtt
51 cagcgcggct gtcagccggt tgacttggtg tgcgccgccg tcgaacgcgg
101 cattcagggt gcggctgaag tcttcagacg gcatagcgtc tgcttcgcc
151 gtttgccccg ccgccggctc gatgccgtct gaaaccgtgt cccacaaatc
201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatggt tcgccccaaat
251 gcccctttgg gacggtttgc aggcaggatg ccgccaagcc gcgcaggttt
301 gggggcaaat cccatatacct gaccggttcg cggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

```

g542.pep
1  MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFRVLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
101 GKGSHILTGS R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

```

m542.seq
1  ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
51  CAGCGCGTCT GTCAGCCGGT TGACTTGGTG TGCGCCGTCG GCAAACGCGG
101 CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCGG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
301 GGGGGCAAAT CCCATATCCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

```

m542.pep
1  MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVLK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRAMF RPNAPLGRNV SPKCPFGTAF
101 RQDAAKPRRF GKGSHILTGS R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

```

m542/g542

                                10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSASVSRLTWCAPSANAAFRVLKSSDGIASASAVCPAAGPMPS
                                |||||
g542      MPKWSRIRRC SVLSLMFSAVVSRLTWCAPP SNAAFRVLKSSDGIASASAVCPAAGSMPS
                                10      20      30      40      50      60

                                70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASXRNVS PKCPFGTAFRQDAAKPRRF GKGSHILTGSRX

```

819

```

|||||
g542      ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100      110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1  ATGCCGAAAT GGTGCGCAT ACGGCGTTGC AGCGTCCTTT CGCTGATGTT
51  CAGCGTGTCT GCCAGCCGGT TGAATTGATG TGCGCCGCCG GCAAACGCGG
101 CATTCAAGAT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG GCGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTT
301 GGGGGCAAAT CCCATATCCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1  MPKWSRIRRC SVLSLMFSVS ASRLT*CAPP ANAAFRMLK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF
101 GKSHILTGS R*

```

m542/a542 94.6% identity in 111 aa overlap

```

              10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSVSASRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
              |||||
a542           MPKWSRIRRC SVLSLMFSVSASRLTXCAPANAAFRMLKSSDGIASASAVCPAAGPMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASXRNVS PKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              |||||
a542           ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1  atggtttgtc gggtatttgc cgcggttttt gggtttcaac tcggcaatca
51  gcccgatgat gcctttggct ttgatgattt cgcgcaattg gttgcggtac
101 acggttaacca ggctcgtgcc ttgatggcg acgttgtagg tacggtattt
151 gccgcccgtt tggtaggttg taaagtccat attgacgggc ttctgaccgg
201 ggatgccgac ttcggcacgg acgacgattt ccttgccgcc cttattgacg
251 atgggattgt ctttgacgtt gacggtcgcy tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattctttg gccaacgctt
351 gtttttgcgc gtcggacgcy gtacgccaag gggtgccgac cgccaatgcy
401 gtcatacggt ggaaatcgaa ataggggaacc gcataggctt cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgtttttgag gatgggtcaa acctgtgtgg
501 cgttttggcg gatttgtccc actgcgtcgg ccggggaggc aaatgccatg
551 ccgatgctca aaataccgat gcccaatgcy ctgatgaagg aggatTTTTT
601 cagcatgtct ttcctgaaaa tggatgtgta tgtttattct gcggctTTTT
651 ccgcatgtcc gccctcagcy tttttctcgg cgaagctggt catgaattta
701 ccgatcaggt ttccagaac cattgcagaa ctgggttacg agatggtgtc
751 gccggcagca aggttttccg tatcgccgcc ctgctgcagc ccgatgtact
801 gttcgcccaa aagtcccga gtcaggattt gcgcggaaac gtcactgctg
851 aactgatact tgccgtccaa atcaaggcgc accctcgcct gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgcc gaccaatacg cctgcggatt
951 tgacgggggc attgacctc aaaccgcca tgctgcggaa atcggcataa
1001 acggcgtaag ttttgtccga accgccgaac gccgcgccgc ccgccacgcy
1051 gaaagcgaga aaggcaaccg ccgcccgcgc gatcaagacg aacagtccga
1101 cccaaaattc caatatgttc tttttcatta a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1  MVCRLFAAVF GFQLGNQPVDF AFGFDDFAEL VAVHGNQARA FDGDVVGTVF

```


820

```

51  AAALVGGKVH IDGLLTGDAD FGTDDDFLAA LIDDGIVFDV DGRVFEFQHR
101 AGIGADQQGL KFFGQRLFLR VGRGTPRVAD RQCGHTLEIE IGNRIGFGFW
151 ACRSRVAAFE DGQNLGCVLA DLSHCVGRGG KCHADAQNTD AQCADEGGFF
201 HDVFPENGCV CLFCGFFRIA ALSVFLGEAG HEFTDQVFQV HCRTGYGDGV
251 AGSKVFRIAA LLQPDVLFQA KRSRQDLRGN VTAEILILAVQ IKAHPRLIGF
301 RVKPSADAP DQYACGFDGG IDLQTADVAE IGINGVSFVR TAERRAARHA
351 ESEKGNRRRA DQDEQSDPKF QYVLFH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1581>:

```

m543.seq
1  ATGGTTTGTC GGTATTGTC CGCCGTTTTT GGCTTTCAAC TCGGCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 GTACGCCGAC TTCGCGCGCG ACGATGATTT CTTTGCCGCG TTTATTGACG
251 ATGGGATTGT CTTTGACGTT GACGTTGGCG TTTTCTAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGTTTGG AAATTCCTTG GCCAACGCTT
351 GTTTTTCGCG GTGCGACGCG GTGCGCCAAG GGTGCGCGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGAGCGGTG TTGGCATCGC CGTTTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTGACG GATTTGCTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAGGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGCGCG
651 CTTTTCCGC ATTGCCGCG TCGGCATTT TCTCGGCAAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCGG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTTGCGC GGAAACGTCG
851 CTGCTGAACT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTGCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCGTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTCT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:

```

m543.pep
1  MVCRLFAAVF GFQLGNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGYAD FGADDDFFAA FIDDGIVFDV DVGVFQFQHR
101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 ASGVGIAVFX DAQYLSGVLT DLAYRVGRGG KCHADAQNTD AQCADEGGFF
201 HDXVSXFEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRGTGYD
251 GVAGSKVFRV AALLQPDVLL AQKRSRQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQADV AEINGVVSF VRTAERRTAG
351 HAESEKGNRR RANQDEQSDP KFQYVLLH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

```

m543/g543
10      20      30      40      50      60
m543.pep MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g543      MVCRLFAAVFGFQLGNQPVDAFGFDDFAELVAVHGNQARAFDGDVVGTVFAAALVGGKVH
10      20      30      40      50      60

70      80      90      100     110     120
m543.pep VDGFLPGYADFGADDDFFAAFIIDDGIVFDVDVGVFQFQHRAGIGADQQGLKFFGQRLFLR
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g543      IDGLLTGDADFGTDDDFLAALIDDGIVFDVDGRVFEFQHRAGIGADQQGLKFFGQRLFLR
70      80      90      100     110     120

130     140     150     160     170     180

```

821

```

m543.pep  VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g543      VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLCGVLADLSHCVGRGG
          130      140      150      160      170      180

          190      200      210      220      230      239
m543.pep  KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIAAGVIFLGKTRHEFADKV
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g543      KCHADAQNTDAQCADEGGFFHDX--FPENGCVCLFCGFFRIAALSFLGEAGHEFTDQV
          190      200      210      220      230

          240      250      260      270      280      290      299
m543.pep  FQNHCRGTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSQDLRGNVAELILAVQIEAHPRL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g543      FQNHCRGTGYGDGVAGSKVFRVAALLQPDVLLFAQKSRSQDLRGNVTAELILAVQIKAHPR
          240      250      260      270      280      290

          300      310      320      330      340      350      359
m543.pep  IGFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNR
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g543      IGFRVKPDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRAARHAESEKGNR
          300      310      320      330      340      350

          360      370      379
m543.pep  RRANQDEQSDPKFQYVLLHX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g543      RRADQDEQSDPKFQYVLFHX
          360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1  ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTTTAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATTCCTTG GCCAACGCTT
351 GTTTTTGCGC GTCGGACGCG GTGCGCCAAG GGTTGCCGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGGGCGGTG TTGGCATCAC CGCTTTTTTA GATGCTCAAT ACTTGAGTGG
501 CGTTTTGACG GATTTGGTTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCCTAGTT TGAATATGAT GGCATACGTT TATTGCGCGG
651 CTTTTTCCGC ATTGCCGCCG TCGGCATTTT TCTCGGCAAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCGG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTCG
851 CTGCTGAAC TACTTTGCC GTCCAAATCG AGGCGCACC TCGCCTGATA
901 GGATTTCCGG TCAAGTCCGA TAGCGCCGAC GCGCCGACC AATACGCCGT
951 CGGATTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATTCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1  MAYGLLAHVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQQL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVL DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRGTGYGD
251 GVAGSKVFRV AALLQPDVLL AQKSRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTADV AEIGINGVSF VRTAERRTAG

```

822

351 HAESEKGNRR RANQDEQSDP KFQYVLFH*

m543/a543 96.0% identity in 378 aa overlap

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGGEVH					
a543	MAYGLLAAXSLQLXNQSVHAFRDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGGEVH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFIIDGIVFDVDVGVFQHRAGIGADQQGLKFFGQRLFLR					
a543	VDGFLPGXADFGADDDFFAAFIIDGIVFDVDVGVFQHRAGIGADQQGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m543.pep	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAXFXDAQYLSGVLTDLAYRVGRGG					
a543	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIAAVGI FLGKTRHEFADKVF					
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGIRLFGGFFRIAAVGI FLGKTRHEFADKVF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m543.pep	QNHCRGTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSQDLRGNVAAELILAVQIEAHPRLI					
a543	QNHCRGTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSQDLRGNVAAELILAVQIEAHPRLI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m543.pep	GFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
a543	GFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
	310	320	330	340	350	360
	370	379				
m543.pep	RANQDEQSDPKFQYVLLHX					
a543	RANQDEQSDPKFQYVLFHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

```

1  atgaaaaaaa tactcaccgc cgccgcgctc gactgatcg gcatcctcct
51  cgccaccgct ctcacccccg acagtaaaac cgcgcccgcc ttctccctgc
101 cggacctgca cggaaaaacc gtttccaacg ccgacctgca aggcaaagtc
151 accctgatta atttttgggt tccctcctgt ccgggttggtg tgagcgaaat
201 gccccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251 tcctcgccgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaagact acggactgcc gtttaccgct atttatgatg cggacaaagc
351 cgtcggacag gcattcggca cacagggtta tccgacttcc gtccttatcg
401 gcaaaaaagg cgaaatcctc aaaacttatg tcggcgaacc cgatttcggc
451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:

g544.pep

```

1  MKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
51  TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1587>:

1	ATGAwAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCmTCCCG	ACAGCAAAC	CGCGCCCGCC	TTCTCCmTGC
101	CCGACCTGCA	CGGAAAAACC	GTTTCCAACG	CCGACCTGCA	AGGCAAAGTA
151	ACCCTGATTA	ATTTTTGGTT	TCCCTCCTGT	CCGGTTGTG	TGAGCGAwAT
201	GCCCAAAATC	ATTA AACCG	CAATGACTA	TAAAwCAAA	AACTTCCAAG
251	TACTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAATAAGG	CGAAATCTTC	AAAACCTACG	TCGGCGAACC	CGATTTCGGC
451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	GCgCAATAG	

MS111_F09
1 MXKILTAAVV ALIGILLAIV LXPDSKTAPA FSXPDLHGKT VSNADLQGKV
51 TLINFWFSPSC PGCVSXMPKI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIQK*GEIF KTYVGEPDFG
151 KLYOEIDTRV AQ*

m544/q544

	10	20	30	40	50	60
m544 . pep	MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGKVTLINFWFPSC					
	:					
g544	MKKILTAAAVVALIGILLATVLI PDSKTAPAFSLPDLHGKTVSNADLQGKVTLINFWFPSC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544 . pep	PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	: : :					
g544	PGCVSEMPKVTKTANDYKKNKDFQVLAVAQPIDPIESVRQYVKDYGLPFTVIYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544 . pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
	: :					
g544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

1	ATGAAAAAAA	TACTACCCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCATCCCCG	ACAGCAAAC	CGCGCCCGCT	TTCTCCCTGT
101	CCGANCTGCA	CGGAAAAANC	GTTTNCAACG	CCGACCTGCA	AGGCNAAGTT
151	ANCCTGATTA	ANTTTTGGTT	TCCCTCCTGT	CCGGGTGTGA	TGAGCGAAAT
201	GNCCANAATC	ATTAATAACG	CAAAATGACTA	TAAAAACAAA	AACTTCCAAG
251	TCCTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCTTTATCG
401	GCAAAAAAGG	CGAAATCCTC	AAAACCTTATG	TCGCGCTAAC	CGATTTCCGG
451	AAACTCTACC	AAGAAATCGA	TACCGCGCTG	GCACAATAG	

```

1  MKKILTAADV ALIGILLAIV LIPDSKTAPA FSLSLHGXKX VVNADLQGXV
51  XLIXFWFPSC PGCVSEMXXI IKTANDYKNK NFOVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

```

824

151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544 . pep	MXKILTA	AVVALIG	ILLAIVL	XPDSKT	APAFSXP	DLHGKT
a544	MKKILTA	AVVALIG	ILLAIVL	IPDSKT	APAFSL	SXLHGK
	10	20	30	40	50	60
	70	80	90	100	110	120
m544 . pep	PGCVS	XM PKI	IKTAND	YKXKN	FQVLAV	AQPIDP
a544	PGCVS	EMXXI	IKTAND	YKXKN	FQVLAV	AQPIDP
	70	80	90	100	110	120
	130	140	150	160		
m544 . pep	AFGTQ	VYPTSV	LIGKXG	EIFKTY	VGEPDF	GKLYQE
a544	AFGTQ	VYPTSV	LIGKKGE	ILKTYV	GEPDFG	KLYQE
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547 . seq

```

1  atgttcgtag ataacggatt taataaaacg gtagcgagtt ttgccccaaat
51  cgtcgaaact ttcgacgtat tcttcttttag gaacgattgc gcctttttta
101 cgcagatgaa acagcgggtgc gggtgggtct gctcgttggg atactctcgtt
151 gatataattta caagatgcgg cttcgagatt ccgaaccgct ccttttaaaga
201 gcttggggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
251 ccgaagtcga gatggatgcc cattacttcc cttactcag aaaatattta
301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaaccgaa
401 aaaagcgggt tgttttttgt tgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547 . pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEDMA HYFPLLRKYL
101 KFIMLHIVTN IRVFCVCVKE LLTILVKNLN PNGKKRFVFC C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547 . seq

```

1  ATGTTTCGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTSTA
101 CGCAGATGAA ACAGCGGTGC GGTTGGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCGCT CCTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251 CCGAAGTCGA GATGGATGCT CATTACTTCC CTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTWTTGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG
401 GAAAAAAGCG GTTGTTTTT TGTGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547 . pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEDMA HYFPLLRKYL
101 KFIMLHIFTN IKVFXVCVK ELLTILVKNL SPNGKKRFV CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKT VASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKT VASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
g547	ELLTILVKNLSPNGKKRFVFCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTTCGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACAATTGC ACCTTTTTTA
101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG CTTGAGATT CCGAACCGCT CCTTTAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251 CCGAAGTCGA GATAGATGCT CATTACTTCC CTTACTCAG AAAATATTTA
301 AAATTATATA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTT.TGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTAGT T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT VASFAQIVET FDVFFFRNNC TFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEIDA HYFPLLRLKYL
101 KFIMLHIFTN IKVFXCVCVK ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKT VASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKT VASFAQIVETFDVFFFRNNTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg taccgcgttc ctttttgccg ggcgttttcg tacttgccgc
51  gcttgccgcc tgcaaacctc aagacaacag tgcggcgcaa gccgcttctt
101 caagtgcata cgcgcgggct gcggaaaatg cggcaaagcc gcaaacgcgc
151 ggtacggata tgcgtaagga agacatcggc ggcgatttca cactgaccga
201 cggcgaaggc aagcctttca gcctgagcga tttgaaaggc aaggtcgtga
251 ttctgtcttt cggcttttacg cactgtcccg atgtctgccc gacagggtt
```

826

```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acgggcgggcc aaaacctgcc ggtcatcaag cagcaatacc gcgtggtttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccgggtgc gtatcttatc gataaaaacg gtgagggttg cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

```

g548.pep
  1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ AASSSASAPA AENAAKPQTR
 51 GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QQYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

```

m548.seq
  1 ATGTTTTCGG TACCGCGTTC CTTTTTGCCG GCGTTTTTCG TACTTGCCGC
 51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGATA TGCGTAAGGA AGACATCGGC GCGGATTTCa CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCAATCAAG CAGCAATACc GCGTGGTTTTc
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTCTCTCG
601 CTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

```

m548.pep
  1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKQXTR
 51 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QQYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAAENAAKQXTRGTD					
	:					
g548	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQAASSSASAPAAENAAKPQTRGTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLTYSDTLKQLGGQAKDVKV					
	:					
g548	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTGLTYSDTLKQLGGQAKDVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPEIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSEN					
	:					
g548	FVSIDPERDTPEIIGKYAKQFNPDFIGLTATGGQNLPIVKQQYRVVSAKINQKDDSEN					
	130	140	150	160	170	180

827

```

                190      200      210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                |||||
g548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTC CG TACCGCGTTC CTTTTTGCCG GCGTTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TGCGTAAGGA AGACATCGGC GCGGATTTCA CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCG GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTCTCTCG
601 CCTTACGGA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTTEL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

```

                10      20      30      40      50      60
m548.pep      MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAENAAXQXTRGTDMRKEDIG
                |||||
a548          MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAENAAXQXTRGTDMRKEDIG
                10      20      30      40      50      60

                70      80      90      100     110     120
m548.pep      GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV
                |||||
a548          GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV
                70      80      90      100     110     120

                130     140     150     160     170     180
m548.pep      FVSIDPERDTPEIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNXDDSENYL
                |||||
a548          FVSIDPERDTPEIIGKYAKQFNPDFIGLTATGDQNLPIVKQQYRVVSAKVNXDDSENYL
                130     140     150     160     170     180

                190     200     210
m548.pep      VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                |||||
a548          VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX
                190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51 tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```


828

```

151 caaatctgca atcggacggg ttgccacgcc gctttccatc gctgctttgg
201 cggcagccgt agcgacgcga ggcagcaggc ggaatcgaa cggagtagga
251 atcaggtatt ccgcgccgaa ttcgaatttc ttaccgtaag cggcaaccac
301 ttcttcgggt acttcttcca tcgccaatc tgccaaagca tacacgcagg
351 cgcgtttcat ttcttcgttg atggtggttg cgcgcacatc caacgcgccc
401 cggaagatga acggaagca caatacgttg ttcacttggt tcgggaagtc
451 ggagcggccg gtaccgataa ccacgtccgg acgggtttct ttcgccagcg
501 gcggcaggat ttccgattc gggttggcca tggcgaacac gatgggtttt
551 tcgttcacatc tgttcaacat ttcaggcgtc agcaggtttg cgcggagag
601 gcccaagaag atgtctttgc ctttaaccgc atcggaagt acgcgcggc
651 cgttgctctt aacggcgtag aatttttttg attcgtccat gcggtctttg
701 tcttcgcggg tttggtaaat cacgcctttg gagttgcaaa cggttacgtt
751 ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgcgg
801 cggcacctgc gccggagcac accaaagtcg cttcttcgat tttacggccg
851 gtataacgca gggcgttcaa tacggcggcg gcggtaatga tggccgtgcc
901 gtgctggtca tcatgaaata cggggatttt gcagcgtttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

```

g550.pep
  1 MITDRFHLFH FPVSFIYQSD NKMPPESSD GILTTNGLQL PFAQLGSVSF
 51 QICNRTGCHA AFHRCFGGSR SDARQQAGIE RSRNQVFRAE FEFLTIVSGNH
101 FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QYVVHLVREV
151 GAAGTDNHVR TGFFRQRQD FRIRVGHGEH DGFFVHRVQH FRRQQVCAGE
201 AQEDVFANR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

```

m550.seq (partial)
  1 ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
 51 GTTTGGACTC GTCCATACGG TCTTTGTCTT CGCGGGTTTG GTAAATCAGC
101 CCTTTGGAGT CGCAAACGGT CACGTTTTCG CGTTTCAAGC CCAAATCCAG
151 CAATTGGWTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTTTA CGGCCGGTAA AACGCAKGGC GTTCAATACG
251 GCGGCGGCCG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301 GATTTGTCAG CGTTTGCCTA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

```

m550.pep (partial)
  1 ..DGIGKHALAV VFNGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
 51 QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

```

m550/g550

                                10      20      30
m550.pep                      DGIGKHALAVVFNGVELFGLVHTVFVFAGLVN
                                |||:| |||||:|:|:|:|:|:|:|:|:|
g550                          DGFFVHRVQHFRQQVCAGEAQEDVFANRIGKYAPAVVFNGVEFFGFVHAVFVFAGLVN
                                190      200      210      220      230      240

                                40      50      60      70      80      90
m550.pep                      HAFGVANGHVFAFQAQIQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDGRA
                                |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g550                          HAFGVANGYVFTFQAQIQLVQAGNRGGTCAGAHQSRFFDFTAGITQGVQYGGGGNDGRA
                                250      260      270      280      290      300

                                100
m550.pep                      VLVVVEYGDFAAFAX
                                |||:|:|:|:|:|:|
g550                          VLVIMKYGDFAAFAX

```

310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGACAATA CATTGTTCAC TTGGTTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTTCG
451 CAGCGGCGGC AGGATTTCCG GATTTCGGGT GGCCATAGCG AACACGATGG
501 GTTTTTTCGT CATGGTGTTT AGTATTTTCA GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTG TCTTCAATGG CGTAGAAGTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTTCG GTTTCAGGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTCGTCGTG GAATACGGGG ATTTTGCAGC GTTTCGCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQRTAE DEREAYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVFEV AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYGS GG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```

                                10      20      30
m550.pep                      DGIGKHALAVVFNGVELFGLVHTVFEVFAGL
                                |||
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVFEVFAGL
              170      180      190      200      210      220

                                40      50      60      70      80      90
m550.pep    VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGNDG
              |||
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYGS GGNDG
              230      240      250      260      270      280

                                100
m550.pep    RAVLVVVEYGDFAAFAX
              |||
a550      RAVLVVVEYGDFAAFAX
              290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttggca cgttggtctg
101 atacgcagaa ttctgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcggtat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcgggtc gtccgtcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaaa tagcgggtatc ttggactgca
```

830

451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt
 501 acggcgcatc atctgcggcg gtatagtga ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

m552.pep
 1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
 151 LSGKIAQHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)
 1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
 51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
 151 AATGCCGGAT TTAAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA
 201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
 251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
 301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
 351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
 401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
 451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
 501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG
 551 CCGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)
 1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
 151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	: : : : : :					
g552	MKLKTLLLPFAALALCANAF AAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	: : : : :					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	: : : : :					
g552	YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq
 1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
 51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
 151 AATGCCGGAT TTAAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA

831

```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 CCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLL PFATLALCTNAF AAPPDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

```

m552.pep      10      20      30      40      50      60
                IKLKTLLL PFATLALCTNAFAAPPDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
                |||||
a552           10      20      30      40      50      60
                IKLKTLLL PFATLALCTNAFAAPPDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK

m552.pep      70      80      90      100     110     120
                ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
                |||||
a552           70      80      90      100     110     120
                ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF

m552.pep     130     140     150     160     170     180
                YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTTEELRRIICGGKNPDAG
                |||||
a552          130     140     150     160     170     180
                YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTTEELRRIICGGKNPDAG

m552.pep     190
                CKQAGQVGKRHQKX
                |||||
a552          190
                CKQAGQVGKRHQKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCGCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCACTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLTLLL PFATLALCTN AFAAPPDAS LARWLDTONF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEFN RYRENVKDL ITPEVKQAVR
101 NTLKNAREI YQEEIDGMI AFYGSPVQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

832

```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCC GCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTTAATG CCGGATTATA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTTG ATTACGCCCC AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEFN RYRENVKDL ITPEVKQAVR
101 NTLKLNAREI YTQEEIDGMI AFYGSVPVQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
m552-1	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a552-1.pep	DKALAEMPEAKKDQAAEFN RYRENVKDL ITPEVKQAVR NTLKLNAREI YTQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEFN RYRENVKDL ITPEVKQAVR NTLKLNAREI YTQEEIDGMI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a552-1.pep	AFYGSVPVQS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGKNPD					
m552-1	AFYGSVPVQS VVAKNPRLIK KSMSEIAVSW TALSGKIAQH HLPFTEELR RIICGKNPD					
	130	140	150	160	170	180
	190					
a552-1.pep	AGCKQAGQVG KRHQKX					
m552-1	AGCKQAGQVG KRHQKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaacct gtctttgggc ttgacaaaaa agctgcccgt
51  tatactgcaa acagaagtag cggagtgtgg cttggcatgt ctacgagctg
101 tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatg gggctgacgg gacgggctgt gaggtggat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcgggtatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgcaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgcttt ggaactgtgg ccaaacacgc gtttcgaggc aggggaagaa
451 aagcaggaaa tccgcatacct acccatgttg cgcgggattt ctgggctggg
501 gcggacattg tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgtttgcg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaagt catgataaat gggcacgaca
701 tttacagctt accgccacct ttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggg ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

m553.seq (partial)

1	ATGGATTATT	TATCAAGACT	GTCCTTTGGA	TTTAACAAAA	AGCTACCTGT
51	CATTCTGCAA	ACAGAAAGTTG	CTGAATGTGG	TTTAGCATGC	CTGACATCCA
101	TCTTGTCTTA	TTATGGCTTT	CACACTGATT	TAAGAACGTT	ACGCCAAAAA
151	TACACCTGT	CATTAAAGGG	CGCAAACTCT	GCAGACATCA	TGAGATTTGG
201	CAATGAAGTG	AATTTAACGC	CACGAGCTTT	GCGTTTAGAG	TTAGATTGAG
251	TGTCAAATTT	ACAACTACCC	TGCATTCTCC	ATTGGAAGTT	AAACCATTTT
301	GTTGTACTTT	GTTCCATTTC	CAAAGACAGT	ATCGTCATTA	TGGACCCTGC
351	TGTCGGTATG	CGAAAAATCA	AAATGGACGA	AGTTTCACAA	AAATTCACAG
401	GGATTGCCCT	AGAATTATTC	CCCAATACCC	ATTTTGAAGA	GAAAAAAGAA
451	ACAAAGAAAA	TCAAAATATT	ATCTCTATTA	AGGGGGGG . T	CAGGCTTAAA
501	ACGCTCTTTA	ATTCAAATGC	TTATATTAGC	TATTTCCTTG	GAAGTCTTTG
551	CATTG...				

m553.pep (partial)

```

1  MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYGYF HTDLRRTLQK
51  YTLSLKGANL ADIMRFGNEM NLTPRALRLE LDELSNLQLP CILHWNLNHF
101 VVLCSSISKDS IVIMDPAVGM RRIKMDEVSQ KFTGIALELF PNTHFECKKE
151 TTKIKILSLR RGXSGLKRSR IQMLILAISS EVFAL...

```

Homology with a predicted ORF from *N. gonorrhoeae*

m553/q553

		10	20	30	40	50	60
g553.pep		MDYLQNLSLGLTKKLPVILQTEVAE	CGLACLA	AVAGFYGFYTDLR	LRSKYCL	SLKG	ENL
		:	: :		: :		
m553		MDYLSRLSFGFNKKLPVILQTEVAE	CGLACLT	SILSYYG	FHTDLR	TLRQKY	TLSLKGANL
		10	20	30	40	50	60
		70	80	90	100	110	120
g553.pep		ADIVRFADDMGLTG	RALRLDL	DELGSRL	PCILHWD	LNHFV	LVESVSSDGA
		: : :	:	: : :	:	: : :	:
m553		ADIMRFGNEMNLT	TPRALR	LELDEL	SNLQL	PCILHWN	LNHFVVLCSISKDSIVIMDP
		70	80	90	100	110	120
		130	140	150	160	170	180
g553.pep		RKVKTEEISRKFT	GIALEL	WPNTR	FEAGEEK	QEIRIL	PMLRGISGLGRTLFQ
		: : :		: :	: : :	:	: : :
m553		RKIKMDEV	SQKFTGIA	LELFP	NTHFE	EKKET	KKIKILSLLRGXSG
		130	140	150	160	170	180
		190	200	210	220	230	240
g553.pep		EVFAFLQNV	SFKIGR	GESLAL	IGRSG	CGKSTLL	DILSGNLPPESGKVMINGHDI
		:					
m553		EVFAL					

a553.seq

```

1  ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT
51  TATCCTGCAA ACAGAAATAT CAGAAATGCGG CTTGGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

```

m553/a553 62.7% identity in 51 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

m554.seq.

1	ATGACAGCAC	ATAAAATCCT	GCCCCGTCCTG	CTTTCATCA	TCTTAGGCGT
51	TTCTCACGCA	ACGGCTGCAT	CGCCCGCGCC	CAACAGACCG	ACGGTACACG
101	CCGCCCCCA	GTTCCAAACA	CCCGAAACCC	TCACAGCGGC	ACACATCGTT
151	ATCGACCTT	AAAGCAAACA	GATTTTATCC	GCCAAAACA	TCAATACCC
201	TGTTGAACCG	CGCGCATAA	CCCAACTGAT	GACCGCATAT	CTGGTTTCA
251	AAAACATGAA	ATCGGGCAAT	ATCCAATCTG	AAGAAAACCT	AAAAATACCC

```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTACATC
751 TCCGGCAACG GCAGGCACAT CCTTGTGATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCTACATC ACTCTGCCAC ATAAGGAAGC GAAATGGCA GAACAAATC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IQSEENLKIP
101 ESAWASEGSR MFVRPGDVS TDKLLKGMIA LSANDAALTL AGRLGNGSIE
151 NFVQQMKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKT V RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554 . pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSKQILS					
	: : : : :					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSRQTL					
	10	20	30	40	50	60
m554 . pep	70	80	90	100	110	120
	AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDVS					
	70	80	90	100	110	120
m554 . pep	130	140	150	160	170	180
	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMKEARRLGMKNTVFNPTGLSREG					
g554	TDKLLKGMIALCANDAALTLADRLGNGSIENFVQQMKEARRLGMKNTVFNPTGLGREG					
	130	140	150	160	170	180
m554 . pep	190	200	210	220	230	240
	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
	:					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554 . pep	250	260	270	280	290	300
	SGGYNLAVSYSGNRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					

836

```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554.pep  QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY
           |||||||||||||||||||||||||||||||||||||||||||||||||||||:
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGH
           310      320      330      340      350      360

           370      380      390
m554.pep  TIAEKEIVALENVKKRSRWQRLWACL TGQX
           |||||||||||||:|||||||:|||||
g554      TIAEKEIVALENVKKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554.seq
1  ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201 TGTCGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTCA
251 AAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAAACCT AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCCGGCCGCG TGGGCAACGG CTCGATTGAA
451 AATTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCAG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTCA AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAGCCCG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CTTGTGCATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAAC TGGCATTGCAAG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAACCGT TGCCCAAATG
901 CAAATTTCCG GAGGCAGCAA AAAAACCCTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554.pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IRSEENLKIP
101 ESAWASEGSR MFVRPGD TVS TDKLLKGMIA LSANDAALT AGRLNGSIE
151 NFVQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFNIEQNN RNILLYRDN VNGLKAGHTE SGGYNLAVSY
251 SGNGRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACL TGQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554.pep  MTAHKILPVL LSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a554      MTAHKILPVL LSIILGVSHATAASPAPNRP TAHAAPTFTQ PETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554.pep  AKNINTPVEPAALTQLMTAYLVFKNMKSNG IQSEENLKIPESAWASEGSRMFVRPGD TVS
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
a554      AKNINTPVEPAALTQLMTAYLVFKNMKSNG IRSEENLKIPESAWASEGSRMFVRPGD TVS

```

837

	70	80	90	100	110	120
	130	140	150	160	170	180
m554.pep	TDKLLKGMIALSANDAALTLAGRLNGSIEFVQQMNKEARRLGKNTVFKNPTGLSREG					
a554	TDKLLKGMIALSANDAALTLAGRLNGSIEFVQQMNKEARRLGKNTVFKNPTGLSREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNLKAGHTE					
a554	QVSTAKDLAQLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m554.pep	SGGYNLAVSYSGNGRHILVITLGSESAETRASNKLLNWALQAFDTPKIYPKGKTVAQI					
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASNKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m554.pep	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY					
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY					
	310	320	330	340	350	360
	370	380	390			
m554.pep	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
a554	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatectgct tgccgcccgc atcgctcgcc cgctgcggg cggctttggt
151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggg ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPRTR QEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC TCGCTTGGGC GGCCTGATTT TACTGACCAC
51  CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTCGCAAA AATGTTCCGG GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

838

101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVAAAAGGFVWTSRRQQRQF					
g556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
g556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
g556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAAAC	GCGCTTGGGC	GGCCTGATTT	TACTGACCAC
51	CGCCGTTTTA	AGCCTCATTA	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT
201	CGACATCGAT	CCCGAAAAAG	GCAGAAATCAA	CGAGGCAAAC	CTGCGCCGTA
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC
301	CTGTCGCAAA	AATGTTTCGGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG
351	CCCGACACGT	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC
401	AGAAACGTCC	GCACCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKTCLRGL	GLILLTTAVL	SLIIVLIVDS	WPLAILLAIV	IVAAAAGGFV
51	WTSRRQQRQF	IERLKKFDID	PEKGRINEAN	LRRMYHSGGQ	HQKDAITLIC
101	LSQKCSVDEA	HAMFKKRPTR	QEINQMAAKQ	SRGQKRPHR*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVAAAAGGFVWTSRRQQRQF					
a556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
a556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
a556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

```
g557.seq
1  atgaacaaaa  tattccttac  tgccgcagcc  ttggtgctgg  gcgcgtgcgg
51  tttccacctg  aaaggtgcag  acggcatttc  tccgccgctg  acctaccgga
101 gctggcacat  cgaaggcgga  caggcattgc  aatttccttt  ggaaaccgcg
151 ctgtatcagg  cttcgggcag  ggtggacgat  gctgccggcg  cgcatatgac
201 cctgcgtata  gacagcgttt  cccaaaacaa  ggaaacctat  accgttaccg
251 gtgcggcagt  catcaacgaa  tatcttttga  tattgacggt  tgaagcgcag
301 gtattgaaac  gcggcgcagc  ggtcggcaaa  ccgatgaccg  tgtccgtccg
351 ccgcattttg  gattatgcgc  acaacgaaat  tttgggcaaa  caggaagaag
401 aagaaaccct  gtgggcggaa  atgcggcagg  atgttgccga  acagattgtc
451 cgccgcctga  cctttctgaa  ggcggaatga
```

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..

1	<u>MNKIFLTAA</u>	<u>LVLGACGFHL</u>	KGADGISPPL	TYRSWHIEGG	QALQFPLETA
51	LYQASGRVDD	AAGAQMTRLI	DSVSQNKETY	TVTRA AVINE	YLLILTVEAQ
101	VLKRGEPVKG	PMTVSVRRIL	DYADNEILGK	QEEETLWAE	MRQDVAEQIV
151	RRLTFLKAE*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

1	ATGAACAAAC	TGTTTCTTAC	TGCCGCAGTG	CTGATGCTGG	GCGCGTGCGG
51	TTTCCACCTG	AAAGGTGCA	ACGGCATTTC	TCCGCCGCTG	ACCTACCGGA
101	GCTGGCACAT	CGAAGCGCGA	CAGGCATTGC	GGTTTCTTTT	GGAAACCGCG
151	CTGTATCAGG	CTTCGGGCAG	GCTGGACGAT	GCTGCCGGCG	CGCAGATGAC
201	CCTGCGTATA	GACAGCGTTT	CCCAAAACAA	GGAAACCTAC	ACCGTTACCC
251	GTGCGGCAGT	CATCAACGAA	TATCTTTTGA	TATTGACGGT	TGAAGCGCAG
301	GTATTGAAAC	GCGGCGAGCC	GGTCGGTAAA	CCGATGACCG	TGTCCTGTCG
351	CCGCGTCCTT	GCTTATGCCG	ACAACGAGAT	CTTGGGCAAA	CAGGAAGAGG
401	AAGCGGCATT	TGGGGCGGAA	ATGCGGCAGG	ATGCCGCCGA	ACAGATTGTC
451	CGCCGCCTGA	CCTTTCTGAA	GGCGGAATGA		

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

```
m557.pep.
1  MNKLFLTAAV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA
51 LYQASGRVDD AAGAQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEPVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151 RRLTFLKAE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKLFLTA	AVMLGACG	FHLKGADG	ISPLTYRS	WHIEGGQAL	RFPLETALYQASGRVDD
	:	:	:	:	:	:
g557	MNKIFLTA	AAVLVLGACG	FHLKGADG	ISPLTYRS	WHIEGGQALQ	FPLETALYQASGRVDD
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQM	TLRIDSVS	QNKETYTV	TRA	AVINEYLL	ILTV
	:	:	:	:	:	:
g557	AAGAQM	TLRIDSVS	QNKETYTV	TRA	AVINEYLL	ILTV
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEI	L	LGKQEEEE	AALWAEM	RQDAAEQ	IVRR
	:	:	:	:	:	:
g557	DYADNEI	L	LGKQEEEE	TLWAEM	RQDVAEQ	IVRR
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

840

```

a557.seq
  1  ATGAACAAAC TGTTCCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGC GG
 51  TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101  GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
151  CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
201  CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
251  GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301  GTATTGAAAC GCGGCGAGCC GGTGCGCAA CCGATGACCG TGTCCGTCGG
351  CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401  AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451  CGCCGCCTGA CCTTCTGAA GGCGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

```

a557.pep
  1  MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
 51  LYQASGRVDD AAGAQMTRLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101  VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151  RRLTFLKAE*

```

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHLKGADGISPPLTYRSWHIEGGQALRFPLETA LYQASGRVDD					
a557	MNKLFLTA AV LMLGACGFHLKGADGISPPLTYRSWHIEGGQALQFPLETA LYQASGRVDD					
	10	20	30	40	50	60
m557.pep	AAGAQMTRLRIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGE PVGK PMTVSVRRVL					
a557	AAGAQMTRLRIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGE PVGK PMTVSVRRVL					
	70	80	90	100	110	120
m557.pep	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE X					
a557	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE X					
	130	140	150	160		
m557.pep	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE X					
a557	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAE X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

```

g558.seq..
  1  ATGGATGCTT GTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
 51  CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
101  TGCCCTTATA TACTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
151  CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG
201  ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251  AGTCCATTTT CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301  CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

```

g558.pep..
  1  MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMMPYTFE ELYMLQQGTA
 51  HQAPHCVLPE RGCPPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP
101  LSDGIV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

```

m558.seq..
  1  ATGAATGCTT GTTTTTCGT CATTCCACA CAGGCGGGAA TTCGGAGATT
 51  CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
101  TGCCCTTATA TACTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA
151  CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG
201  ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251  AGTCCATTTT CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301  CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m558/g558

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

m558/a558 70.2% identity in 141 aa overlap

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1649>:

q560.seq

1 atgctcatca tccgcaacct gatttactgg ctgatactct gttccagcct

	10	20	30	40	50	60
m560.pep	MLII RNLIYWLILCSTLIFLPFFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
	:					
q560	MLII RNLIYWLILCSSLIFLPFFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICA KHQSGWETLALQDIFPPQVYVAKRELFKI PFFGWGLKLVKTIGIDR					
	: : :					
q560	GAEHIPDRPSVICA KHQSGWETLALQEIFPPQVYVAKRELFKI PFFGWGLKLVKTIGIDR					

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVIICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1   ATGCTCATCA TCCGCAACCT GATTTACTGG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGAGACGGGG
101 CGCACAAGAT GGCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAATCC  CCTTTTTCGG CTGGGGCTTG AAACGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
401 GGTGGCGCGC CAAAAACGAA GGCTATTGGA TTACCATTTT CCCCGAAGGC
451 ACACGCCCTT CGCCCCGAAA ACGCGGCAAA TACAAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCGCGTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAC  TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAAA TGCGAACACC TCATCGAAAC GCAGCAGCCG CTCATTCCG
701 GCGCAGGCCC GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1   MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAM MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*

```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

844

	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMGKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

```
m561.seq.
1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCCTGCGC AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCCT
301 TCGGACACCC CTCTTGCTTA TGATTTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCCTCCA GTCTTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAAAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCTGC TGTACTGATG CTGTTTTGGC
551 ACCAGATTTC GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTTGTTCCTA TCAAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTTC GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCCCTG CTGTACCAAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTTC CATTTCATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTTC GGGGAAGTACC ATGAGGAAAT CTTCCCCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTTCCTCT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGCGCT
1101 ATCGCTTGCC GGCGCAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAA CCGCCTTTGC
1251 CGAAAACAAA CGGGAGGAAG CCGCAGAAAA CATCAGCTTT ATCAAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTTCCTG
1351 ACCAAAATCA GCAATAAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCGC
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTCGTTCCG GCCGCCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCCCGCGCCA CCCATGTAAA
1551 ATTCACCCCT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTGACACAG GAGAAAATAG GAGAACCCAC GGGCAGCCAT
1651 GTCGGACTGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA
```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

```
m561.pep
1  MILPARFSDG ISLSRLRLKL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFHWQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRKILYDDL EGQVAEQTRS
251 LEKQNQNLT LYTTRDLHQ SYIPQAAEH FLNRILPAVG ADGSRVCLDG
301 GSDVYVSIH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFAENK REEAENISF IKTVGQECYE DVRELLLNFR
451 TKISNKEFPE AVADLFARFT QQTGITVETA WENGSLFPQ EAQLQMIFIL
```

845

501 QESLSNIRKH ARATHVKFTL SEHGGRFTMT IQDNGQGFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS	SVVLTLLLSRL	LENAASVIEE	EAGNLR	MQAY	
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALS	SVVLTLLLSFRL	ENAASVIEE	EAGNLK	MQAY	
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAE	FEKSLKRIAQSDAIHPLIPSDT	PLAYDLIQSMLIIDWQA			
g561	RLAYMAGEGSPRAQIDNQIAE	FEKSLKRISQSDAIHPLIPSDN	PLAYDLIQSMLIIDWQA			
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIE	LFQALENANEKNTWWLRRFQWAIM	MLTLVSSVLM			
g561	NILPPLQAYRRPTQIELYRFAGNIE	LFQALENAGEKNTWWLRRFQWVIM	MLTLVSSVLM			
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRRC	FDPVPEGGTPEFKQVGRCFNQMG	GRKLKILYDDL			
g561	LFWHQIWVIRPLQALREGAERIGRHF	DPVPEDVRPNSNRSGGVSTKWR	SGX			
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQNQNLTLLYQT	TRDLHQSYIPQQA	AHFLNRILPAVGADSGR	VC	LDG	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCCCT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCTTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAACA	TCGAAGTGT	TTTGCAGGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCAATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTACTGATG	CTGTTTTGCG
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTGCGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCCCTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTTCATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCGGATTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCCATT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCCTG	CTTGCAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCTTTTGC
1251	CGAAAACAAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCTC

846

```

1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCAATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCACGCCA CCCATATCAA
1551 ATTCAAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
  1 MILPARFSDG ISLSRLRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
  51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
 101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
 151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
 201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
 251 LEKQNQNLTLYQTTRDLHQ SYIPQQAEEH FLNRILPAVG ADSGRVCLDG
 301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRLLSFPNGISL
 351 DEDDRILLQT LGRQLGVSLA GAKQEEERLL LAVLQERNLIA QGLHDSIAQ
 401 ALTFLNLQVQ MLETAFENK REEAENIGF IKTGVQECYE DVRELLLNFR
 451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
 501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFDI ENIGEPSGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

          10      20      30      40      50      60
m561.pep  MILPARFSDGISLSRLRLKLLTGLWVGLAALSVVLTLLLSLRLLENAASVIEEAGNLRMQAY
          |||||||
a561      MILPARFSDGISLSRLRLKLLTGLWVGLAALSVVLTLLLSLRLLENAASVIEEAGNLRMQAY
          10      20      30      40      50      60

          70      80      90      100     110     120
m561.pep  RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA
          |||||||
a561      RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA
          70      80      90      100     110     120

          130     140     150     160     170     180
m561.pep  HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
          |||||||
a561      HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
          130     140     150     160     170     180

          190     200     210     220     230     240
m561.pep  LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGRLKILYDDL
          |||||||
a561      LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGRLKILYDDL
          190     200     210     220     230     240

          250     260     270     280     290     300
m561.pep  EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQSYIPQQAEEHFLNRILPAVGADSGRVCLDG
          |||||||
a561      EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQSYIPQQAEEHFLNRILPAVGADSGRVCLDG
          250     260     270     280     290     300

          310     320     330     340     350     360
m561.pep  GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT
          |||||||
a561      GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT
          310     320     330     340     350     360

          370     380     390     400     410     420
m561.pep  LGRQLGVSLAGAKQEEERLLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK
          |||||||
a561      LGRQLGVSLAGAKQEEERLLAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK

```

847

	370	380	390	400	410	420
	430	440	450	460	470	480
m561.pep	REEAAENISFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFARFTQQTGITVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m561.pep	WENG SFLPPQEAQLQMIFILQESLSNIRKHARATHVKFTLSEHGGRFTMTIQDNGQGFD T					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLKQDGSFTMTIQDNGQGFD T					
	490	500	510	520	530	540
	550	560	570	580	590	
m561.pep	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKX					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKX					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

```

1  atggcaagcc cgctcgagtct gcctttcaat tcgggcaaga ccaaaccgac
51  ggcttttgcc ggcgcggttt tggtcggaat catgttttcc acgccgctgc
101 gggcgcggcg caggtctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtgcgt ggatggtggt cattgcgcct ttgacgatgc cgacgctttc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tggaaacgac ggtcatgtcg gcggtcagga cgctgtcgtt caccgcgtac
301 acgacggttg catcgacatc gtcgccgccc ggtgcggaaa tgaggacttt
351 tttcgcgcgg ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggg tgcgggtcga gaagaagggg attttgcgcg cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcgttg
601 acggcgacga tttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

```

1  MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNLT LATGERQLVV QEAL ETVMS AVRTLSFTPY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM T KSTPSSFHGS
151 SAGLRVEKKG ILSPLTMR L PWDTSASKR PCTVSNLVRW ALVSR LPLAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

```

1  ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
101 GGGCGCGGCG CAGGTCTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGT CATGTCG GCGGTCAGGA CGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCGCGCCG CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 CCGCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TCGGGTCTGA GAAGAAGGGG ATTTTGTGCG CGTTGACGAT
501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
551 TGTCGAATTT GGT CAGATGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

```

1  MASPSSLPFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNLT LATGERQLVV QEAL ETVMS AVRTLSFTPY

```

848

101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVEKKG ILSPLTMLRP PSWDTASASKR PCTVSNLVRW ALVSRLPLAL
 201 TATSWWS*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	:					
g562	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALTTVMSAVRTLSTPYTTVASTSSPPGAEMRTFFAP					
g562	LTMPTLSLNTLATGERQLVVQEALTTVMSAVRTLSTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPSPWDTASASKR					
g562	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPSPWDTASASKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWWSX					
g562	PCTVSNLVRWALVSRLPLALTATIWSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq
 1 ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC
 51 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
 101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
 151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
 201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
 251 TGGAAACGAC GGTCATGTCG GCGGTCAGGA TGCTGTCGTT CACGCCGTAC
 301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
 351 TTTCCGCGCG CTTTCCAGAT GAACTTTGGC TTTTCTTTG CTGGTGAACG
 401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
 451 TCGGCAGGGT TCGGGGTCNA GAAGAANGG ATTTTGTGCG CGTTGACGAT
 501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG
 551 TGTCGAATTT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
 601 ACGGCACGA TTTGGAGTTG GTCTTGA

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep
 1 MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
 51 VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALTTVMS AVRMLSTFPY
 101 TTVASTSSPP GAEMRTFFAP LSR*TLAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVXKXG ILSPLTMLRP PSWDTASASKR PCTVSNLVRW ALVSRLPLAL
 201 TATIWSWS*

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
a562	MASPSSLSFN SGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60

849

	70	80	90	100	110	120
m562 . pep	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R T L S F T P Y T T V A S T S S P P G A E M R T F F A P					
a562	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R M L S F T P Y T T V A S T S S P P G A E M R T F F A P					
	70	80	90	100	110	120
m562 . pep	L S R W I L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V E K K G I L S P L T M R L P P S W D T S A S K R					
a562	L S R X T L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V X K X G I L S P L T M R L P P S W D T S A S K R					
	130	140	150	160	170	180
m562 . pep	P C T V S N L V R W A L V S R L P L A L T A T S W S W S X					
a562	P C T V S N L V R W A L V S R L P L A L T A T I W S W S X					
	190	200	209			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563 . seq

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1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTTCTTTAT GTTTGGCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCcc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCAGTTT GATGTGGGTA ATcgcGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GGCGTTTGA TTCAAGGCAA TCCTTGGTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTGTAAC CAAATCAACA GCAGCCATCC
501 TTCACAACCT AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAACTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTTAAGATAA GGCAAGGCAA TGCTGTAATC GCCCGACACG
701 GTTTGGATGC CCGTGATACC GATTTACACG GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTC GTAATCAAGG
801 GCAGTTGTTT GCTTCTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCACGATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAGTCAA TATCCGAGT CAAGCCTTGT AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACACTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTCAGG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATTT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACCTTGC AAGCAGGAAA ACGCATTCCG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CGGTACGACA GACATTGGCA CGCAGCACAA TTAAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAACCAA ATCCAAGCCG GGCAAAATGAA TAATATCGGT
1501 ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGGCGA TTAGATACCA ATGACCAAGC
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1851 AGCATTTGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGGTTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAAGTG CGCTTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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2101 GGCGGCCAAT TGCTTGTGCA AACAGAAAAA GACGGTTTGC ATAACGAGCA
2151 AACCTTTTGGC GAGAAGAAAG TCTTCAGCGA AAATGGTAAG TTGCACAACCT
2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA
2251 AATTATACCT TGCCGGAGGA AATCACACGC GACATTTTAC TGGGTTTCACT
2301 TGCCTATGAA TCGCATAGCA AAGCATTAAAG CCGTCATGCG CCCAGCCAAG
2351 GCACTGAGTT GCCACAAAGT AACCAGGGATA ATATCCGTAC TGCGAAAAGC
2401 AACGGTATTT CGCTACCCTA TACGCCCAAT TCTTTTACCC CATTACCCGG
2451 CAGCAGCTTA TACATTATCA ATCTTGCCAA TAAAGGCTAT CTGTGTGAAA
2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGGGTAG TGACTATATG
2551 CTGGGCAGCC TCAAACCTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA
2601 TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA GAGCTGACAG
2651 GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC
2701 TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC TCAGCGTTGG
2751 CATTGCATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT
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2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA
2901 AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT TCAGGCAGCC
2951 TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT TATCAATACC
3001 GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA AATCAGCGGT
3051 TACGGCCACA CAAGACATCA ATAATATTGG CGGCATTCTT TCTGCCGAAC
3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC
3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC
3201 AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA GCGCAGGCAG
3251 GCAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA ATCAGATCAA
3301 GGGCAAACCC GGCTGCAGGC AGGACGCGAC ATTAACCTGG ATACGGTACA
3351 AACCAGCAAA TATCAAGAAA TCCATTTTGA TGCCGATAAC CATACCATCC
3401 GAGGTTCACG GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT
3451 ACCCTatTGT CAGGGAATAA TCTCAATGCC AAAGCTGCCG AAGTCGGCAG
3501 CGCAAAAGGC ACACTTGCCG TGTATGCTAA AAATGACATT ACTATCAGCT
3551 CAGGCATCCA TGCCGGCCAA GTTGATGATG CGTCCAAACA TACAGGCAGA
3601 AGCGGCGGCG GTAATAAATT AGTCATTACC GATAAAGCCC AAAGTCATCA
3651 CGAAACTGCT CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT GTATTGCAGG
3701 CAGGAAACGA TGCCAACATC CTTGGCAGTA ATGTTATTTT CGATAATGGC
3751 ACCCGGATTC AAGCAGGCAA TCATGTTCCG ATTGGTACAA CCCAAACTCA
3801 AAGCCAAAGC GAAACCTATC ATCAAACCCA AAAATCAGGA TTGATGAGTG
3851 CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA AGAAAAACCA
3901 TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCC TGAAAGGCGA
3951 TACCACCATT GTTGCAAGCA AACACTACGA ACAAACCGGC AGCAACGTTT
4001 CCAGCCCTGA GGGCAACAAC CTTATCAGCA CGCAAAGTAT GGATATTGGC
4051 GCAGCACAAA ACCAATTAAA CAGCAAAACC ACCCAAACCT ACGAACAAAA
4101 AGGCTTAACG GTGGGCATTG AGTTCGCCCC TTACCGATTT GGCACAACAA
4151 GCGATTGCCG TAGCACACAA AGCAGCAAAC AAGTCGGACA AAGCAAAAAAC
4201 GACCGCGTTA ATGCCATGGC GGCTGCCAAT GCAGGTGGC AGGCCTATCA
4251 AACAGGCAAA GGCGCACAAA ACTTAGCCAA TGGTACAACC AATGCCAAAAC
4301 AAGTCAGCAT CTCATAACC TACGGCGAAC AGCAAAACCG ACAAAACCACC
4351 CAAGTTCAAG CCAATCAAGC CCAAGCGAGT CAAATTCAAG CAGGCGGCAA
4401 AACTACCCCT TATTGCCGAA GGTGCGGCGA ACAATCCAAT ATCAACATCA
4451 CAGGCTCAGG TGTTTCAGGC AGAGCAGGAA CCGGCCTGAT TGCCGATAAG
4501 CAAATCCATC TGCAATCAGC CGAGCAAAGC AATACCGAAC GCAGCCAAAA
4551 CAAATCAGCA GGCTGGAACG CAGGTGCTGC CGTATCATTC GGACAAGGAG
4601 GCTGGTCATT AGGCGTTGCC GCAGGCGGCA ATGTCGGCAA AGGCTACGGC
4651 TATGGCGATA GCGTAACCCA CCGCCATAGC CATATTGGCG ACAAAGGCAG
4701 CCAAACCCCT ATCCAAAGTG GTGGCGATAC CATCATCAAA GGCAGCGAAG
4751 TACGCGGCAA AGGCGTACAA GTCAATGCCA AAAACCTAAG CATTCAAAGT
4801 GTACAAGATA GAGAACTTA TCAAAGCAAA CAACAAAACG CCGGTGCACA
4851 AGTTACCGTA GGTTATGGCT TCAGTGCCAG TGCGGATTAC AGCCAAAGCA
4901 AAATCCGAGC CGACCATGCT TCGGTAACCG AGCAAAGCGG TATTTATGCC
4951 GGAGAAGACG GCTATCAAAAT CAAGGTCGGA AACCATACAG GCCTCAAAGG
5001 CGGCATCATC ACCAGCAGCC AAAGCGCAAA AGACAAGGGT AAAAAACCAT
5051 TCAGCACAGG CACACTCGCC GGCAGTGATA TTCAAATTA CAGCCAATAC
5101 GAAGGAAAAA GTTTTGGATT GGGTGCCAGC GTTGCCGTAA GCGGCAAAAC
5151 ACTGGGACAG GGCGCAAAAA ATAAACCTCA AGACAAACAC CTGACAAGCA

5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
 5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT
 5301 TCAAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
 5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
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 5451 TGAAGTGGAT TTACAAAGaA CCGTCAGCCA AGATTTTAGT AAAAATGTTC
 5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
 5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
 5601 GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG
 5651 CAGATAATTG GCAACAAGGC AAAGTCATT CTAACATGTT AGCCTCAGGT
 5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
 5751 GCCagA CGTA TCGTATGCGA TTGGACAGCA CTTTAAagaT TTAGCCGGTC
 5801 AAAACGCGAA TGGCAAATA ACCGCCAGTC AagaAACCGC TCACGTTCTT
 5851 CCCCACGCGG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC
 5901 CCCGGCAGGA GCATTGGGTG CGGGCGGGTc ggAagcggCC GCCCCAATCA
 5951 TCGGCAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgcgag
 6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggtA cGgctGCCGG
 6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGGT TGTTTTcaaa
 6101 cggctTCaga TTTTCGTTCC TCTTTTTCAT ATCCTATAAA CATGTGA

This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:
 g563.pcp..

1 MNKTLRYVIF NRKRGA VAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
 51 SKAFCF~~SALG~~ FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTGNIP
 101 QVNIQTPTSA GVSVNQYAF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
 151 TRGEARVVVN QINSSHPSQL NGYIEVGRR AEVVIANPAG IAVNGGGFIN
 201 ASRATLTGQ PQYQAGDFSG FKIRQGNVAV AGHGLDARDT DFTRILLYAN
 251 KITLISTAEQ AGIRNQQLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
 301 TAEHKVNIRS QAFENSGTAV SQQGTQIHSQ SIQNTGKLLS AGTEDLAVSG
 351 SLNNQNGEIA TNQQLIIHDG QQSTVVIDNT NGTIQSGRDV AIQAKSLNN
 401 GTLAADNKL DIALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
 451 IKANNLDNAV QGNIQSGGTT DIGTQHNLTN RGLIDGQQTQ IQAGQMNNIG
 501 TGRIYGDNIA IAATRLDNQD ENGTGAAIAA RENLNLGIEQ LNNRENSLIY
 551 SGNDMAVCGA LDTNDQATGK AQRHNAAGI IEAAGKMRLG VEKLHNTNEH
 601 LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGWVFNYN ESDHLRTPDG
 651 VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
 701 GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHNRYWRARRK GHDETGHREQ
 751 NYTLPEEITR DISLGSFAYE SHSKALSRHA PSQGTLPQS NRDNIRTAKS
 801 NGISLPYTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YRQWLGS DYM
 851 LGSLKLDPN LHKRLGDGYE EORLINEQIA ELTGHRRLDG YQNDEEQFKA
 901 LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVVLVQKEV KLPDGGTQTV
 951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
 1001 DTLDNIGGRI HAQKSAVTAT QDINNIGGIL SAEQTLILLNA GNNINNQSTA
 1051 KSSQNAQGS TYLDRMAGIY ITGKEKGVLA AQAGKDINII AGQISNQSDQ
 1101 GQTRLQAGRD INLDTVQTGK YQEIHFADN HTIRGSTNEV GSSIQTGKDV
 1151 TLLSGNNLNA KAAEVGSAKG TLAVYAKNDI TISSGIHAGQ VDDASKHTGR
 1201 SGGGNKLVI DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVISDNG
 1251 TRIQAGNHVR IGTQTQTSQS ETYHQTQKSG LMSAGIGFTI GSKTNTQENQ
 1301 SQSNEHTGST VGS LKGDTTI VASKHYEQTG SNVSSPEGNN LISTQSM DIG
 1351 AAQNQLNSKT TQTYEQKGLT VGIQFARYRF GTTSDCRSTQ SSKQVGQSKN
 1401 DRVNAMAAN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQONRQTT
 1451 QVQANQAQAS QIQAGGKTTL YCRRCEQSN INITGSGVSG RAGTGLIADK
 1501 QIHLQSAEQS NTERSQNKSA GWNAGAAVSF GQGGWSLGVA AGGNVKGKYG
 1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTI IK GAQVRGKGVQ VNAKNLSIQS
 1601 VQDRETYQSK QQNAGAQT V GYGFASGDY SQSKIRADHA SVTEQSGIYA
 1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFSTGTLA GSDIQNYSQY
 1701 EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH LSIADKNGA SSSVGYGSDS
 1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVTDTAE
 1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDFS KNVQQTNTTEI NQHLDKLLAD
 1851 KEAAETA~~AAE~~ ALANGDMETA KRKAHEAQDA AAKADNWQQG KVILNMLASG
 1901 LAEPTQSGAG IAAATASPDV SYAIGQHFKD LAGQNANGKL TASQETAHVL
 1951 AHAVLGA~~AVA~~ AAXGNNAPAG ALGAGGSEAA APIIGKWL~~YG~~ KGDGGS~~LNAE~~
 2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPINM*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

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1   ATGAATAAAA CTCTCTATCG TGTAATTTTC AACCGCAAAC GTGGGGCTGT
51  GGTAGCCGTT GCTGAACTA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGATTCAGG CAGCGCTCAT GTGAAATCTG TTCCTTTTGG TACTACTCAT
151 GCACCTGTTT GTCGTTCAAA TATCTTTTCT TTTTCTTTAT TGGGCTTTTC
201 TTTATGTTTG GCTGTAGGTA CGGCCAATAT TGCTTTTGCT GATGGCATTAA
251 TTGCTGATAA AGCTGCTCCT AAAACTCAAC AAGCCACGAT TCTGCAAACA
301 GGTAAACGCA TACCGCAAGT CAATATTCAA ACCCCTACTT CGGCAGGGGT
351 TTCTGTTAAT CAATACGCC AGTTTGATGT GGGTAATCGC GGGGCGATTT
401 TAAACAACAG CCGCAGCAAC ACCCAAACAC AGCTAGGCGG TTGGATTCAA
451 GGTAAATCCTT GGTGGCAAG GGGCGAAGCA CGTGTGGTTG TAAACCAAAT
501 CAACAGCAGC CATTCTTCAC AAATGAATGG CTATATTGAA GTGGGCGGAC
551 GACGTGCAGA AGTCGTTATT GCCAATCCGG CAGGGATTGC AGTCAATGGT
601 GGTGGTTTTA TCAATGCTTC CCGTGCCACT TTGACGACAG GCCAACCGCA
651 ATATCAAGCA GGAGACCTTA GCGGCTTTAA GATAAGGCAA GGCAATGTTG
701 TAATCGCCGG ACACGGTTTG GATGCCCCGTG ATACCGATT CACACGTATT
751 CTCAGTTATC ATTCCAAAAT TGATGCACCC GTATGGGGAC AAGATGTTCC
801 TGTCGTCGCG GGACAAAACG ATGTGGTCGC AACAGGTAAT GCACATTCCG
851 CTATTCTCAA TAATGCTGCT GCCAATACGT CAAACAATAC AGCCAACAAC
901 GGCACACATA TCCCTTTATT TCGGATTGAT ACAGGCAAAT TAGGAGGTAT
951 GTATGCCAAC AAAATCACCT TGATCAGTAC GGCCGAGCAA GCAGGCATTC
1001 GTAATCAAGG GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA
1051 AATGGCCGTT TAGTCAATAG TGGCACGATG GCTGCCGCCA ATGCGAAAGA
1101 TACGGATAAT ACAGCGGAAC ACAAAGTCAA TATCCGCAGT CAGGGCGTTG
1151 AAAACAGCGG TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAG
1201 TCGATTCAAA ACACTGGCAC ATTATTGTCC TCAGGCGAAA TATTGATTCA
1251 CAATTTCGGC AGCCTGAAAA ATGAAACATC AGGCACCATT GAAGCCGCTC
1301 GTTTGGCTAT TGATACCGAC ACACTTAATA ATCAAGGCAA ACTCTCTCAA
1351 ACAGGTTTCA AAAAATCCA TATTGATGCA CAAGGCAAAA TGGATAACCG
1401 TGGCCGCATG GGTTTACAAG ATACCGCACC AACCGCGTCA AATGGTTCAA
1451 GCAATCAAAC CGGCAATAGT TACAATGCAT CTTTCCATT CACTACTACC
1501 ACACCAACAA CGGCAACAGG TACGGGTACT GCAACCGTTT CTATATCAAA
1551 CATAACTGCG CCTACCTTTG CTGATGGGAC AATTCGCACT CATGGTGCAC
1601 TGGATAATTC AGGCAGTATT ATTGCCAATG GTCAAACAGA TGTTAGTGCG
1651 CAACAAGGTT TAAATAATGC AGGACAAATA GACATTCATC AGTTAAATGC
1701 AAAAGGTTTC GCGTTTGACA ATCACAATGG AACAATTATC AGTGATGCGG
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1801 CGCCAACAGT TAGAGATTGA AACCGATCAA CTGGATAACG CTCATGGCAA
1851 GTTATTATCA GCAGAAATAG CGGATTTAGC CGTTTCAGGC AGCCTGAACA
1901 ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT TCACGATGGT
1951 CAGCAATCTA CCGCTGTCAT TGATAATACG AATGGCACGA TACAATCAGG
2001 CCGTGATGTT GCTATTCAGG CAAAATCGTT ATCCAACAAC GGCACACTTG
2051 CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATTT TTATGTAGAA
2101 CGCAATATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC GAGGCAGCCT
2151 GAAAAATTCA CATACTTTGC AAGCAGGAAA ACGCATTTCG ATTAAAGCAA
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2251 GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA TTGACGGACA
2301 ACAAACCAAA ATCCAAGCCG GGCAATGAA TAATATCGGT ACAGGTCGGA
2351 TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA CAATCAAGAT
2401 GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGTGAAAACC TGAATTTAGG
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2601 GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT TTGAAAACGC
2651 AGTTGGTAGA AACAGGGCGC GAGCATATTG TTGATTACGA AGCATTTGGA
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2801 AAAATTGGCA TAAATACGAT TATGAAAAAG TCACCCAAAA AACCCAAGTT
2851 ACCCAAACCTG CGCCAGCCAA AATCATTTCA GGTAATGATT TAACCATTTGA
2901 TGGTAAAGAA GTATTTAATA CCGATAGCCA AATCATTGCT GGTGGCAATC
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3001 GAAAAGAAAG TATTCAGTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA
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3101 TGCCGGAGGA AATCACACGC AACATTTCAC TGGGTTCATT TGCCTATGAA
3151 TCGCATCGCA AAGCATTAAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT
3201 GCCGCAAAGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC
3251 CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT
3301 CTTGTTGAAA CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGCGGTAG
3351 TGACTATATG CTGGACAGCC TCAAACCTAGA CCCAAACAAT TTACATAAAC
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3451 GAGCTGACAG GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA
3501 ATTTAAAGCC TTAATGGATA ATGGCGCGAC TCGGCGACGT TCGATGAATC
3551 TCAGCGTTGG CATTGCATTA AGTGCCGAGC AAGTAGCGCA ACTGACCAGC
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3651 ACAAAACCGTA TTGGTGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGACA
3701 TAGACGGTAA AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT
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3801 TATCAATACC GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA
3851 AATCAGCGGT TACGGCCACA CAAGACATCA ATAATATTGG CGGCATGCTT
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3951 AAGCACCACC GCCAGCAGTC AAAATACACA AGGCAGCAGC ACCTACCTAG
4001 ACCGAATTGGC AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA
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4101 ATCAGAGCAA GGGCAAACCC GGCTGCAAGC AGGGCGCGAC ATTAACCTAG
4151 ATACGGTACA AACCAGCAAA CATCAAGCAA CCCATTTTGA TGCCGATAAC
4201 CATGTTATTC GCGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA
4251 AGGCGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGTGCCG
4301 AAGTCAGCAG CGCAAACGGT ACACTCGCTG TGTCTGCCAA AAATGACATC
4351 AACATCAGCG CAGGCATCAA CACGACCCAT GTTGATGATG CGTCCAAACA
4401 CACAGGCAGA AGCGGTGGTG GCAATAAATT AGTCATTACC GATAAAGCCC
4451 AAAGTCATCA CGAAACCGCC CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT
4501 GTATTGCAGG CAGGAAACGA TGCCAACATC CTGGCAGCA ATGTTATTTT
4551 CGATAATGGC ACCCAGATT CAGCAGGCAA TCATGTTTCG ATTTGGTACAA
4601 CCCAAACTCA AAGCCAAAGC GAAACCTATC ATCAAACCCA GAAATCAGGA
4651 TTGATGAGTG CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA
4701 AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT
4751 TGAAAGGCGA TACCACCATT GTTGCAAGCA AACACTACGA ACAAATCGGC
4801 AGTACCGTTT CCAGCCCGGA AGGCAACAAT ACCATCTATG CCCAAAGCAT
4851 AGACATTCAA GCGGCACACA ACAAATTAAA CAGTAATACC ACCCAAACCT
4901 ATGAACAAAA AGGCCTAACG GTGGCATTCA GTTCGCCCCT TACCGATTG
4951 GCACAACAAG CGATTGCCGT AGCACAAGC AGCAAACAAG TCGACAAAG
5001 CAAAAACGAC CGCGTTAATG CCATGGCGGC TGCCAATGCA GGCTGGCAAG
5051 CCTATCAAAC AGGTAAGAGT GCACAAACT TAGCCAATGG TACAACCAAT
5101 GCCAAACAAG TCAGCATCTC CATAACCTAC GGCGAACAGC AAAACCGACA
5151 AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAGCAG
5201 GTGGTAAAAA CACATTAATC GCCACAGGCG CAGCAGAAACA ATCCAATATC
5251 AACATCGCAG GCTCAGATGT TGCCGGCAAA GCAGGCACAA TCCTGATTGC
5301 CGATAACGAC ATCACACTCC AATCAGCCGA GCAAAGCAAT ACCGAACGCG
5351 GCCAAAACAA ATCGGCAGGC TGAACGCAG GTGCTGCCGT ATCATTCGGA
5401 CAAGGAGGCT GGTCAATTAG CGTTACCGCA GGCGCAATG TCGGCAAGG
5451 CTACGGCAAT GGCACAGCA TCACCCACCG CCATAGCCAT ATCGGCGACA
5501 AAGGCAGCCA AACCCTTATC CAAAGCGGTG GCGACACTAC CATCAAAGGC
5551 GCGCAAGTAC GCGGCAAAGG CGTACAAGTC AATGCCAAAA ACCTAAGTAT
5601 TCAAAGCGTA CAAGATAGAG AAACCTATCA AAGCAAACAA CAAAACGCCA
5651 GTGCACAAGT TACCGTAGGT TATGGCTTCA GTGCCGGTGG CGATTACAGC
5701 CAAAGCAAAA TCCGAGCCGA CCATGTTTCA GTAACCGAGC AAAGCGGTAT
5751 TTATGCCGGA GAAGACGGCT ATCAAATCAA GGTGCGAAAC CATACAGACC
5801 TCAAAGGCGG CATCATCACC AGTACCCAAA GCGCAGAAGA CAAGGGTAAA
5851 AACCCTTTTC AGACGGCCAC CCTCACCCAT AGCGACATCA AAAACCACAG
5901 CCAATACAAA GGCGAAAGTT TTGGATTGGG CGCAAGTCG TCCATAAGCG
5951 GCAAAACACT GGGACAGGGC GCACAAAATA AACCTCAAAA CAAACACCTG
6001 ACAAGCGTAG CCGATAAAAA CAGCGCAAGT TCATCAGTGG GTTATGGCAG
6051 CGACAGCGAC AGTCAAAGCA GCATCACAAA AAGCGGCATC AACACCCGCA

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6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
6201 CGAACGACAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
6251 AAAGTGAAGT GGATTTACAA AGAACCGTCA GCCAAGATT TAGTAAAAAT
6301 GTTCAACAAG CCAATACCGA GATTAACCAA CATTTAGACA AACTCAAAGC
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6401 ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TGCGGCAGCA
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6601 GGTCAAACCG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
6701 ATGCTCTAGC AGGAGCATTG AGTGCGGGCG GGTGGAAGC GGCTGCGCCT
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6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
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7001 ATCCTGGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
7051 CAATTAAATT TATTTCTTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTTG
7151 GCAAAGATAT TGCTGTTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAAATACCA
7301 ATAGGTTAAA CACAAAAGAG TTAGTTGGAT TAATTCTGGA AACTTATAAA
7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
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7451 TGATTCACCT AGATAATACT GGTGCCGGAT TTTAAATTCA GCAGAGGAGA
7501 AAACAAATCA GAGCACAAAT TTCAGCCAGA CAATGGAGAA GATAA

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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

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1 MNKTLRYRVIF NRKRGAUVAV AETTKREGKS CADSDSGSAH VKSVFPFGTTH
51 APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIADKAAP KTOQATILQT
101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIO
151 GNPWLARGEA RVVVNQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
201 GGFINASRAT LTTGQPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
251 LSYHSKIDAP VWGQDVRVVA QONDVVATGN AHSPILNNA ANTSNNTANN
301 GTHIPLFAID TGKLGGMYAN KITLISTAEQ AGIRNQQLF ASSGNVAIDA
351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QVENS GTAV SQQTQIHSQ
401 SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQKLSQ
451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSSTT
501 TPTTATGTGT ATVSISNITA PTFADGTIRT HGALDNSGSI IANGQTDVSA
551 QOGLNNAQOI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
601 RQQLIETDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIHDG
651 QQSTAVIDNT NGTIQSGRDV AIQAKSLSNN GTLAADNKLD IALQDDFYVE
701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
751 DIGTQHNLTN RGLIDGQOTK IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
801 ENGTGAAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGGA LDITNGQATGK
851 AQRHINAGAT IEAAGKMRLG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
901 RHELLREGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSFAYE
1051 SHRKALSHHA PSQGTELPQS NGISLPYTSN SFTPLPSSSL YIINPVNKGY
1101 LVETDPRFAN YRQWLGS DYM LDSLKLDPNN LHKRLGDGY EORLINEQIA
1151 ELTGHRRLDG YQNDEEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
1201 DIVVLVQKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKGAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQKSAVTAT QDINNIGGML
1301 SAEQTLLLNA GNNINSQSTT ASSQNTQGS TYLDRMAGIY ITGKEKGVLA
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1451 NISAGINTTH VDDASKHTGR SGGGNKLIVIT DKAQSHHETA QSSTFEGKQV
1501 VLQAGNDANI LGSNVISDNG TQIQAGNHVR IGTQTQSQS ETYHQTQKSG

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Homology with a predicted ORF from *N.gonorrhoeae*

m563/g563

	10	20	30	40	50	
g563.pep	MNKTLYRVIFNRKRGAVVAVAETT	KKREGKSCADSGSGSVYVKSVSFI	PTH-----SKAFC			
m563.pep	MNKTLYRVIFNRKRGAVVAVAETT	KKREGKSCADSDSGSAHVKSVPFGT	THAPVCRSNIFS			
	10	20	30	40	50	60
	60	70	80	90	100	110
g563.pep	FSALGFSLCLALGTVNIAFADGII	ITDKAAPKTQQATILQTGNGI	PQVNIQTPTSAGVSVN			
m563.pep	FSLLGFSLCLAVGTANIAFADGII	IADKAAPKTQQATILQTGNGI	PQVNIQTPTSAGVSVN			
	70	80	90	100	110	120
	120	130	140	150	160	170
g563.pep	QYAQFDVGNRGAILNNSRSNTQT	QLGGWIOGNPWLTRGEARVVVN	QINSSHPSQLNGYIE			
m563.pep	QYAQFDVGNRGAILNNSRSNTQT	QLGGWIOGNPWLARGEARVVVN	QINSSHSSQMNGYIE			
	130	140	150	160	170	180
	180	190	200	210	220	230
g563.pep	VGGRRAEVVIANPAGIAVNGGGF	INASRATLTGQPQYQAGDFSGF	KIRQGNVIAIGHGL			
m563.pep	VGGRRAEVVIANPAGIAVNGGGF	INASRATLTGQPQYQAGDLSGF	KIRQGNVVIAGHGL			
	190	200	210	220	230	240
	240					
g563.pep	DARDTDFTRIL-----					
m563.pep	DARDTDFTRILSYHSKIDAPVWG	QDVRVVAGQNDVVATGNAHSPI	LNNAANTSNNTANN			
	250	260	270	280	290	300
	250	260	270	280	290	
g563.pep	-----LYANKITLISTAEQAGI	RNQQLFASSGNVAIDANGRLV	NSGTM			
m563.pep	GTHIPLFAIDTGKLGMYANKITL	ISTAEQAGIRNQQLFASSGNVA	IDANGRLVNSGTM			
	310	320	330	340	350	360

856

g563.pep	300 310 320 330 340	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----
m563.pep	370 380 390 400 410 420	AAANAKDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG
g563.pep		-----
m563.pep	430 440 450 460 470 480	SLKNETSGTIEAARLAIDTDTLNNQKLSQTSQKLHIDAQGMKNRGRMGLQDTAPTAS
g563.pep		-----
m563.pep	490 500 510 520 530 540	NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSIENITAPTADFRTIRTHGALDNSGSI
g563.pep		-----
m563.pep	550 560 570 580 590 600	IANGQTDVSAQQGLNAGQIDIHQLNAGSAFDNHNGTIISDAVHIQAGSLNNQNGNITT
g563.pep	350 360 370 380	-----EDLAVSGSLNNQNGEIAATNQQLIIHDGQQSTVVIDNT
m563.pep	610 620 630 640 650 660	RQQLIEIETDQLDNAHGKLLSAEIALAVSGSLNNQNGEIAATNQQLIIHDGQQSTAVIDNT
g563.pep	390 400 410 420 430 440	NGTIQSGRDVAIQAKSLNNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS
m563.pep	670 680 690 700 710 720	NGTIQSGRDVAIQAKSLNNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS
g563.pep	450 460 470 480 490 500	HTLQAGKRIRIKANNLDNAVQGNISGGTTDIGTQHNLNTRGLIDGQQTQKIAGQMNNIG
m563.pep	730 740 750 760 770 780	HTLQAGKRIRIKANNLDNAAQGNISGGTTDIGTQHNLNTRGLIDGQQTQKIAGQMNNIG
g563.pep	510 520 530 540 550 560	TGRIYGDNIAIAATRLDNQDENGTTGAAIAARENLNLGIEQLNNRENSLIYSGNDMAVGGA
m563.pep	790 800 810 820 830 840	TGRIYGDNIAIAATRLDNQDENGTTGAAIAARENLNLGIGQLNNRENSLIYSGNDMAVGGA
g563.pep	570 580 590 600 610 620	LDTNDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFF
m563.pep	850 860 870 880 890 900	LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFF
g563.pep	630 640 650 660 670 680	RHELLREGTQHELGFVYNNESEDHLRTPDGAHENVHKKYDYKVTQETQVTGTAPAKIIA
m563.pep	910 920 930 940 950 960	RHELLREGTQHELGWSVYNNESEDHLRTPDGAHENVHKKYDYKVTQKTQVTGTAPAKIIS
	690 700 710 720 730 740	

	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLAHAVLGA AVAAAXGNNAPAGALGAGGSEAAAPIIGKWLYGKGDGGSLSNAE					
	: : : : :					
m563 . pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAPYISKWLYGKEKGSDLTAE					
	2210	2220	2230	2240	2250	2260

	2010	2020	2030	2040	2049	
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFTASDFASSFSYPINMX					
	: : : : : :					
m563 . pep	EKETVTAITNVLTATGA AVGNSATDAAQGSLSNAQSAVENNDTVEQVKFALRHPRIAI					
	2270	2280	2290	2300	2310	2320

m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLFNSEFGGEGGVGNAFRHVLWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

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m564 . seq
1   ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAAATGATA TTGCGGGCTT TGCGGGTTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTC
201 TGCCCTTATC CTGACTTCTT CTTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CTTGGTTGG CAAGGGGCGA AGCACGTGTG GTTGTAACC AAATCAACAG
501 CAGCCATTCT TCACAACTGA ATGGCTATAT TGAAGTGGG GACGACGTG
551 CAGAAGTCGT TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCTGTC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAATCG
701 CCGGACACGG TTGGATGCA CGTGATACCG ATTACACACG TATTCTCAGT
751 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCGT
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTTTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCGA GCAAGCAGGC ATTCGTAATC
1001 AAGGGCAATG GTTTGCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
1051 AAATGGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT
1101 TTCACTTCAT GCCCGCAATG TTCATAATAG CCGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTCAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA
1251 CAACGGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGTA
1351 TCTGCCGCA AATTCGATAA CAGTGGCAAG ATTGGTGTA GTGACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CCGTATCTAA GCCTGGTTCA
1501 AACAAATCCG TTTCACCTAC AGCACCTGCA AAAAATACG CCGTAGGACG
1551 CATTCAAACA ACAGGAGCAT TTGACAATGC AGGATCAATT AATGCGGGTG
1601 GGCAAATTGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG
1651 AATGCGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTAAA
1701 AGGCAAACTC CAGGCACACG ATCTGGCTGT TAACACTCAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAATC CAAACGGCA AGATTGATAA CCGTGAATG
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1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTACAGC
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1951 ACCGTTACCA CCAAGAATAA TCTTCGCAAT ACAGGAAAAG TTTCTGTTGC
2001 ACGACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG
2051 AGGCTGAAAC GGTAAACATC CAAAGTCAGC AACTGACTAA CCAAGACGGC
2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
2151 CCAAACGGC AAATCCTAT CTGCAAACCA AGCACAATTA GCTGTTTCAG
2201 ACGGCTATA CAACCAACAT GGTGAAATTG CCACCAACCG GCAGTTGTCT

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6051 TGAACCTAT CAGAGCAAAC AGCAAAACGG CAATGTCCAA GTTACTGTCG
6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCAC AGCCGCTACG AAGGCAGAA
6351 CTTCGGCATA GGCGGCAGTT TCGACCTGAA CGGCGGCTGG GACGGCACGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCGG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAACAGCT TCGACAAAGA
6651 CGCGGTGCGC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCC
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCG TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAA AGCCGCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGGCGGC GGCACCTCCC
7001 TTGCCGCACC GTATTTGGAC AAAGCGGCGG AAAACCTCGG TCCGGCGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAGATTGG AACAATAGGC
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CTTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAATGACGA GCCTTGTCAG CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA CCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GGCGGGTGCG GGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

```

1 MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51 IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QQPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRRVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGMYANKI TLISTVEQAG IRNQGWQFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNSVIPQ IPSTATSGS STVSVSKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLNCSGL
551 NAAKLRVSGD SFNNTVKGKL QAHD LAVNTQ TAKNSGHLIT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLDNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

```

901	ILLNREETTE	GSTKAGATAA	RKRLDIGAKE	IHNQEGALLS	SEGI FAVGNR
951	LDEQHHAAGM	ADTFVNGSAG	LEVQGDALMS	VRNMQNINNH	FKTETYLAKA
1001	EKQVRDYTVL	GQNTYYQAGK	DGLFDNSQDQ	KDQTTATFHL	KNGSRIEANQ
1051	WHVRYDHIET	YKERIENRNP	AHITVGGDLT	ASGQNWLNKD	SRIVVGGRII
1101	TDDLNQKEIT	NQSTTGKGRG	DAVGTQWDSV	TKKGWYSGRK	RQRRTERNHT
1151	PYHDTQLFTH	DFDTPVSVIQ	QNAASPSFQP	AASAIKLIDG	VSTA AVNGQP
1201	IHTGNVVSLN	NATVTLPNSS	LYTTHPDNKG	WL VETDPQFA	DYRRWLGS DY
1251	MLQQQLQD TN	HLHKRLGDGY	YEQKLVNEQI	HQLTGYRRLD	GYRSDEEQFK
1301	ALMDNGLTAA	KTFGLTPGIA	LSAEQVARLT	SDIVWMENQT	VTLSDGSTQT
1351	VLVPKYVALA	RKGLDLNTSGG	LISAEQVLLK	LDNGNLNTSG	TIAGRQAVLI
1401	QARNINSNGN	IQADQIGLKA	EKSINIDGGQ	VQAGRLLTAQ	AQNINLNGTT
1451	QTSGNERNGN	TAIDRMAGIN	VVGSHTEQVD	NRTSDGILSL	HASNDINLNA
1501	ATVSNQVKGD	TTQITAGNNL	NLGTIRTEHR	EAYGTLDDEN	HRHVRQSTEV
1551	GSSIRQTONGA	LLRAGNDLKI	RQGELEAAEG	KTVLAAGRDV	TISEGRQITE
1601	LDTSVSGSKS	GILSSTKTHD	RYRFSHDEAV	GSNIGGGKMI	VAAGQDINVR
1651	GSNLISOKGI	VLKAGHDIDI	STAHNRYTGN	EYHESKKSGV	MGTGGLGFTI
1701	GNRKTTDDTD	RTNIVHTGSI	IGSLNGDVT	VAGNRYRQTG	STVSSPEGRN
1751	TVTAKSIDVE	FANNRYATDY	AHTQEQQKLT	VALNVPPVQA	AQNFIQAQNN
1801	VGKSKNKRVN	AMAAANAAWQ	SYQATQOMQO	FAPSSSAGQG	QNNNQSPSIS
1851	VSITYGEOQS	RNEQKRHYTE	AAASQIIGKG	QTTLAATGSG	EQSNINITGS
1901	DVIGHAGTAL	IADNHIRLQS	AKQDGESEQS	NKSSGWNAGV	AVKIGNGIRF
1951	GITAGGNIGK	GKEQGGSTTH	RHTHVGSTTG	KTTIRSGGSDT	TLKG VQLIGK
2001	GIQADTRNLH	IESVQDTEY	QSKQONGNVQ	VTVGYGFSAS	GSYRQSKVKA
2051	DHASVTGQSG	IYAGEDGYQI	KVRDNTDLKG	GIITSSQSAE	DKGNLFTQTA
2101	TLTASDIQNH	SRYEGRSFGI	GGSF DLNGGW	DGTVTDKQGR	PTDRISPAAG
2151	YGS DGD SKNS	TTRSGVNTHN	IHITDEAGQL	ARTGRTAKET	EAR IYTGIDT
2201	ETADQHSGLH	KNSFDKDAVA	KEINLQREVT	KEFGRNAAQA	VAAVADKLGN
2251	TQSYERYQEA	RTLLEAELQN	TDSEAEKAAF	RASLGQVNAY	LAENQSRYDT
2301	WKEGGIGRSI	LHGAAGGLTT	GS LGGILAGG	GTSLAAPYLD	KAAENLGPAG
2351	KAAVNALGGA	AIGYATGGSG	GAVVGANVDW	NNRQLHPKEM	ALADKYAEAL
2401	KREVEKREGR	KISSQEAAMR	IRRQILRWVD	KGSQDGYTDQ	SVISLIGMKG
2451	EDKALGYTDW	YRDYGARNPQ	TYNDPKLFEE	YRRQDKPEYR	NLTWLHSGTK
2501	DTKIRQGERK	NEEFALNVAE	GLTSLVNPNP	RIKQVPILAGI	RNLNKIKPTV
2551	TGSDPLLAGA	GNIRIPANGN	VAKGDRIPDT	ALASKGIKHK	DRKDQLEKK*

Homology with fha

```
m564/fha
ID   FHAB_BORPE          STANDARD;          PRT;   3591 AA.
AC   P12255;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE   FILAMENTOUS HEMAGGLUTININ. . . .
```

SCORES Init1: 190 Initn: 524 Opt: 594
Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

		10	20	30	40	50	60
m564	.pep	MNRTLYKVVFENKHRNCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS					
fhab_borpe		: :: :: : : :: :: : : : : ::					
		10	20	30	40	50	
		MNTNLRLVLFSHVRGMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA					
		70	80	90	100	110	119
m564	.pep	LSLLLG-SALILTSSSATAQGIVADKSAPAAQQOPTILQTNGIPQVNIQTPTSAGVSVNQ					
fhab_borpe		: :: : :: : :: :: : : : :: :					
		WALMLACTGLPLLVTH---AQGLV-----P-QGQTQVLQGGNKVPVVNIADPNSSGGVSHNK					
		60	70	80	90	100	
		120	130	140	150	160	170
m564	.pep	YAQFDVGNRGAILNNRSRNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQLNGYIEV					
fhab_borpe		: :: : :: :: : : : : : : : : : : : : : :					
		FQQFNVANPGVFFNNGLTDGVSRIGGALTKNPNLTR-QASAILAEVTDTPSPRLAGTLEV					
		110	120	130	140	150	160

864

m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTDDFVVERDLTAGKQL-NLS					
fhab_borpe		RL-----DGA-HAGGQLRVSSDQAALGSLAAKGELTVSAARAATVA-EL---KSLDNIS					
			720	730	740	750	760
m564	.pep	820	830	840	850	860	870
		IKGRLK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLNSDGLT					
fhab_borpe		VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-					
		770	780	790	800	810	
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGAIAARKRLDI-GAKEIHN					
fhab_borpe		--GSDGAISVSGRDAVRVDQARSLADISLG---AEGGATLGAVEAAGSIDVRGGSTV--					
		820	830	840	850	860	
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGIFAVGNRLDEQHHAAGMADTFVNGSAGLEVQGDALMSVRNMQINNHFKT					
fhab_borpe		AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
		870	880	890	900	910	920
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--QVRDYTVLGQNTYYQAGKDGLFDNSQGQKQDQTATFHLKNGSRLEANQ-					
fhab_borpe		ALQSAKASGTLHVQGGEHLDLGTLAAGVAVDV---NGTGDVRVAKLVSDAGADLQAGRS					
		930	940	950	960	970	
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNWLNKDSRIVVGGRIITDDLNQKE					
fhab_borpe		MTLGIVDTTGDLDQARAQQKLELGSVKSDDGGLQAAAGGALSAAAAEVAGALELS---GQGV					
		980	990	1000	1010	1020	1030
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGKGRTDVGTQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
fhab_borpe		TVDRASASRARIDSTGSGVIGALKAGAVEAASPRRARRALR-----QDFFFTP					
		1040	1050	1060	1070	1080	
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QQNAASPSFQPAASAIKLIDGVSTAAVNGQRIHTGNVVSNNATVTLPNSSLYT					
fhab_borpe		SVVVRAGQGNVTVGRGDPHQGVLAQGDIIIMDA--KGGTLLLRNDALTENGTVTISADSAVL					
		1090	1100	1110	1120	1130	1140
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQLDTNHLHKLRLGDGYEQLVNEQIHQ					
fhab_borpe		EHSTIESKISQSVLAAKGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRQIDV					
		1150	1160	1170	1180	1190	
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLDGYSDEEQFKALMDNGLTAAKTFLTPG-IALSAEQVARLTSDIVWMENQTV					
fhab_borpe		VDGRPQI----TDAVTGEARKDES SVSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
		1200	1210	1220	1230	1240	1250

865

m564	.pep	1350	1360	1370	1380	1390	1400
		TLSDGSTQTVLVPKYYALARKGDLNTSSGLISAEQVLLKLQNGNLNTSGTIAGRQAVLIQ					
fhab_borpe		--ENGASVTVRTT-----GNLVNKGYSAGKQGVLEV-GGALTNEFLVGS DGTQRIE					
		1260	1270	1280	1290	1300	
m564	.pep	1410	1420	1430	1440	1450	
		ARNINSNGNIQ-----ADQIGLKA EKSINIDGGQVQAGRLLTAQ----AQNINLNGTT					
fhab_borpe		AQRIENRGTFQSQAPAGTAGALVVKAAEAIVHDGVMATKGEMQIAGKGGGSPTVTAGAKA					
		1310	1320	1330	1340	1350	1360
m564	.pep	1460	1470	1480	1490	1500	
		QTSGNERNGNTAI-DRMAGINVV-GSHT EQVDNRTSD-GILSLHASNDINLNAATVSNQV					
fhab_borpe		TTSANKLSVDVASWDNAGSLDIKKGAQVTVAGRYAEHGEVSIQGDYTVSADAIALAAQV					
		1370	1380	1390	1400	1410	1420
m564	.pep	1510	1520	1530	1540	1550	
		--KDGTQTITAGNNLNLGT-IRTE---HREAYGTLD DENHRHVRQST-----EVGS					
fhab_borpe		TQRGGAANLTSRHDTRFSNKIRLMGPLQVNAGGPVSNTGNLKVREGVTVTAASFDNETGA					
		1430	1440	1450	1460	1470	1480
m564	.pep	1560	1570	1580	1590	1600	
		SIRTQNGALLRAGNDLKIRQGELEAE EGKTVLAAGRDV--TISEGRQITELDTS---VSG					
fhab_borpe		EVMAKSATLTTSGAARN--AGKMQVKEAATIVAASVSNPGTFTAGKDITVTSRGGFDNEG					
		1490	1500	1510	1520	1530	
m564	.pep	1610	1620	1630	1640	1650	1660
		K---SKGILSSTKTHDRYRF---SHDEAV-GSNIGGGKMIVAAGQDINVRGSLISDKGI					
fhab_borpe		KMESNKDIVIKTEQFSNGRVLD AKHDLT VTASGQADNRGSLKAGHDFTVQAQRI--DNSG					
		1540	1550	1560	1570	1580	1590
m564	.pep	1670	1680	1690	1700	1710	
		VLKAGHDIDISTAHNRYTG-----NEYHESKKS GVMGTGGLGFTIGNRKTTDDTDRTNIV					
fhab_borpe		TMAAGHDATLKAPHLRNTGQVVAGHDIHIINS AKLENTGRV--DARN DIALDVADFTN--					
		1600	1610	1620	1630	1640	1650
m564	.pep	1720	1730	1740	1750	1760	1770
		HTGSIIGSLNGDVTTVAGNR YRQT---GSTVSSPEGRNTVTAKSIDVEFANNRYATDYA					
fhab_borpe		-TGSLYAEHDA-TLTLAQGTQRDLVVDQDHILPVAEGTLRVKAKSLTETGNPGSLIA					
		1660	1670	1680	1690	1700	1710
m564	.pep	1780	1790	1800	1810	1820	1830
		HTQE QKGLTVALNVPVQAAQNFIAAQNVGKSKNKR VNAMAAANAA-WQSYQATQMQQ					
fhab_borpe		EVQE-----NIDNKQA-----IVVGKDLTLS-SAHGNVANEANALLWAAGELTVKAQN					
		1720	1730	1740	1750		
m564	.pep	1840	1850	1860	1870	1880	1890
		FAPSSSAGQGQNNNQSPSISVSITYGEQKSRNEQKRHYTEAAASQIIGKGQTTLAATGSG					
fhab_borpe		ITNKRAALIEAGGNARLTA AVALLNKLGRIRAGEDMHL D---APRI-----ENTAKLSGEV					
		1760	1770	1780	1790	1800	1810
m564	.pep	1900	1910	1920	1930	1940	1950
		EQSNINITGSDVIGHAGTALIADNHIRLQSAKQD GSEQSKNKSSGWNAGVAVKIGNGIRF					
fhab_borpe		QRKGVQDVGGGEHGRWSGIGYVNYWLRAGNGK KACT-----IAAPWYGGDLTAEQSLIEV					
		1820	1830	1840	1850	1860	

866

```

      1960      1970      1980      1990      2000      2010
m564 .pep  GITAGGNIGKGKEQGGSTTHRHVHGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
fhab_borpe GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGHIGG-----DVDNRSV-
      1870      1880      1890      1900

      2020      2030      2040      2050      2060
m564 .pep  IESVQDTETYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE
      : : : | | : : : : : | | : | | : | : | | : | |
fhab_borpe VRTVSAMEYFKTFLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY
      1910      1920      1930      1940      1950      1960

      2070      2080      2090      2100      2110      2120
m564 .pep  DGYQIKVRDNTDLKGGIITSSQSAEDKGKNLFQTATLTASDIQNHS--RYEGRSFGIGGS
      : : : | | | | : : | | | | | | | | | | | | | | | |
fhab_borpe TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDRGHTLESAGRKI-FGEY
      1970      1980      1990      2000      2010

      2130      2140      2150      2160      2170
m564 .pep  FDLNGGWDGT-----VTDKQGRPTDRISPAAGYSGDGSKNSTTRSGVNTNHIHITDEAG
      | | : : : : : | | | | | | | | | | | | | | | | |
fhab_borpe KKLQGEYEKAKMAVQAVEAYGEATRVRVDQLG-----QRYGKALGGMDAETKEVDGIIQ
      2020      2030      2040      2050      2060      2070

      2180      2190      2200      2210      2220      2230
m564 .pep  QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKEFGRNAA
      : : | | : : | | | | | | | | | | | | | | | | | |
fhab_borpe EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPRVT--LAKALS
      2080      2090      2100      2110      2120

      2240      2250      2260      2270      2280      2290
m564 .pep  QAAVAADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----
      | : | | | : | : | : : : : | | : | | | | | : :
fhab_borpe AALGADWRALGHSQMLQWRKDFKAGKRGAEIAFYPKQTVLAAGAGLTLSNGAIHNGENA
      2130      2140      2150      2160      2170      2180

      2300      2310      2320      2330      2340      2350
m564 .pep  AENQSRDYDTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK
      | : | : | : | | : : : : | : |
fhab_borpe AQNRGRPEGLKIGAHSATSVSGSFDALRDVGLEKRLDIDDALA AVLNPHIFTRIGAAQT
      2190      2200      2210      2220      2230      2240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1   atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accatthttcg cccgtcccag accggcggct tccaatactt
101 ccctgcgttt cgcacgcgcg aacgacaccg gctcgcctgc acttctgget
151 acctgcacgc gtgcgatgtc caagtcgagc gcgaaatacg gaatacctc
201 tttgggcgaa gacgcgtccg accgtctgcc cgccctgcc gaagccgaca
251 atcagcacat gatcagactt gctcatcgct tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1   MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1   ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

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867

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251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCGTCCG CGCCTGTTC CATTCTGGCG AAACCATATC AAGCTGCCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCCG CGACCGAATG TTTCATTTT AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRТААVААC S HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

              10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
              |||||||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
              10      20      30      40      50      60

              70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
              |||||||
g565           AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
 51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCGTCCG CGCCTGTTC CATTCTAGCG AAACCATATC AAGCTGCCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTTG AGGCTGTCCG CGACCGAATG TTTCATTTT AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRТААVААC S HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

              10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
              |||||||

```


868

```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
           70      80      90     100     110     120
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSLCRSSDFMSQLDLTKRPTSASLP
           |||||
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSLCRSSDFMSQLDLTKRPTSASLP
           70      80      90     100     110     120
           130     140     150     160     170     180
m565.pep  PKRKGAIIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           |||||:|||||
a565      PKRKGAIIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
           190     200     210
m565.pep  KAMANTTSAFNTSSSIANSINTCRQPPINAX
           |||||
a565      KAMANTTSAFNTSSSIANSINTCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat ggggggtaac
51 ggttggtcag cccgagtacg tcctgcatat cgtacaaacc cgttttgccg
101 ttaccctaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggct
151 gccggccttg tgggtgattt ccacgcgttc gccgtcggtg gcgaagaggg
201 cggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgcggcg gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTTAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTTGCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACCG GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51  AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m566/g566  93.1% identity in 116 aa overlap
           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||

```

869

```

g566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60

           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG AACAATATCT TTTCAGACGG CATTGTGTAT GGGGGTTAAC
51 GGTGTGTTTACG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTACCG
101 TTTACCCAAA CTGCGGCGCG GACGCGCCG GCGGCAAAGG TCATGCGGCT
151 GCTTGCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCCGCGC GGACGGTGGC AAAGCCGATG
251 GTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFTVYPNCGA DGAGGKGHAA
51  ACLVGDFHAL AVGGEEGGVV ADDVARADGG KADGGRIARA GVAFAAVNGA
101 LFEVSAERAG DDFAHA*

m566/a566  94.0% identity in 116 aa overlap

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      MPSEQYLFRRHFWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60

           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq..
1  atgcgacgac gggcagcggc atcgacaagg cgggtttgca gtccggcggt
51  tatcaggtct tattgggcga tgcggacgtg cagtcggcgg cggtagcgag
101 caaagagggc ggatacggcg tgttgggtgc gaacgcgcgc gcttgccggc
151 gcggaaatcg agctggtgca ggaaatcgcc cgggaagtgc gtttgaaaaa
201 cgcgctcaag gcagtgccgg aagattacga ctttatcctg atcgactgtc
251 cgccttcgct gacgctgttg acgcttaacg gcttggtggc ggcgggcggc
301 gtgattgtgc cgatgttggt cgaatattac gcgctggaag ggatttccga
351 tttgattgcg accgtgcgca aaatccgtca ggcggtcaat cccgatttgg
401 acatcacggg catcgtgcgt acgatgtacg acagccgcag caggctgggt
451 gccgaagtca gcgaacagtt gcgcagccat ttcggggatt tgctttttga
501 aaccgccatc ccgcgcaata tccgccttgc ggaagcgccg agccacggtg
551 tgccggtgat ggcttacgac gcgcaggcaa aggggtgccaa ggcgtatcct
601 gccttgccgg acgaactggc ggcgaggggtg tcggggaaat ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAATR RVCSPAFIRS YWAMRTCSR RYAAKRADTA CWVRTRALAG
51  AEIELVQEIA REVRKLNALK AVAEDYDFIL IDCPPSLTLL TLNGLVAAGG
101 VIVPMLCEYY ALEGISDLIA TVRKIRQAVN PDLDITGIVR TMYDSRSRLV
151 AEVSEQLRSH FGDLLFETAI PRNIRLAEAP SHGMPVMAYD AQAKGAKAYL
201 ALADELAARV SGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
  1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
 51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101  GCGTGCTGGT GGTTCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151  GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201  CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
251  CTGTGTTGGG TGCGAACC GCCTGGCCG GCGCGGAAAT CGAACTGGTG
301  CAGGAAATCG CCCGGAAGT GCGTTTGA AAACGCGCTCA AGGCAGTGGA
351  AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401  TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451  TGCGAATATT ACGCGCTGGA AGGGATTTC GATTTGATTG CGACCGTGCG
501  CAAAATCCGT CAGGCGGTCA ATCCCGATT GGACATCACG GGCATCGTGC
551  GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601  TTGCGCAGCC ATTTGCGGGA TTTGCTTTT GAAACCGTCA TCCCGCGCAA
651  TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701  ACGCGCAGGC AAAGGTACC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751  GCGGCGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
  1  MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
 51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101  QEIAREVRLK NALKA VEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151  CEYYALEGIS DLIATVRKIR QAVNPDLDI GIVRTMYDSR SRLVAEVSEQ
201  LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251  AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

      60      70      80      90      100      110      119
m567.pep  G V Y Q V L L G D A D V Q S A A V R S K E G G Y A V L G A N R A L A G A E I E L V Q E I A R E V R L K N A L K A V E E D
g567      A F I R S Y W A M R T C S R R R Y A A K R A D T A C W V R T R A L A G A E I E L V Q E I A R E V R L K N A L K A V A E D
           20      30      40      50      60      70

      120     130     140     150     160     170     179
m567.pep  Y D F I L I D C P P S L T L L T L N G L V A A G G V I V P M L C E Y Y A L E G I S D L I A T V R K I R Q A V N P D L D I
g567      Y D F I L I D C P P S L T L L T L N G L V A A G G V I V P M L C E Y Y A L E G I S D L I A T V R K I R Q A V N P D L D I
           80      90      100     110     120     130

      180     190     200     210     220     230     239
m567.pep  T G I V R T M Y D S R S R L V A E V S E Q L R S H F G D L L F E T V I P R N I R L A E A P S H G M P V M A Y D A Q A K G
g567      T G I V R T M Y D S R S R L V A E V S E Q L R S H F G D L L F E T A I P R N I R L A E A P S H G M P V M A Y D A Q A K G
           140     150     160     170     180     190

      240     250
m567.pep  T K A Y L A L A D E L A A R V S G K X
g567      A K A Y L A L A D E L A A R V S G K X
           200     210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
  1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
 51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101  GCGTGCTGGT GGTTCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151  GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201  CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
```

871

```

251 GCGTGTGGG TGCGAACC GC GCGTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCC GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCTGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVVKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
 51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYGVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSFHDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

```

m567/a567 97.7% identity in 257 aa overlap

	10	20	30	40	50	60
m567.pep	MSANILAIANQKGGVVKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKAGLQSG					
a567	MSANILAIANQKGGVVKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG					
	10	20	30	40	50	60
m567.pep	VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY					
a567	VYQVLLGDADVKSAAVRSKEGGYGVLGANRALAGAEIELVQEIAREVRLKNALKAVAEDY					
	70	80	90	100	110	120
m567.pep	VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY					
a567	VYQVLLGDADVKSAAVRSKEGGYGVLGANRALAGAEIELVQEIAREVRLKNALKAVAEDY					
	70	80	90	100	110	120
m567.pep	DFILDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT					
a567	DFILDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT					
	130	140	150	160	170	180
m567.pep	DFILDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT					
a567	DFILDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT					
	130	140	150	160	170	180
m567.pep	GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAGT					
a567	GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA					
	190	200	210	220	230	240
m567.pep	GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAGT					
a567	GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA					
	190	200	210	220	230	240
m567.pep	KAYLALADELAARVSGKX					
a567	KAYLALADELMARVSGKX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgctcaggg tcagaccggt attatttgcc gtcaaggcct ccgcctcttc
 51 gataccttgc agaatctgcc gattaaagcg ttcgaggctg cccaatatatt
101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
151 tgtaaaaaca gccccatcag gaacgaaact tcgtcttcg ggcgacgcca
201 gttttcgggt gaaaaggcaa acacggctcag atattgcacg cccagtttgg
251 cgcaatgctt caccatatatt tccaacgcgt ccaagccgcg tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```

```
g568.pep
  1  MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCKA
 51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101  IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSFAFKRL
151  NAAP*
```

```
m568.seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
51  GATGCGCTTGC AGAATCTGCC GGTGAAGCG TTCCGCGGTG CCCAATATCT
101 TCAGGCCGAT ATTGTTTTCG TCAGGCCGCG GTACCTGTTT TCGCAAGACC
151 TGTAAAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTTCGCC CAACGGCCGT TTGCGTCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CGGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAAGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTT ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA
651 CGCGGCCCTT TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTCTCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

```
m568.pep..
1  MLRVRPVLFA  VNASASSMPC  RICRLKRSRL  PNIFRRILFS  CRRRTCFCKA
51  CKNSPIRNET  SSSGRRQFSV  EKANTVRYCT  PSLAQCFITF  SNASKPRLCP
101 IMRGRKRFFA  QRPLPSIITA  ICLGMAVCSK  TACVLLFMSA  FRGSAFKCRL
151 NAEPCRLNCH  QIFFFGSQEF  VGFGNVFVGQ  FLNRFFAATC  LVFGNFFVFE
201 EFFDVVVGIA  AHVADRDAAF  FRFAAYDFNQ  VFAAFLGQHG  HRHADQVADS
251 CRVOSOV*
```

```

m568/g568      94.8% identity in 154 aa overlap

                10          20          30          40          50          60
m568.pep      MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET
                |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g568          MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET
                10          20          30          40          50          60

                70          80          90          100         110         120
m568.pep      SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA
                |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g568          SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIIRGRKRFFAQRPLPSIITA
                70          80          90          100         110         120

                130         140         150         160         170         180
m568.pep      ICLGMAVCSKTACVLLFMSAFRGSFAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFGVQ
                :|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g568          MCLGMAVCSKMVCVLLFISAFRGSFAFKCRLNAAPX
                130         140         150

                190         200         210         220         230         240
m568.pep      FLNRFFAATCLVFGNFFVEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
  1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
 51 GATGCCCTTC AGGATTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAAACT TCGTCTTCGG GGCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTAGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGCTTGCC TTTCGCGGTT CGGCATTCAA ATGCCGTCGT
451 AACGCCGAAC CGTGCAGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTT TTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
  1 MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
 51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCLRNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIKRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLRNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLRNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADGDAAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADGDAAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
  1 atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
 51 gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgccggc
101 tgattgcctt gaccgccttg tgggagatg cccgatggc cggtttgtgc
```

874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa tttggtttgg tatgttggtt
251 tggcattttt gctcgccggt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgat cctggcgcc cgcacccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNNGWQVYAV GWLLLMPEFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTITG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGTTTC GCGCTCGTAT CCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CTTGCTGCTCG CTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGCGCG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTGGTGTCTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGGACAC GGCGGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCACGCTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNNGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAIKPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDLSL
251 IAVISVYAAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGWQVYAVGWLLLMPEFWF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m569.pep	ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAIKPGKSWEGAIGGAVC					
g569	ALVSLAPASRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```

875

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGGTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGCGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

a569.pep

```

1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLI GLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRDTS
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
a569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
a569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m569.pep	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
a569	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
	130	140	150	160	170	180
	190	200	210	220	230	240
m569.pep	VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSKLLPGH					
a569	VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSNLLPGH					
	190	200	210	220	230	240
	250	260				
m569.pep	GGVFDRDTSLIAVISVYAAMMSVLNX					
a569	GGVFDRDTSLIAVISVYAAMMSVLNX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1  atgatccgtt tgaccgcgc gtttgccgcc gccctgatcg gtttatgctg
51  caccacaggc gcgcacgcgc acaccttcca aaaaatcggc tttatcaaca
101 cggagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttgaaa ggcagctcgc cggcgcaaa ctaaggacg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggt cgaagcgttc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgccaa ccgcgtcatc gtcaaaatcg

```



```

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
451 acccaatacg acgttaccga cagcgtcatt aaagaaatga acgcccgtg
501 a

```

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

```

g570.pep..
  1 MIRLTRAFAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151 TQYDVTDSVI KEMNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

```

m570.seq..
  1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
 51 CACCGCAGGC GCGCAGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
501 A

```

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

```

m570.pep
  1 MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIYVN
151 TQYDVTDSVI KEMNAR*

```

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD					
g570	MIRLTRAFAAALIGLCCTTGAAHADTFQKIGFINTERIYLESKQARNIQKTLTLDGEFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLDKAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIKIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

```

a570.seq
  1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
 51 CACCGCAGGC GCGCAGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

```

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101  RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIIYVN
151  TQYDVTDSVI KEMNAR*

m570/a570  97.6% identity in 166 aa overlap

              10      20      30      40      50      60
m570.pep    MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD
a570        MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD
              10      20      30      40      50      60

              70      80      90     100     110     120
m570.pep    ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
a570        ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              70      80      90     100     110     120

              130     140     150     160
m570.pep    SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX
a570        SLQQNANRVIVKIAKQEGYDVILQDVIIYVNTQYDVTDSVIKEMNARX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttggt gttaccgttt tcggcggcgg
 51  tataggttct gccgtccac acgtgcctg cgtcgcaaa caggctcagg
101  cggacggtgc gtgcgtcttt cgcaccgggc atcggaaga gcagctcggc
151  ggagacgttg gcttttttgt tgcgcgcta gctgattttt tcgccgtatt
201  cgtcatacac ttccgggccc agcgtgccgc ttctgtagcc gcgcaccgaa
251  cccaggccgc cgcgtagaa gttttcaaag aaggggattt ctttggttct
301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351  ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRFV VTVEGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
 51  GDVGFFVAAV ADFFAVFVIH FRAERAAVFA AHRTQAAAVE VFKEGDFFGS
101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTCGCGG
 51  AACTGCTGTT GTCGTCGTAG GTTTGCCGT CCCACACGCT GCCTGCGTCG
101  GCAAACAGGC TCAGGCGGAC GGTGCGCGC TCTTTCGCGC CGGGCATCGG
151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201  TTTTTCGCC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
251  TATCCGCGCA CCGAACCCAG GCCGCGCGC TAGAAGTTT CAAAGAAGGG
301  GATTTCCTTG GTTCTGCCGT AGCCGCCGC AATGCCGACT TCGCCGCCGA
351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGGT TTGGTTGTGG
401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCGGCGTT
451  CACGCCCGTC AGGTAGCCGC GCGTCGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 51  EEQLGGDVGF FVAAVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101  EFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDFGV
151  HARQVAARRP *

```

878

m571/g571 93.1% identity in 102 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLNPAAGRGTAVVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
g571      MRVFRVNRFFVVTVFEGGIGSAVPHAACVKGQAQADGACVFRTGHREEQLGGDVGF
           10      20      30      40      50

      70      80      90      100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQR
g571      FVAAVADFFAVFVIHFRAERAAFVAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQR
           60      70      80      90      100     110

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGGVVLQFAARQGDGFGVHARQVAARRPX
g571      EGFA
           119

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1   ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTCGCGG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTGCGC CCGTAGCTGA
201 TTTTTCGCC GTATTCGTCA TACACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCCGCGG TAGAAGTTT CAAAGAAGGG
301 GATTCTTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGGTTTTG CTTAAGGGGA AGAACCAGGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCG GGCAGGGCGA TTTCGGCGTT
451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1   MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVKGQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQR EGFA*GEEPG LVVGGGVVLQ FAAGQGDFGV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVLNPAAGRGTAVVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
a571      MGIAGAVNVLNPAAGRGTAVVVVGFAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           10      20      30      40      50      60

      70      80      90      100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQR
a571      FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQR
           70      80      90      100     110     120

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGGVVLQFAARQGDGFGVHARQVAARRPX
a571      EGFAXGEEPLVVGGGVVLQFAAGQGDGFGVHARQVAARRPX
           130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..

g572.pap. .

m572.seq.

m572.pap. .

m572/g572 92.9% identity in 295 aa overlap

```

              10      20      30      40      50      60
m572.pep      MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVPVDEHNAVF
              |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
g572           MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVPVDEHNAIF
              10      20      30      40      50      60

              70      80      90      100     110     120
m572.pep      QVLPDRDYAGRLNEHGIASIIILTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
              |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
g572           QVLPDRDYDRLNEHGIDSIIILTASGGPFLTDLSTFDSITPEOAVKHPNWRMGRKISVDS

```

880

	70	80	90	100	110	120
	130	140	150	160	170	180
m572 . pep	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
g572	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572 . pep	CLGLPERIDSGVGLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGLDFGALSALTFOKPDFGRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572 . pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGQIKFTDIAKTVAHCLAQDFSNGMGDIEGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```

a572 . seq
1   ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGCGGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGCTG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTT CAAGTTTTGC CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGGCC GTTCTGACC GCCGATTAA ACACGTTCTG CAGCATTACG
301 CCCGACCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCT GGTGTCGGCG ACCTGGATTT CGACGCATTG
601 TCCGCGCTGA CCTTCCAAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TGCCTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCGCCT TTTTGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGCATA GCGACATAG GGGGGCTCTT GCGCAAGAT GCCCGACAC
851 GCGACAAGC GCGGCATTT ATCGGCACAC TGCGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```

a572 . pep
1   MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPRDYTGR LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFQKPDF DRFPCLKLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*
  
```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572 . pep	QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPRDYTGRLNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

881

	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDPKLEVVIIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDPKLEVVIIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1   atgccctggt  tgtgccgcct  taatcgcaat  atcggcagtt  tccaaatcac
51  gaatctcacc  gaccataatg  atgtccgggt  cctgacgcag  gaaagacttc
101 aaagcagcgg  caaaagtcag  accctgctta  tcattgacgt  taacctgatt
151 gatgcccgcc  aggttaatct  cggcagggtc  ttccgccgtt  gcaatattta
201 ccgactccgt  attcaaaata  ttcaaacagg  tatagagcga  caccgtctta
251 cccgaacccg  tcggacccgt  taccagcacc  atcccgttaag  gacggtgaat
301 cgcttccaac  aacaattttt  tctggaacgg  ctcaaaaccg  agctggtcga
351 tgttcaaaga  cgccgcatcg  gaattcaaaa  tccgcacac  gaccttttcg
401 ccaaacagcg  tcggcaatgt  gctgacacgg  aaatcgacag  gcttgccgcc
451 cttttgaaag  gtcagctgca  tcctaccgtc  ctgccgtatc  cgtttttcgg
501 aaatgtccaa  acgcgacatt  accttaatcc  gggaagcaag  ctgccccctt
551 accgcaatgg  cgggctgaac  cacctcgccg  agctgcccgt  ccacacggaa
601 accgatacgc  gcatttgtgt  cgtaaaactc  gaaatggatg  tcggatgccc
651 cgctacgcaa  ggcacccgac  aaagttttat  ggataaacct  cggaacaggg
701 ccgtctctcg  cctcctcgtc  gtcgatatac  aggggtgtgc  ttctctcttc
751 ctcttgcccc  tccccaaagt  cctgaagcag  cgatgtcgaa  cggaaccca
801 cccaatcgag  caaacccgcc  aactgggtcat  cctcgacaat  gaccaactca
851 accgcaatcc  ctgcggcaga  aaccgttttc  tgaatttgcg  gcattctgggt
901 cggatcggaa  accgcaaaaa  atactttgtc  gccccacgg  aaaaccggca
951 cacagtggaa  ctccaccatc  tgctcctcgg  tcaacacccc  catcagcacc
1001 ctgtggcgcg  gataatgacg  caaatcaaga  atcgaataac  tgaacaccct
1051 cgcaatcaat  gccgaagcgg  acttgggcga  aatgacaccg  tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1   MPCLRLNRN  IGSFQITNLT  DHNDVRVLTQ  ERLQSSGKSQ  TLLIIDVNLI
51  DARQVNLGRV  FRCNIYRLR  IQNIQTGIER  HRLTRTRRTG  YQHPVVRTVN
101 RFQQQFFLER  LKTELVDVQR  RGIGIQNPHH  DLFAKQRRQC  ADTEIDRLAA
151 LLKGQLHPTV  LRYPPFGNVQ  TRHYLNPGSK  LPPYRNGRLN  HLAELPVHTE
201 TDTRIVFVKL  EMDVGCPATQ  GIRQSFMDKP  RNRAVFCLLV  VDIQGVAFLE
251 LLPLPKLLKQ  RCRTRTHPIE  QTRQLVILDN  DQLNRNPGCR  NRFLNLRHLG
301 RIGNRKKYFV  APTENRHTVE  LHHLLLRQHP  HQHPVARIMT  QIKNRITEHP
351 RNQCRKRLGR  NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1   ATGCCCTGTT  TGTGCCGCCT  TAATCGCAAT  ATCGGCAGTT  TCCAAATCAC
51  GAATCTCACC  GACCATAATG  ATGTCGGGGT  CCTGACGCAG  GAAAGACTTC
101 AAAGCAGCGG  CAAAAGTCAG  GCCCTGCTTA  TCATTGACGT  TAACCTGATT
151 GATGCCCGGC  AGGTAAATCT  CGGCAGGGTC  TTCCGCCGTT  GCAATATTTA
201 CCGACTCCGT  ATTCAAAATA  TTCAAACAGG  TATAGAGCGA  CACCGTCTTA
251 CCCGAACCCG  TCGGACCGGT  TACCAGCACC  ATCCCGTAGG  GACCGTGAAT
301 CCTACCAAC  aCaw.TTTT  TCTGAAACGG  CTCAAAACCG  AGCTGGTCGA
351 TGTTCAAAGA  CGCGGCATCG  GAATTCAAAA  TCCGCATCAC  GACCTTTTCG
401 CCAAACAGCG  TCGGCAATGT  GCTGACACGG  AAATCGACAG  GCTTGCCGCC
451 CTTTGTAAAG  GTCAGCTGCA  TCCTGCCGTC  CTGCGGTATC  CGTTTTTCGG
501 AAATGTCCAA  ACGCGACATT  ACCTTAATCC  GTGAAGCAAG  CTGCCCCCTT

```

```

551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCCG CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

m573.pep..

```

1  MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51  DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXXFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

m573.pep	10	20	30	40	50	60
	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
g573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
m573.pep	70	80	90	100	110	120
	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRYQHXXFLKRLKTELVDVQR					
g573	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRYQHXXFLKRLKTELVDVQR					
m573.pep	130	140	150	160	170	180
	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPPFGNVQTRHYLNPXSK					
m573.pep	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
m573.pep	250	260	270	280	290	300
	VDIQGVAFLELLPLPKLLKQRCRTTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLELLPLPKLLKQRCRTTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
m573.pep	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

883

a573.seq

```

1   ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAAATTTT TCTGAAACGG CTCAAACCCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGTAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GCGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCCG CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1   MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51  DARQVNLGRV FRRCNIRLRL IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPFEGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAQ GIROSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQTLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m573.pep	FRRCNIRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXXFFLKR LKTELVDVQR					
a573	FRRCNIRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRFFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFEGNVQTRHYLNXPXSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFEGNVQTRHYLNPGSK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAQGIRQSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAQGIRQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

884

	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLLRQHPHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLLRQHPHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
a573	NDTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1  atgtctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct ttgcccgtc ttcttcacga
101 tgggctgggt tggcgccgcg gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttcgggatt ttataaaagc ctggacgctt tggcgcaccg
201 caacagcggg cgcgcggcaa gggagttggc ggaagtcgtc gacggccggc
251 ggcaatcgta tgatttgaac cttaccctcg gcaaatctta ccgtcagcgc
301 cgcgaaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaag cgcgggtttg gtcgatcgtg ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaagcc agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgttt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgcgcgcgtc
751 gaagcctatg ccgccatcga gcagcaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaccg tctgacagga tatatgcaga cgtttcccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg ctttaagggcg agaagaagc
951 cgcgcaaac ccctgcgagc ttgtccgcgc caagcccgac cttaacggcg
1001 tgtaccgcct gctcggtttg aaactcagcg atttggatcc ggcttggaaa
1051 gccgatgccg acatgatgcg ttcggttatc ggacggcagc tccagcgcag
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1  MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLF LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQAAALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKGEKEAAQT AVELVRRKPD LNGVYRLGL KLSLDLPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1  ATGCGCCCGA ATCTACCAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCCGGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCTCG GCAAACCTTA CCGCCAGCGT
301 GGCGAAAACG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGTC GCGGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGG
451 CTGCAAGACG GTAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTCGATG TCGCGGTTT

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885

```

651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAATA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAAAC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAACCTCAGC ATATGAATCC GGCTTGGAAA
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCCTGCCCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```

1 MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQKG PEEGLNRLTG YMQTFPELDL
301 INVVEKSLK LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSMDNPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFESQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

m573/g573 97.8% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
g574	MLPNLPNSLKADMDNELWIILLPIILLPVFTMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
g574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
	70	80	90	100	110	120
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
g574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
	70	80	90	100	110	120
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
g574	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
g574	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
g574	AQLLSHDEQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
g574	AQLLSHDEQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					
	190	200	210	220	230	240
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGPKEEGLNRLTGYMQTFPELDL					
g574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGPKEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGPKEEGLNRLTGYMQTFPELDL					
g574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGPKEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
m574.pep	INVVEKSLKCEKEAAQTAVELVRRKPDNLGVYRLGLKLSMDNPAWKADADMMRSVI					
g574	INVVEKSLKCEKEAAQTAVELVRRKPDNLGVYRLGLKLSMDNPAWKADADMMRSVI					
	310	320	330	340	350	360
m574.pep	INVVEKSLKCEKEAAQTAVELVRRKPDNLGVYRLGLKLSMDNPAWKADADMMRSVI					
g574	INVVEKSLKCEKEAAQTAVELVRRKPDNLGVYRLGLKLSMDNPAWKADADMMRSVI					
	310	320	330	340	350	360
m574.pep	GRQLQRSVMYRCRNCHFESQVFFWHCPACNKWQTFTPNKIEVX					
g574	GRQLQRSVMYRCRNCHFESQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFESQVFFWHCPACNKWQTFTPNKIEVX					
g574	GRQLQRSVMYRCRNCHFESQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1   ATGCGCCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTGCCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCCG GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GCGGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG CCGCGCGTTT
651 CAATGTGCGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCGCTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTGCG GTTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTCAACGCGG
1001 TGTACCGCCT GCTTGGTTTG AAACTCAGCG ATTTGGATCC GGCTTGGAAA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTCT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1   MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLTDSPTT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAALEFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMOTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDLDPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*
```

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
a574	MRPNLPNSLEKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLLDSPDTT					
	70	80	90	100	110	120
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLLDSPDTT					
	70	80	90	100	110	120
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
a574	GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					
	130	140	150	160	170	180
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					

887

	190	200	210	220	230	240
	250	260	270	280	290	300
m574 . pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
	310	320	330	340	350	360
m574 . pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPD L NGVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPD L NGVYRLLGLKLSDLPAWKADADMMRSVI					
	370	380	390	400		
m574 . pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTF TPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTF TPNKIEVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575 . seq (partial)
1  ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51  ccgtaacaaca gtccgctttc ggtttcttct tcggcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggaacttc actggctgtt tccgcaacag
151 gttcggaaac ggtgttaccg gtttcgtcgg tcggcgtgtc gatggcagaa
201 gcggcggtct cttggggggg cggtatcggc agcgggttcc gatgcggcag
251 tatttgcagc gggtaacagg cgggttggtc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggttcgggt cgaacggccg gtttttcgc
351 ttttgcttcg ggcgcggcaa cttttgttc aggtttttca accggttttt
401 cgacagggtt ctctatcggt ttctccacag ttgcctgttt ggacgggtta
451 gacggcatgg atgcagtttc ggctttgggt ttcgccgttt gcggtttggg
501 ttgttccgct ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575 . pep (partial)
1  ..MPCLRRQAAR CTNRRTDRQT VRFRLLRQK FVRQVRQVR RQLHWLFPPQ
51  VRKRCYRFR SACRWQKRRL LGGADSAAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSG RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAAALI LFRFGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575 . seq .
1  ATGTTTCGG GCGAGGAAG CTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGCAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGT
401 TTGCCGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGCGCGC CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAAATGCC GCGCCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACGCCGA ACAGACCGTC AAACAGTCCG CTTTCGGTTT
701 CTTCTTCGGC AGAACTCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTGAT GGCAGAAGCG GCGGCTTCTT GGGGGGCGGA
801 TTCGGCAGCG GTTTCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 GTCGAACGGC CGGTTTTCCT GCTTTTGCTT CGGGCGCGGC AACTTTTGCT
901 TCAGGTTTTT CAACCGGTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTCGGGTT
1001 GTTCCGCTTT GATCCTGTTC AGATTCGGAA TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

```
m575.pep
  1  MVSGEAEFRK PASPEGEAGF AEAUVSSVPIW LFEGRLSEKS VSTVSGLFSA
 51  VWATDSGSGV SMTISTGLYG LKVSQSYTSL VDSMAFQSAS ARFWVSSSCV
101  SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
151  TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201  RKSSSRINA APPPASSKVY EPPNRPNSP LSVSSAETC STGSETALPV
251  SSVGVSMAEA AASWGADSA VSDAAVFAAG TGSGRTAGFS AFASGAATFA
301  SGFSTGFSTV ACLDGS DMD AVSALGFAVC GLGCSALILF RFGM*

m575/g575 70.2% identity in 114 aa overlap

      240      250      260      270      280
m575.pep  SSAETCTGSETALPVSSVGVSMEEAAASWGADSAVSDAAVFAAGT-----
              |||||
g575      LHWLFPPQVRKRCYRFRSACRWQKRLLGGADSAVSDAAVFAAGTGPWRSVAEAGVS
              50      60      70      80      90     100

      290      300      309      310      320
m575.pep  -----SGRTAGFSAFASGAATFASGFSTGFST-----VACLDGSDGMDAVSALGFA
              |||||
g575      DTAGLGSRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA
              110     120     130     140     150     160

      330      340
m575.pep  VCGLGCSALI-----LFRFGMX
              |||||
g575      VCGLGCSALIFLGAAALILFRFGMX
              170     180
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

```
a575.seq
  1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
 51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101  GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151  GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201  GTTGACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251  TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301  AGTGCGCCGG ATAAATGCC GTTTGCGCG GCTGCCAGGC TGTCGAAATC
351  CAAGTCGATG CGGTTGGAAG GCGTATCGGT TCGACATCG AACGTTTGTT
401  TTGCCGACAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT
451  ACATCGTTTT TCGAGCGGG TTCGGGCGTT GCCGAGTTT CGACTTCGGC
501  AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAGG TCAGGCTCTT
551  CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601  CGCAAAGCA GCAGCAGGGC GATCAATGCC GCGCTCCGC CGGCAAGCAG
651  CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TCGGTTTCT TCTTCGGCAG
701  AACCTGTTT GACAGGTTTC GAAACGCGT TACCGGTTT GTCGGTCGGC
751  GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
801  TTCCGATGCG GCAGTATTTC CAGCGGTGAC AGGTCGGGT CGAACGCGCG
851  GTTTTCCGC TTTTGCTTCG GGCGCGGCAA CTTTGTCTTC AGGTTTTTCA
901  ACCGGTTTCT CTACCGTTGC CTGTTTGGAC GGTTCGGACG GCATGGATGC
951  GGTTTCGGCT TTGGGTTTCG CCGTTTGGCG TTTGGGTTGT TCCGCTTGA
1001 TCCTGTTTCA ATTCCGAATG TGA
```

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

```
a575.pep
  1  MVSGEAEFRK PASPEGEAGF AEAUVSSVPIW LFEGRLSEKS VSTVSGLFSA
 51  VWATDSGSGV SMTISTGLYG LKVSQSYTSL VDSMAFQSAS ARFWVSSSCV
101  SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
151  TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201  RKSSSRINA APPPASSKVY EPPNPLSVS SSAETCTSGS ETALPVSSVG
251  VSMEEAAASW GADSAVSDA AVFAAGTSGS RTAGFSAFAS GAATFASGFS
301  TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *
```

889

m575/a575 98.8% identity in 344 aa overlap

m575.pep	10	20	30	40	50	60
	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVSTV	SGLFSAVWATD	SGSGV
a575	10	20	30	40	50	60
	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVSTV	SGLFSAVWATD	SGSGV
m575.pep	70	80	90	100	110	120
	SMTISTGLYGL	KVSGSYTSLVSD	MAFQASARFW	VSSSCVSAPDK	MPFCAAARLSK	SKSM
a575	70	80	90	100	110	120
	SMTISTGLYGL	KVSGSYTSLVSD	MAFQASARFW	VSSSCVSAPDK	MPFCAAARLSK	SKSM
m575.pep	130	140	150	160	170	180
	RLEGVSVSTSN	VCFADNSSSDSP	KASVSFTSFFG	AGSGVAGVST	SAKVISMPSSA	AASSR
a575	130	140	150	160	170	180
	RLEGVSVSTSN	VCFADNSSSDSP	KASVSFTSFFG	AGSGVAGVST	SAKVISMPSSA	AASSR
m575.pep	190	200	210	220	230	240
	SGSSSGTDSSV	RRARLDWARRK	SSSRANAAPPP	PASSKVYEPN	RPSNSPLSVSS	SAETC
a575	190	200	210	220	230	
	SGSSSGTDSSV	RRARLDWARRK	SSSRANAAPPP	PASSKVYEPN	----SPLSVSS	SAETC
m575.pep	250	260	270	280	290	300
	STGSETALPV	SSVGVSMAEAAA	SWGADSAAVS	DAVFAAGTGS	GRTAGFSAFAS	GAATFA
a575	240	250	260	270	280	290
	STGSETALPV	SSVGVSMAEAAA	SWGADSAAVS	DAVFAAGTGS	GRTAGFSAFAS	GAATFA
m575.pep	310	320	330	340		
	SGFSTGFSTV	ACLDGSDGMDA	VSALGFAVCG	LGCSALILFR	FGMX	
a575	300	310	320	330	340	
	SGFSTGFSTV	ACLDGSDGMDA	VSALGFAVCG	LGCSALILFR	FGMX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1  ..atgggctggtg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttccctgcagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgtaa ccgtggaata
351 cgaagccgcg ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcggcgc acccgaaaac
601 gcgcccgcca agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1  ..MGVDIGRSLK QMKEQGA EID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGAEFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```

51	GCAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGAAG
101	CCATGCAGCG	AGTGTATGAC	GGCAAGAGAA	TCAAATACAG	CGAAGAGCAG
151	GCTCAGGAAG	TCATGATGAA	ATTCTTTCAG	GAACAACAGG	CTAAAGCCGT
201	AGAAAAACAC	AAGGCGGACG	CGAAGGCCAA	TAAAGAAAAA	GGCGAAGCCT
251	TTCTGAAAGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGC
301	CTGCAATACA	AAATCACCAA	ACAGGCGCAA	GGCAACATGC	CGACCAAAAG
351	CGACATCGTT	ACCGTGGAAAT	ACGAAGGCCG	CCTGATTGAC	GGTACGGTAT
401	TCGACACGAG	CAAAGCCAAAC	GCGGCGCCGG	TCACCTTCCC	TTTGAGCCAA
451	GTGATTCCGG	GTTGGACCGA	AGCGGTACAG	CTTCTGAAAG	AAGGCGGGCGA
501	AGCCACGTTT	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG
551	GGCAGAAAAA	CGGTCCGAAC	GCCACTTTGG	TATTTGATGT	GAAACTGGTC
601	AAAATCGCGC	CACCCGAAAA	CGCGCCCGCC	AAGCAGCCGG	CTCAAGTCGA
651	CATCAAAAAA	GTAAATTAA			

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1      .MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51     AQEVMMKFLQ  EQQAKAVEKH KADAKANKEK GEAFLEKENAA KDGVKTTASG
101    LQYKITKQGE  GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151    VIPGWTEGVQ  LLKEGEATEF YIPSNLAYRE QGAGDKIGPN ATLVFVDKLV
201    KIGAPENAPA  KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

```

m576.pep      10      20      30      40      50      60
MQQASYAMGVDIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAQEVMMKFLQ
|||||
g576          10      20      30      40      50
MGVDIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQ

m576.pep      70      80      90      100     110     120
EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQEGEKQPTKDDIV
|||||
g576          60      70      80      90      100     110
EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTTASGLQYKITKQEGEKQPTKDDIV

m576.pep      130     140     150     160     170     180
TVEYEGRLIDGTVFDDSSKANGGPVTFPLSQVIPGWTEGQLLKEGGEATFYIPSNLAYRE
|||||
g576          120     130     140     150     160     170
TVEYEGRLIDGTVFDDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYRE

m576.pep      190     200     210     220
QGAGDKIGPNATLVFVDVKLVKIGAPENAPAKQPAQVDIKKVN
|||||
g576          180     190     200     210
QGAGEKIGPNATLVFVDVKLVKIGAPENAPAKQPDQVDIKKVN

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

```
a576.seq
1  ATGAACACCA TTTTCAAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCG TGCGGCAAAA AAGAAGCGCG CCCCGCATCT GCATCCGCAAC
101 CTGCCGCGCG TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAA TCAAAATGAC CGAAGAGCAC
301 GCTCAGGAAG TCATGTAGAA ATTCTTCCAG GAACAACAGG CTAAGAGCCGT
351 AGAAAAACAC AAGGCGGACG ATTAGGCCAA TAAAGAAAAA GCGGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATACCCAA ACAGGGCGAA GGCAAAACAG CGACCAAATA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCGTATTGAC GGTACGGTAG
551 TCGACAGCAG CAAAGCCAAAC GCGGCGCCGG TCACCTTCCC TTTGAGCCAA
```

891

```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
  1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

                                10      20      30
m576.pep                                MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                |||||
a576      CGKKEAAPAS ASEPAASSA QGDTSSIGSTM MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m576.pep      FTEAMQAVYDG KEIKMTEEQAQ EVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
                                |||||
a576      FTEAMQAVYDG KEIKMTEEQAQ EVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m576.pep      KDGVKTTASGLQYKITKQEG GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
                                |||||
a576      KDGVKTTASGLQYKITKQEG GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m576.pep      VIPGWTEGVQLLKEGGEATFYIPSNLAYRE QGAGDKIGPNATLVFDVKLV KIGAPENAPA
                                |||||
a576      VILGWTEGVQLLKEGGEATFYIPSNLAYRE QGAGDKIGPNATLVFDVKLV KIGAPENAPA
                                210     220     230     240     250     260

                                220
m576.pep      KQPAQVDIKKVN
                                |||||
a576      KQPAQVDIKKVN
                                270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

g576-1.seq

```

  1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCGGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCGCG TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCTGTCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAGTACA AAATCACCAC ACAGGGTGAA GGCAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCGCCGG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```


This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAAASAA  QGDTSSIGST
51  MQQASYAMGV  DIGRSLKQMK  EQGAEIDLKV  FTDAMQAVYD  GKEIKMTEEQ
101 AQEVMMKFLQ  EQQAKAVEKH  KADAKANKEK  GEAFLENAA   KDGVKTTASG
151 LQYKITKQGE  GKOPTKDDIV  TVEYEGRLID  GTVFDSSKAN  GGPATFPLSQ
201 VIPGWTEGVR  LLKEGGEATF  YIPSNLAYRE  QGAGEKIGPN  ATLVDVKLV
251 KIGAPENAPA  KQPDQVDIKK  VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq

```

1  ATGAACACCA  TTTTCAAAAT  CAGCGCACTG  ACCCTTTCCG  CCGCTTTGGC
51  ACTTTCCGCC  TGCGGCAAAA  AAGAAGCCGC  CCCC GCATCT  GCATCCGAAC
101 CTGCCGCGCG  TTCTTCCGCG  CAGGGCGACA  CCTCTTCGAT  CGGCAGCAGC
151 ATGCAGCAGG  CAAGCTATGC  GATGGGCGTG  GACATCGGAC  GCTCCCTGAA
201 GCAAATGAAG  GAACAGGGCG  CGGAAATCGA  TTTGAAAGTC  TTTACCGAAG
251 CCATGCAGGC  AGTGTATGAC  GGCAAAGAAA  TCAAATGAC   CGAAGAGCAG
301 GCTCAGGAAG  TCATGATGAA  ATTCTTCAG  GAACAACAGG  CTAAAGCCGT
351 AGAAAAACAC  AAGGCGGACG  CGAAGGCCAA  TAAAGAAAAA  GGCGAAGCCT
401 TTCTGAAAGA  AAATGCCGCC  AAAGACGGCG  TGAAGACCAC  TGCTTCCGGC
451 CTGCAATACA  AAATCACCAC  ACAGGGCGAA  GGCAAACAGC  CGACCAAAGA
501 CGACATCGTT  ACCGTGGAAT  ACGAAGGCCG  CCTGATTGAC  GGTACGGTAT
551 TCGACAGCAG  CAAAGCCAAC  GGCGGCCCGG  TCACCTTCCC  TTTGAGCCAA
601 GTGATTCCGG  GTTGGACCGA  AGGCGTACAG  CTTCTGAAAG  AAGGCGGCGA
651 AGCCACGTT  TACATCCCGT  CCAACCTTGC  CTACCGCGAA  CAGGGTGCGG
701 GCGACAAAT  CCGTCCGAAC  GCCACTTGG  TATTTGATGT  GAAACTGGTC
751 AAAATCGGCG  CACCCGAAAA  CGCGCCCGCC  AAGCAGCCGG  CTAAGTCGA
801 CATCAAAAAA  GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL  TLSAALALSA  CGKKEAAPAS  ASEPAAASSA  QGDTSSIGST
51  MQQASYAMGV  DIGRSLKQMK  EQGAEIDLKV  FTEAMQAVYD  GKEIKMTEEQ
101 AQEVMMKFLQ  EQQAKAVEKH  KADAKANKEK  GEAFLENAA   KDGVKTTASG
151 LQYKITKQGE  GKOPTKDDIV  TVEYEGRLID  GTVFDSSKAN  GGPVTFPLSQ
201 VIPGWTEGVQ  LLKEGGEATF  YIPSNLAYRE  QGAGDKIGPN  ATLVDVKLV
251 KIGAPENAPA  KQPAQVDIKK  VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TL	SAALALSAC	KGKKEAAPAS	ASEPAAASAA	QGDTSSIGSTM
m576-1	MNTIFKISAL	TL	SAALALSAC	KGKKEAAPAS	ASEPAAASSA	QGDTSSIGSTM
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	QAQEVMMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ	QAQEVMMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
g576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTAS	GLQYKITKQ	GEGKQPTKDDIV	TVEYEGRLID
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTAS	GLQYKITKQ	GEGKQPTKDDIV	TVEYEGRLID
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGV	RLLEKGEATF	YIPSNLAYRE	QGAGEKIGPN
m576-1	GTVFDSSKAN	GGPVTFPLSQ	VIPGWTEGV	QLLEKGEATF	YIPSNLAYRE	QGAGDKIGPN
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPAQVDIKK	VN		
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGGCGCAAAA AAGAAGCCGC CCCC GCATCTCT GCATCCGAAC
101 CTGCCGCGCG TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAG ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGTGCGCG
701 GCGACAAAT CCGCCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLEKNA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISAL	TL	SAALALSA	CGKKEAAPAS	ASEPAASSA	QGDTSSIGST
m576-1	MNTIFKISAL	TL	SAALALSA	CGKKEAAPAS	ASEPAASSA	QGDTSSIGST
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ	AQEVMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ	AQEVMKFLQ	EQQAKAVEKH
	130	140	150	160	170	180
a576-1.pep	KADAKANKEK	GEAFLEKNA	KDGVKTTAS	GLQYKITKQ	GEGKQPTKD	DIVTVEYEGRLID
m576-1	KADAKANKEK	GEAFLEKNA	KDGVKTTAS	GLQYKITKQ	GEGKQPTKD	DIVTVEYEGRLID
	190	200	210	220	230	240
a576-1.pep	GT	VFDSSKAN	GGPVTFPLS	QVILGWTEGV	QLLKEGGEAT	FYIPSNLAYRE
m576-1	GT	VFDSSKAN	GGPVTFPLS	QVILGWTEGV	QLLKEGGEAT	FYIPSNLAYRE
	250	260	270			
a576-1.pep	ATL	VDVKLV	KIGAPENAP	AKQPAQVDIKK	VNX	
m576-1	ATL	VDVKLV	KIGAPENAP	AKQPAQVDIKK	VNX	

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipathic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
  1  atggaaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
 51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101  ttaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggt
151  tttatttacg gagcaaacat gaaacttata tataccgtca tcaaaatcat
201  tatcctgctg ctcttcctgc tgcttgccgt cattaatatg gatgccgtta
251  ccttttcta tcttcgggg cagagtgtca atctgccgt gattgtcgta
301  ttgttcggcg cgttgtcgt cggcatcgtg ttcggaatgt ttgccctggt
351  cgggcggctg ctgtccttgc gcggcgaaaa cagccgcctg cgtgcggaag
401  tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451  caaaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
  1  MERSGVFGKI VGNRILRMPS EHAAAFYPKP CKSFKLTQSW FRVRSCTCGV
 51  FIYGANMKLI YTVIKIILL LFLLLAVINM DAVTFSYLPQ QSVNLPLIVV
101  LFQAFVVGIV FGMFALFGR LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151  QNAAESAKQP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
  1  ATGGAAGGA ACGGTGTATT TGGTAAATTT GTCGGCAATC GCATACTCCG
 51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101  TTAAGTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151  TTTATTTACG GAGCAAACAT GAACTTATC TATACCGTCA TCAAAATCAT
201  TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAAATACG GATGCCGTGA
251  CCTTTTCTA CCTGCCGGG CAAAATTTCG ATTTGCCGCT GATTGTCGTA
301  TTGTTCCGCG CATTGTAGT CCGTATTATT TTTGGAATGT TTGCCTTGT
351  CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401  TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451  CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
  1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGGV
 51  FIYGANMKLI YTVIKIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101  LFQAFVVGII FGMFALFGR LSLRGENGRL RAEVKKNARL TGKELTAPPA
151  QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

	10	20	30	40	50	60
m577.pep	MERNGVFGKIVGNRILRMSS	EHAAASYPKPCKSFKLAQSW	FRVRSCLGGVFIYGANMKLI			
g577	MERSGVFGKIVGNRILRMP	SEHAAAFYPKPCKSFKLTQSW	FRVRSCTCGVFIYGANMKLI			
	10	20	30	40	50	60
	70	80	90	100	110	120
m577.pep	YTVIKIILL	LFLLLAVINT	DAVTFSYLPQ	QKFDLPLIVV	LFQAFVVGII	FGMFALFGR

895

```

      |||||
g577  YTVIKIIILLFLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFVVGIVFGMFALFGR
      70      80      90      100     110     120

      130      140      150      160
m577.ppep  LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
      |||||:|||||:||||:||||| ||| ||:||||
g577  LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAESAQKQPX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1   ATGGAAAGGA  ACGGTGTATT  TGGTAAAATT  GTCGGCAATC  GCATACTCCG
51  TATGTCGTCC  GAACACGCTG  CCGCATCCTA  TCCGAAACCG  TGCAAATCGT
101 TTAAGTAGC   GCAATCTTGG  TTCAGAGTGC  GAAGCTGTCC  GGGCGGCGTT
151 TTTATTTACG  GAGCAAACAT  GAACTTATC   TATACCGTCA  TCAAAATCAT
201 TATCCTGCTG  CTCTCCTGCT  TGCTTGCTGT  CATTAATACG  GATGCCGTTA
251 CCTTTTCCTA  CCTGCCGGGG  CAAAAATTCG  ATTTGCCGCT  GATTGTCGTA
301 TTGTTCCGCG  CGTTTGTCTG  CGGCATCGTG  TTCGGAATGT  TTGCCTTGTT
351 CGGACGGTTG  TTGTCGTTAC  GTGGCGAGAA  CGGCAGGTG   CGTGCCGAAG
401 TAAAGAAAAA  TGC GCGTTT  ACGGGGAAGG  AGCTGACCGC  ACCACCGGCG
451 CAAAATGCGC  CCGAATCTGC  CAAACAGCCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.ppep
1   MERNGVFGKI  VGNRILRMSS  EHAAASYPKP  CKSFKLAQSW  FRVRSCPGGV
51  FIYGANMKLI  YTVIKIIILL  LFLLLAVINT  DAVTFSYLPQ  QKFDLPLIVV
101 LFGAFVVGIV  FGMFALFGR  LSLRGENGRL  RAEVKKARL  TGKELTAPPA
151 QNAPESAKQP  *

```

m577/a577 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577.ppep  MERNGVFGKIVGNRILRMSSEHAAASYPKPKCSFKLAQSWFRVRSCLGGVFIYGANMKLI
      |||||
a577  MERNGVFGKIVGNRILRMSSEHAAASYPKPKCSFKLAQSWFRVRSCPGGVFIYGANMKLI
      10      20      30      40      50      60

      70      80      90      100     110     120
m577.ppep  YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIIFGMFALFGR
      |||||
a577  YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGR
      70      80      90      100     110     120

      130      140      150      160
m577.ppep  LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
      |||||
a577  LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESAKQPX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq..
1   atgggaaagc  tcgacatcgg  gatattgttt  gccgatttct  tcaaagattt
51  cgcgccacag  ttcggtggtt  tccaaaacgt  tggctttgcc  tacggagcag
101 acttttttgc  tgcgtttttg  ggcggattgg  aaggccacgt  gggcgatgcg
151 gcggtatttcg  ctttcgctgt  atttcaggtt  gttgtagcct  tcgtgttcgc
201 cgttttccaa  aacacggatg  ccgcgcggtt  cgccgaaata  aatatcgccg
251 gtaagtctgc  gcacaatcaa  aatatccaaa  ccggcaacga  tttcaggctt
301 gagcgtggag  gcgttggcta  a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.ppep
1   MGKLDIGILF  ADFFKDFAPQ  FGGFQNVGFA  YGADFFAAFL  GGLEGHVGD
51  ADFAFVVFHG  VVAFVFAVFQ  NTDAARFAEI  NIAGKFAHNQ  NIQTGNDFRL

```

101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

m578.seq..

```

1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTTGC TCGTTTTTGC GCGGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGGCAACGA TTTCAGGCTT

```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

m578.pep..

```

1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*

```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	:					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGHVGDADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	:					
g578	VVAFVFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

a578.seq

```

1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCT TCAAAGATT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTTGC TCGTTTTTGC GCGGATTGG AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

a578.pep

```

1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*

```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	:					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	:					
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

g579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

```

897

```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGC GCGGGT TGGCGGTGGC GTTGTCTTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CCGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGC GCGGGT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCG CCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CCGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCCACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

```

1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120

898

	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGV DYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
g579	GNSIVNRSSLPLCRAQVIVGV DYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWT LQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
g579	DNAIEITLWAWANEADRWT LQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```

a579.seq
1   ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCTTGG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCGG CCCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGTGATG GGCAACAGCA TCGTCAACCG TTCCCACTG CCGCTGTGCC
401 GCGCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT TAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCCGCCG OCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAACG AAGCAGACCG CTGGACGCTG
601 CAATCGGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```

a579.pep
1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSLRRTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWT L
201 QCDLNEQVVE NLRKVNINIP FPQORDIHIIN S*

```

m579/a579 100.0% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILV IIAALGRLGVSTTSVTALIGGAGLAVALSL					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILV IIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRRTDNEEVVLPNSVVM					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRRTDNEEVVLPNSVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGV DYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
a579	GNSIVNRSTLPLCRAQVIVGV DYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWT LQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
a579	DNAIEITLWAWANEADRWT LQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

899

```

1  ATGGA CTCA  AACAA TTTGA  TTTT TACAC  CTGAT CAGTG  TTTCC GGTG
51  GGGGC ATCTG  GCTGA AAAAG  CGTGG GCGTT  CGGGC TGAAC  CTTGC CGCCG
101 CGCTG CTTAT  TTTCT TGGTC  GGGAA ATGGG  CGGCG AAAAC  CATTG TCGCC
151 GTAAT GAGGG  CGGCG ATGAC  GCGCG CGCAG  GTCGA TGCCA  CGCTG ATTAG
201 TTTT TTTGT  AATGT TGCCA  ATATC GGCCT  ATTGA TTTTG  GTGAT TATTG
251 CCGCA TTGGG  ACGGT TGGGC  GTTCC ACACA  CATCC GTAAC  CGCCT TAATC
301 GCGCG CGCGG  GTTTG GCGGT  GGCCT TGTC  TTAAG AGACC  AGCTG TCCAA
351 TTTTG CCGCC  GGCGC GCTGA  TTATC CTGTT  CCGCC CGTTC  AAAGT CGGCG
401 ACTTT ATCCG  TGTCG GCGGT  TTTGA AGGAT  ATGTC CGGGA  AATCA AAATG
451 GTGCA GACTT  CTTTG CGGAC  GACCG ACAAC  GAAGA AGTCG  TGCTG CCCC
501 CAGCG TGGTG  ATGGG CAACA  GCATC GTCAA  CCGTT CCAGC  CTGCC GCTTT
551 GCCG CGCCCA  AGTGA TAGTC  GGCCT CGATT  ACAAC TCGCA  TTTGA AAGTG
601 GCGAA AGAGG  CCGTG TTGAA  AGCCG CCGCC  GAACA CCCCT  TGAGC GTTCA
651 AAACA GAGAG  CGGCAG CCGC  CCGCT ACAT  CACCG CCCTG  GCGCA CAATG
701 CCATC GAAAT  CACATT ATGG  GCTTG GGCAT  ACGAA GCAGA  CCGCT GGACG
751 CTGCA ATGCG  ACTTG AACGA  ACAAG TGGTC  GAAAC CTTCC  GCAAAG TCAA
801 TATCA ACATC  CCGTT CCCGC  AACGC GACAT  ACACA TCATC  AATTCT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQ FDFLH  LISVS GWGHL  AEKAW AFGLN  LAAALL IFLV  GKWAA KRIVA
51  VMRAA MTRAQ  VDATL ISFLC  NVANI GLLIL  VIIAAL GRLG  VSTTS VTALI
101 GGAGL AVALS  LKDQL SNFAA  GALIIL FRPF  KVGDF IRVGG  FEGYV REIKM
151 VQTSR LRTDN  EEVVL PNSVV  MGNSI VNRSS  LPLCRA QVIV  GVDYN CDLKV
201 AKEAV LKAAA  EHPLS VQNEE  RQPAAY ITAL  GDNAIE ITLW  AWANE ADRWT
251 LQCDL NEQVV  ENLRK VNNIN  PFPQR DIHII  NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGA CTCA  AACAA TTTGA  TTTT TACAC  CTGAT CAGTG  TTTCC GGTG
51  GGAGC ATCTG  GCTGA AAAAG  CGTGG GCGTT  CGGGC TGAAC  CTTGC CGCCG
101 CGCTG CTTAT  TTTT TGGTC  GGGAA ATGGG  CGGCG AAAAC  CATTG TCCTG
151 GTGAT GAGGG  CGGCG ATGAC  GCGCG CGCAG  GTCGA TGCCA  CGCTG ATTAG
201 TTTT TTTGT  AATGT TGCCA  ATATC GGCCT  ATTGA TTTTG  GTGAT TATTG
251 CCGCA TTGGG  CAGAT TGGGC  GTTCC ACACA  CATCC GTAAC  CGCCT TAATC
301 GCGCG CGCGG  GTTTG GCGGT  GGCCT TGTC  CTGAA AGACC  AGCTG TCCAA
351 TTTTG CCGCC  GGCGC ACTGA  TTATC CTGTT  CCGCC CGTTC  AAAGT CGGCG
401 ATTTT ATCCG  CGTCG GCGGT  TTTGA AGGAT  ATGTC CGAGA  GATTA AAATG
451 GTGCA GACTT  CTTTG CGGAC  GACCG ACAAC  GAAGA AGTCG  TGCTG CCCC
501 CAGCG TGGTG  ATGGG CAACA  GCATC GTCAA  CCGTT CCACA  CTGCC GCTGT
551 GCCG CGCCCA  AGTGA TAGTC  GGCCT CGATT  ACAAC TCGCA  TTTGA AAGTG
601 GCGAA AGAGG  CCGTG TTGAA  AGCCG CCGTC  GAACA CCCCT  TGAGC GTTCA
651 AAACA GAGAG  CGGCAG GCTG  CCGCT ACAT  CACCG CCCTG  GCGCA CAATG
701 CCATC GAAAT  CACATT ATGG  GCTTG GGCAT  ACGAA GCAGA  CCGCT GGACG
751 CTGCA ATGCG  ACTTG AACGA  ACAAG TGGTC  GAAAC CTTCC  GCAAAG TCAA
801 TATCA ACATC  CCGTT CCCGC  AACGC GACAT  ACACA TCATC  AATTCT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQ FDFLH  LISVS GWEHL  AEKAW AFGLN  LAAALL IFLV  GKWAA KRIVA
51  VMRAA MTRAQ  VDATL ISFLC  NVANI GLLIL  VIIAAL GRLG  VSTTS VTALI
101 GGAGL AVALS  LKDQL SNFAA  GALIIL FRPF  KVGDF IRVGG  FEGYV REIKM
151 VQTSR LRTDN  EEVVL PNSVV  MGNSI VNRST  LPLCRA QVIV  GVDYN CDLKV
201 AKEAV LKAAV  EHPLS VQNEE  RQAAAY ITAL  GDNAIE ITLW  AWANE ADRWT
251 LQCDL NEQVV  ENLRK VNNIN  PFPQR DIHII  NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQFDFLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWA	KRIVAVMRAAMTRAQ				
g579-1	MDFKQFDFLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWA	KRIVAVMRAAMTRAQ				
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	130	140	150	160	170	180
m579-1.pep	GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST					

900

```

|||||
g579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.ppep LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||||
g579-1  LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.ppep AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX
          |||||||
g579-1  AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1  ATGGACTTCA  AACAAATTGA  TTTTITACAC  CTGATAAGTG  CTTCCGGCTG
51  GGAGCATCTG  GCTGAAAAGG  CGTGGGCGTT  CGGGCTGAAC  CTTGCCGCGG
101 CGCTGCTTAT  TTTTITGGTC  GGAAAATGGG  CGGCGAAACG  CATTGTCGCC
151 GTGATGAGGG  CGGCGATGAC  GCGCGCGCAG  GTCGATGCCA  CGCTGATTAG
201 TTTTITGTGT  AATGTTGCCA  ATATCGGCTT  ATTGATTTTG  GTGATTATTG
251 CCGCATTGGG  CAGATTGGGC  GTTCCACAA  CATCCGTAA  CGCCTTAATC
301 GCGGCGCGCG  GTTGGCGGCT  GCGGTTGTCC  TTGAAAGACC  AGCTGTCCAA
351 TTTTGCCGCG  GCGCGCTGA  TTATCCTGTT  CCGCCCGTTC  AAAGTCGGCG
401 ATTTATCCG  CGTCGGCGGT  TTTGAAGGAT  ATGTCCGAGA  GATTAAATG
451 GTGCAGACTT  CTTTGGCGAC  GACCGACAAC  GAAGAAGTCG  TGCTGCCCAA
501 CAGCGTGGTG  ATGGGCAACA  GCATCGTCAA  CCGTTCACA  CTGCCGCTGT
551 GCCGCGCCCA  AGTGATAGTC  GCGCTCGATT  ACAACTGCCA  TTTGAAAGTG
601 GCGAAAGAGG  CGGTGTTGAA  AGCCGCCGTC  GAACCCCT  TGAGCGTTCA
651 AAACGAAGAG  CGGCAGGCCG  CCGCTACAT  CACCGCCTTG  GCGGACAATG
701 CCATCGAAAT  CACATTATGG  GCTTGGGCAA  ACGAAGCAGA  CCGTGACG
751 CTGCAATGCG  ACTGAACGA  ACAAGTGGTC  GAAAACCTCC  GCAAAGTCAA
801 TATCAACATC  CCGTCCCGC  AACGCGACAT  ACACATCATC  AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.ppep
1  MDFKQDFDLH  LISASGWEHL  AEKAWAFGLN  LAAALLIFLV  GKWAAKRIVA
51  VMRAAMTRAQ  VDATLISFLC  NVANIGLLIL  VIIAALGRLG  VSTTSVTALI
101 GGAGLAVALS  LKDQLSNFAA  GALIILFRPF  KVGDFIRVGG  FEGYVREIKM
151 VQTSRLRTDN  EEVLPNSVV  MGNSIVNRST  LPLCRAQVIV  GVDYNCDLKV
201 AKEAVLKAAV  EHPLSVQNEE  RQAAAYITAL  GDNAIEITLW  AWANEADRWT
251 LQCDLNEQVV  ENLRKVNINI  PFPQRDIHII  NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.ppep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          |||||||
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.ppep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||||
m579-1  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.ppep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          |||||||
m579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.ppep LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||||
m579-1  LPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.ppep AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQRDIHIINSX

```

901

```

|||||
m579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

```

g580.seq
1  atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51  cgcgtcgcag ccatttcga tggcaaggca gacttcgccg atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
151 tcgaaaaatca gcttggtaaa gccgttgctg caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
251 ctttggcaga caattcggtt tcaccgacct atgccacttc gggggaagtg
301 tag

```

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

```

g580.pep.
1  MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

```

m580.seq..
1  ATGGATTTCGC CCAAGGTTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCGGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTGTGCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCCACGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCGGA CAGTTCGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
301 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

```

m580.pep..
1  MDSPKVGCGW MVLPMASASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101 *

```

m580/g580 97.0% identity in 100 aa overlap

```

          10      20      30      40      50      60
m580.pep  MDSPKVGCGWMVLPMASASQPISMARQTSP IISPPFGPTM PPPMMRPVSASKISLVKPLS
          |||||
g580       MDSPKVGCGWMVLPMASASQPISMARQTSP IMSPPFGPTM PPPMMRPVSASKISLVKPLS
          10      20      30      40      50      60

          70      80      90      100
m580.pep  QPLAIARPEAAHGKLALVILRPEALADSSVSPTHATSGEVX
          |||||
g580       QPLAIARPEAAHGKLALVILRPDALADNSVSPTHATSGEVX
          70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

```

a580.seq
1  ATGGATTTCGC CCAAGGTTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51  CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCCG
101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTGCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG
251 CTTTGGCAGA CAATTCGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
301 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

```

a580.pep
1  MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51  SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

```

902

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX					
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1  atgcacttcg cccagcttgt gggcacaacc ggtatagaac aaaatacgtt
51  ctgtcgtcgt ggttttaccg gcatcgatat gggcggaaat accgatgttg
101 cggtagacagg tgatcggggg cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagtgagaga atgctttgtt ggcttcagcc atacggtgta
201 cttcttcacg ttttttcaac gcaccgccac ggccttcgga cgcacatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttcggggc
301 cgcgtcgcgga acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHQCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCCTTCAAG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGGLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAQADRGGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLTTFAGRVANPTHQCSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

```

a581.seq
  1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
 51  CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101  CGGTACAGGC TGATCGGGGT CTACGAGCC ATTTTATTAG CCTTTCAAAA
151  TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201  CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251  AATTCGCGTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGCGGC
301  CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
  1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTQADRG LTSHFISLSK
 51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101  RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
	:					
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
a581	GFSHTVYFFTFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
  1  atgcgcctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51  agagaccgcg ctgcaatgcg ccgctttgac ggacaatgtt acgcgtttgg
101  cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151  gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201  cagcttggat aagggcgagg cggtcattgt tgttgaaaaa ggcggggatg
251  cgcttcctgc gcacagtgcg ggcgaaaccg ccgatatcta tacgcctttg
301  agcctgatgt acgacttggc caaaaacgat ttgcgcgggc tgttggcggt
351  acgcgaacac aatccgatgt accttatgcc gttttggtat aacaattcgc
401  ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451  ttcggacagc agaaacgtgc ggaaaccaa ttgcaggttt cgttcaaaag
501  caaaattgcc gaaaatttgt ttaaaacccg cgcggatctg tggttcgggt
551  acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601  ccgttccgca atacggatta caaacctgaa attttctga cccagcctgt
651  gaagggcagg ttgccgttcg gcggcaggct gcgtatgctc ggtgcggggt
701  ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcgtggaac
751  aggatttatg ccatggcagg catggaatgg ggcaaattga cggtgattcc
801  gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851  ccgatattgc cgactatatg gggatatggc acgtgaagct gcagtaccgc
901  ctgaacgaca ggcagaatgt gtattccgta ttgcgtaca accccaaaac
951  gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcgggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
  1  MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
 51  EQQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101  SLMYDLKND LRGLLGVRH NPMYLMPFY NNSPNYAPSS PTRGTTVQEK
151  FGQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSDW QIYNQGRKSA
201  PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNG QSRPESRSWN
251  RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301  LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI GKGLKGVVRG FHGYGESLID
351  YNHKQNGIGI GLMFNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
  1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
 51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101  CGTGTTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151  GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201  CAGCCTGGAT AAGGGCGAGG CCGTCATTGT TGTGAAAAA GGCGGGGATG
251  CGCTTCTGCG CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301  AGCCTGATGT ACGACTTGGG CAAAAACGAT TTGCGCGGGC TGTGGGCGGT
351  ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401  CCAACTATGC CCCGGGTTCC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451  TTCGGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTCAAAAG
501  CAAAATTGCC GAAGATTTGT TTAACACCCG CCGGATCTCG TGGTTCGGCT
551  ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601  CCGTTCGGCA ATACGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651  GAAGGCGGAT TTGCCGTTCC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701  TTGTCCACCA GTCCAAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751  AGGATTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
801  GCGCGTGGG GTGCGTGCCT TCGATCAGAG CCGCGATAAA AACGACAATC
851  CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901  CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951  GGGCTACGGC GCGATTGAAG CCGCTACAC GTTTCGGATT AAGGGCAAAC
1001 TCAAAGCGGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
  1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
 51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101  SLMYDLKDND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151  FGQQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSWQ QIYNQGRKSA
201  PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNG QSRPESRSWN
251  RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYDM GYGDVKLQYR
301  LNDRQNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKVVVRG FHGYGESLID
351  YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

m582.pep	10	20	30	40	50	60
	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
	10	20	30	40	50	60
m582.pep	70	80	90	100	110	120
	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKDNDLRLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKDNDLRLLGVREH					
	70	80	90	100	110	120
m582.pep	130	140	150	160	170	180
	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLFWYNNSPNYAPSSPTRGTTVQEKFGQKRAETKLQVSFKSKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	190	200	210	220	230	240
	WFGYTQRSWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNG					
g582	WFGYTQRSWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNG					
	190	200	210	220	230	240
m582.pep	250	260	270	280	290	300
	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYDMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYDMGYGDVKLQYR					
	250	260	270	280	290	300
	310	320	330	340	350	360

905

```

m582.pep  LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGPHGYGESLIDYNHKQNGIGI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
g582      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGPHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          ||||| ||||
g582      GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTTGAAAAA GCGCGGGATG
251 CGCTTCCTGC CGACAGTGC GCGGAAACCG CCGACATCTA TACGCCTTGT
301 AGCCTGATGT ACGACTTGA CAAAAACGAT TTGCGCGGGC TGTTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
401 CCAACTATGC CCCGGGTTGC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAAACCAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTGT TTA AACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGCGGAT TTGCCGTTGC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAAATG GTATTCCGTA TTGCGCTACA ATCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCCTACAC GTTTCGGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLGVRH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GLTVIPRVW VRAFDQSGDK NDNPDADYD GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHNKQNGIGI GLMFNDLDGI *

m582/a582  100.0% identity in 370 aa overlap

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLGVRH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

m582.pep	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAETKLQVSFKSKIAEDLFKTRADL
a582	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAETKLQVSFKSKIAEDLFKTRADL
	130 140 150 160 170 180
m582.pep	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
a582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ
	190 200 210 220 230 240
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIADYMGYGDVKLQYR
a582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIADYMGYGDVKLQYR
	250 260 270 280 290 300
m582.pep	LNDRQNVYSVLRYNPKTG YGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
a582	LNDRQNVYSVLRYNPKTG YGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
	310 320 330 340 350 360
m582.pep	GLMFNDLDGIX
a582	GLMFNDLDGIX
	370

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg  accaaagcca  aatatttacc  catcttgcc  tctgtgcctt
51  ttgcgggatt  ggagccgtaa  ctgccggcaa  tcgactgcat  aatcggatgt
101  ataatgccgc  cgccgcgcgc  ggtattggaa  ggggtaacgg  gagccagcag
151  cagttcggaa  agagcgagac  tgtaaccgat  gccagcggtt  tttcttccaa
201  aaacggcgat  aaacaaatat  ccgatacgca  tccccagccc  tgttttgagc
251  aaaccgcgcg  aaatcataac  tgcgatggca  atcagccaaa  tcaacggatt
301  ggcgaaacga  ctcaacgcat  cgctcatcgc  cgcgcccggg  ttgtcggcgg
351  ttacgcgggt  tactgcgacc  aaccgcgacg  caataatcga  cagcgcgccc
401  aacggcataa  ccttgccgat  aatggcggca  atcacaccga  caaacatagc
451  cagcagcgtc  caagcctgag  gcttgacccc  gtcgggtacg  ggcagtgcca
501  aaaccagggc  gcacaatact  gcggcaatgg  cgaggggtat  cggtttgaaa
551  cccaatttca  tcattattgac  ctccgtaaaa  aagaccgtcc  cgaaaaatcg
601  gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSQIFT  HLAFCFAFCGI  GAVTAGNRLH  NRMYNAAAAR  GIGRGNGSQQ
51  QFGKSETVTD  AQRFSKNGD  KQISDTHPQP  CFEQTARNHN  CDGNQPNQRI
101  GERTQRIahr  RARFVGGYAG  YCDQPDGNNR  QRAQRHNLAD  NGGNHTDKHS
151  QQRPSLRldp  VGYGQCQNQG  AQYCGNGEGY  RFETQFHHID  LRKKDRPEKS
201  EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG  ACCAAAGCCA  AATATTTACC  CATCTTGCCT  TCTGTGCCTT
51  TTGCGGGATT  GGAGCCGTAA  CTGCCGCAAA  TCGACTGCAT  AATCGGATGT
101  ATAATGCCGC  CGCCGCGCGC  GGTATTGGAA  GGGGTAACGG  GAGCCAGCAG
151  CAGTTCGGAA  AGAGCGAGAC  TGTAACCGAT  GCCCAGCGTT  TTTCTTCCAA
201  AAACGGCGAT  AAACAAATAT  CCGATACGCA  TCCCCAGCCC  TGTTTTGAGC
251  AAACCGCGCG  AAATCATAAC  TGCGATGGCA  ATCAGCCAAA  TCAACGGATT
301  GGCGAACGCA  CTCAACGCAT  CGCTCATCGC  CGCGCCCGGT  TTGTCGGCGG
351  TTACGCCGGT  TACTGCGACC  AACCCGACGG  CAATAATCGA  CAGCGCGCCC
401  AACGGCATGG  CCTTGCGGAT  AATGGCGGCA  ATCACACCGA  CAAACATGGC
451  CAGCAGCGTC  CAAGCCTGAG  GCTTGACCCC  GTCGGGTACG  GGCAGTGCCA
501  AAACCAGGGC  GCACAATACT  GCGGCAATGG  CGAGGGGTAT  CGGTTTGAAA

```

551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNQSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSLRLLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

m583.pep	10	20	30	40	50	60
	MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNQSQQ QFGKSETVTD					
g583	MIIDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNQSQQ QFGKSETVTD					
	10	20	30	40	50	60
m583.pep	70	80	90	100	110	120
	AQRFSKNGDK QISDTHPQPCFEQTARNHNC DGNQPNQRIGERTQRIahr RARFVGGYAG					
g583	AQRFSKNGDK QISDTHPQPCFEQTARNHNC DGNQPNQRIGERTQRIahr RARFVGGYAG					
	70	80	90	100	110	120
m583.pep	130	140	150	160	170	180
	YCDQPDGNNR QRAQRHGLADNGGNHTDKHG QQRPSLRLLDPVGYGQCQNQGAQYCGNGEGY					
g583	YCDQPDGNNR QRAQRHNLADNGGNHTDKHSQQRPSLRLLDPVGYGQCQNQGAQYCGNGEGY					
	130	140	150	160	170	180
m583.pep	190	200				
	RFETQFHHD LKKDRPEKSEKX					
g583	RFETQFHHD LKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTGCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGCGCAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCGGCGG
351 TTACGCCGGT TACTGCGACC AACC CGACGG CAATAATCGA CAGCGACCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTTC TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNQSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSLRLLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHD LKKDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

m583.pep	10	20	30	40	50	60
	MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNQSQQ QFGKSETVTD					

908

```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQQFGKSETVTD
           10      20      30      40      50      60
m583.pep  AQRFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
           70      80      90      100     110     120
a583      AQRFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
           70      80      90      100     110     120
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRRLDPVGYGQCQNQGAQYCGNGEGY
           130     140     150     160     170     180
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRRLDPVGYGQCQNQGAQYCGNGEGY
           130     140     150     160     170     180
m583.pep  RFETQFHHIDLRRKKDRPEKSEKX
           190     200
a583      RFETQFHHIDLRRKKDRPEKSEKX
           190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

```

g584.seq..
1  atgctgcgtt ctatcttggc ggcttccctg ctggcggtat cttttccggc
51  ggcggtgag gcattgaatt acaatattgt cgaattttcc gaatcgcgcg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcgcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagttgtta aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cgcgcagtgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggagggca gggatttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcggttctg ggtgcgtccg gttataaaat cgtcaaattg aattttgggc
551 aaatcggcag ccatattgcy ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc ccatattgcy ggcgatgggg ctgttcgggc aaaaatgctg
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

```

g584.pep Length:..
1  MLRSILAASL LAVSFPAABE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNVANA EFVKKFNFT RKSKNGSFKT ELVRSAMPR YQYTNRRRIQ
101 TGWEERAEPK AGRDFDALN RFIADVQTD SLEDTDFSVS RERRNEVDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

```

m584.seq..
1  ATGTTGCGTC TTGTTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAATATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTCATC AGAAAAATCGA AAAATGGTAG CTTTAAACCC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTTAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGmAT
401 ATACGGATTT CCATGTGTGC CGCGAACGCC GCAACGAGGT CATCKATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCGC CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

m584.pep..

```

1  MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNGRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

	10	20	30	40	50	60
m584.pep	MLRLVLAASLSAVSFPAAAEALNYNIVEFS	ESAGVEVAQDTMSARFQVTA	EGRDKNVNA			
	:					
g584	MLRSILAASLLAVSFPAAAEALNYNIVEFS	ESAGIEVAQDTMSARFQVAAEGRDKNVNA				
	10	20	30	40	50	60
	70	80	90	100	110	120
m584.pep	EFVKKFNKFI	RSKNGSFKT	ELVSRSAMPR	YQYTNGRRIQ	TGWEERAEFK	VEGRDFDELN
		:				
g584	EFVKKFNNTFR	RSKNGSFKT	ELVSRSAMPR	YQYTNGRRIQ	TGWEERAEFK	AEGRDFDALN
	70	80	90	100	110	120
	130	140	150	160	170	180
m584.pep	RFIADIQADA	ALXYTDFHVS	RERRNEVIXQ	VSKDAVLRFK	KARAEKLAGVL	GASGYKIVKL
		:		:		
g584	RFIADVQTDAS	LEDTFDSV	SRRNEVIDQ	VSKDAVLRFK	KARAEKLAGVL	GASGYKIVKL
	130	140	150	160	170	180
	190	200	210	220	230	
m584.pep	NLGHIGSHIAG	GGAAQAKML	RAMPMAASVN	MEGADSAAPG	VEEISISVNG	TVQFX
		:		:		
g584	NFGQIGSHIAG	DGAVRAKML	RAMPMAASVN	MMKGTDSAAPG	VEEISISVNG	TVQFX
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

a584.seq

```

1  ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51  .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTACAC AGAAAATCAA AAAATGGTAG CTTTAAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TCGGTTGAAC CGTTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGATTTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTGG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

a584.pep

```

1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNVNA EFVKKFNFT RSKNGSFKT ELVSRSAMPR YQYTNGRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

	10	20	30	40	50	60
m584.pep	MLRLVLAASLSAVSFPAAAEALNYNIVEFS	ESAGVEVAQDTMSARFQVTA	EGRDKNVNA			
	:					
a584	MLRSILAASLL-----	IVEFS	ESAGVEAVQDTMSARFQVTA	EGRDKNVNA		
	10	20	30	40	50	60

910

	70	80	90	100	110	120
m584.pep	EFVKKFNKFKIRKSKNGSFKTELVSRSAMPYQYTNGRRITQGWEEERAEFKVEGRDFDELN					
a584	EFVKKFNNFTRKSKNGSFKTELVSRSAMPYQYTNGRRITQGWEEERAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADALEYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcat  tttcgccaca  ttttgcgcg  ttatcgctctg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctggtgcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattattt  ccgcattcaa  gacacggggc  gacaacggcg  cgcgcgaaat
201  cctgaccgaa  tggaaaaaca  gccccgtctc  atccgccgtt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaacc  gctatatcga  caattacacc
301  atagaacgcg  cccggtgtgt  tgccgccaac  aacccccatt  ccaaccttgt
351  ccgcattcgaa  tacgaccgtt  tcggcggaaga  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggccctgccg  ttgccccgat  ttggcacgaa  ttcattcatc  tctccttcat
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aaccctcag  aatcttaggc  aacggcatgg  acagggtggc  agaacgagaa
601  cttgaagacc  gcgtttgcca  acaggttcgc  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgcaattcg  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFQRI FAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETTLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQGDDEK  IILNRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGEEYLF  FIKGWDNHQA  QRLPSPLFIP
151  GLPLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCQQVR  DRDDELADVA  MQFDTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAAACTGT  TCCAACGCAT  TTTCGCCACA  TTTTGC GCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCAG  AACACCCTTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATTCG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCTGACGGA  TGGAAAGACA  GCCCCGTCTC  ATCGGCGGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCGGCTTTT  CGCCGCCGGA  CACCCGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACCGCT  TCGGCGAAGA  ATACCTGTTT  TTCACCAAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCCGCCTGC  CCAGCCCTCT  GTTGATCCCC
451  GGCCTGCCGC  TCGCCCCGAT  TTGGCAGGAA  CTCATCATAT  TGTCTTCAT
501  CATCATCGTC  GGACTGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AACCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGGTGGC  AACCGGAGAA
601  CTTGAAACCC  CTATCTCCCA  ACAGGTCGAC  GACCGCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTCG  ACAAATGGT  GGAAAACTC  GAAAACTCG
701  TTGCCAAGA  ACGCCACCTG  CTCCATCAG  TCTCCCATGA  AATGCGTTCT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTGCGA  CTGATTGAGG  CGCAGCCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAAGTG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAAGTG  TTAACCCTGT  CCCGTCTCGA  AACTTCCAAT
901  ATGGCTTTGG  AAAAAAGAA  CCTGAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAGAAGAC  AATCAAAGCA  TTGCCAGAA  AAACGGACAA  ACGGTTACCC
1001  TGCTTGCCGA  CGGAAAAATC  CCCGAAAACA  CAACCATCCT  TGCCAACGAA

```

```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGET TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```

1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKDD ILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQVVD DRDDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPKQKE QYLRLEGELE TRMDTLAGELE LTLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNQO TVTLSADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNYSPG GSTILINIQO DHKHWIIDVT DNGPGVDEMO
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

```

          10      20      30      40      50      60
m585.pep  MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRTIETTLMGSIISAFRARG
          |||
g585       MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRTIETTLMGSIISAFKTRG
          10      20      30      40      50      60

          70      80      90      100     110     120
m585.pep  DAGAREILTEWKDSPVSSGVYVIQGDEKDDILNRYIDSYTIERARLFAAGHPHNSNLVHIE
          |||
g585       DNGAREILTEWKNSPVSSAVYVIQGDEKDDILNRYIDNYTIERARLFAANNPHNSNLVRIE
          70      80      90      100     110     120

          130     140     150     160     170     180
m585.pep  YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
          |||
g585       YDRFGEEYLF FIKGWDNHQAQRRLPSPLFIPLGLPLAPIWHEFIILSFIIIVGLLMAYILAG
          130     140     150     160     170     180

          190     200     210     220     230     240
m585.pep  NIAKPIRILNGMDRVANGELETRISQVVD DRDDELSHLA IQFDKMVEKLEKLVAKERHL
          |||
g585       NIAKPIRILNGMDRVAERELEDRVCQVDRDRDELADVAMQFDTMVEKLEX
          190     200     210     220     230

          250     260     270     280     290     300
m585.pep  LHHVSHEMRSPLARMQAIVGLIQAQPKQKEQYLRLEGELETRMDTLAGELELTLRLETSN

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```

1 ATGAAACTGT TCCAACGCAT CTTCGCCACA TTTTGCGCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCGAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAGACA GCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTT TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
451 GGCTGCGCG TCGCCCGAT TTGGCAGGAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC

```

```

651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAAGA ACGCCACCTG CTCCATCAG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTGAG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAACTG TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAAGAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGCTGCGCGA CGGAAAAATC CCCGAAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAAGTGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

```

a585.pep
  1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
 51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEK KD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLI
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDEL SHLA IQFDKMVEKL EKLVAKE RHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPQKQE QYLKRLEGE LTRMDTLAGE LTLRSLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIQ DHKHWIIDVT DNGPGVDEM Q
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKI IA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

m585/a585 99.8% identity in 468 aa overlap

      10      20      30      40      50      60
m585.pep MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG
a585      MKLFQRI FATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRARG
      10      20      30      40      50      60

      70      80      90      100     110     120
m585.pep DAGAREILTEWKDSPVSSGVYVIQGDEKKDILNRYIDSYTIERARLFAAGHPHNSNLVHIE
a585      DAGAREILTEWKDSPVSSGVYVIQGDEKKDILHRYIDSYTIERARLFAAGHPHNSNLVHIE
      70      80      90      100     110     120

      130     140     150     160     170     180
m585.pep YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
a585      YDRFGEEYLF FTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
      130     140     150     160     170     180

      190     200     210     220     230     240
m585.pep NIAKPIRILGNMMDRVANGELETRISQQVDDRDEL SHLA IQFDKMVEKLEKLVAKERHL
a585      NIAKPIRILGNMMDRVANGELETRISQQVDDRDEL SHLA IQFDKMVEKLEKLVAKERHL
      190     200     210     220     230     240

      250     260     270     280     290     300
m585.pep LHHVSHEMRSPLARMQAIVGLIQAQPQKQE QYLKRLEGE LTRMDTLAGE LTLRSLRLETSN
a585      LHHVSHEMRSPLARMQAIVGLIQAQPQKQE QYLKRLEGE LTRMDTLAGE LTLRSLRLETSN
      250     260     270     280     290     300

      310     320     330     340     350     360
m585.pep MALEKESLKL LPFLGNLVEDNQSIAQKNGQTVTLSADGKI PENTTILANESYLYRAFDNV
a585      MALEKESLKL LPFLGNLVEDNQSIAQKNGQTVTLSADGKI PENTTILANESYLYRAFDNV

```

913

	310	320	330	340	350	360
	370	380	390	400	410	420
m585.pep	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1   atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatattt
51  ttggaaaacc acgggcaaat ggctgtttgc cctgctgatt ttggcggcac
101 tccgctactt gggatacacg gtttaccaaa accgtgcggc ttcccaaaat
151 caggaagcgg cgcggtgctt ggcaaacatc gtggaaaagg cgcaaaacaa
201 agccccgcga agcgaaatca atgccgaact gtccaaactc caacaaagct
251 acccccattc catttcggcc gcccaagcca cgctgatggc ggcggaacc
301 gaatttgacg cgcagcggtt cgatgttgcc gaaggtcatt tgaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttgccg gcgcagcgtc
401 tggcggttgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctgcacacgc cggttgaggg ggacttcgcc cccctgctga tggaaactaa
501 aggcgatgtt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551 acggacaggg tttggaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1   MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNR AASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAElskl QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHlKWVLSN QKDSLlQALA AQLGvvllQ QKKYDAALAA
151 LDTpVEADFA PLLMETKGDV YAAQEKsQEA LKNYgQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1   ATGCGAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAAC TTAATATTT
51  TTGGA AAAACC ACGGGCAAAT GGCTGTTTGC CTTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTAAAGT TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTAGAAAAGG CGCAAAGCAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GACCAAATC CAACAAAGCT
251 ACCCGCATTC CATTTCCGCC GCCCAAGCCA CACTGATGGC GCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 GTTGTC CAAC CAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGCGTGTGT GTTGTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCG
451 CTCGATACGC CGGTTGAAGC GGA CTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGA AAAAG CCAGGAAGCC TTA AAAA ACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCAATTG
601 GTTCAAATGA AACTTGATT C GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1   MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNR KVSN
51  QEAAAVLANI VEKAQSKAPQ SEINAEltkl QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHlKWVLSN QKDSLlQALA AQLGvvllQ QKKYDAALAA
151 LDTpVEADFA PLLMETKGDV YAAQGKSQEA LKNYgQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQE LDNFKYFWKT TGKWL Falli LAALGYLGYT VYQNR KVSN QEAAAVLANI					

914

```

g586      MAAHLEEQQE LDNFKYFWKT TGKWLFA LLI L AALGYLG YTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKAPQSEINAELSKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSLIIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQEKSQEA
           130     140     150     160     170     180

           190     200     210
m586.pep  LKNYGQALEKMPQDSVGRELVQMKLDSLKX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      LKNYGQALEKMPQDSVGRELLQMKLDSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1   ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51  TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTGCGGC TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 ATTGTCCAAC CAAAAAGACA GCCTGATCCA GCGTGTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TAAAAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1   MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLG YTVYQNRAASQN
51  QEAAAVLANI VEKAQNKAPQ SEINAELAKL QQSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLKWVLSN QKDSLIIQALA AQLRGVVLLQ QKKYDAALAA
151 LDTPEADFA PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

m586/a586  97.6% identity in 209 aa overlap

           10      20      30      40      50      60
m586.pep  MAAHLEEQQE LDNFKYFWKT TGKWLFA LLI L AALGYLG YTVYQNRAASQNQEAAAVLANI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI L AALGYLG YTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKAPQSEINAELAKLQQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWVLSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSLIIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           130     140     150     160     170     180

```

915

	190	200	210
m586.pep	LKNYGQALEKMPQDSVGR	ELVQMKLDSLKX	
a586	LKNYGQALEKMPQDSVGR	ELVQMKLDSLKX	
	190	200	210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
  1  atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
 51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101  aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151  gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201  ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251  ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301  ggacgaggca gctatctgtg gcacgaagaa cgcaaaactcg acggcaacgg
351  caaaacccgc aacaaacgga tgtccgacat atccgccggc atcagccaca
401  ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451  acggttttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501  gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
  1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNSR
 51  AALAAPVYIQ TGATSFIPIP TEIQENGST DMLAGTLGLR YGLTGNTDIY
101  GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151  TVYEKSRNKA SLIKRGLCP FYNLRYNEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
  1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
 51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101  AATGGAAACT GGAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151  GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201  CCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251  TCGGCACGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301  GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACAG
351  CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401  CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451  ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501  CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551  CCGCCGCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601  TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGTGCTG
651  CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701  CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751  GCCCATTTG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801  ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851  GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
  1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
 51  AELAAPVYIQ TGATSFIPIP TEIQENGST DMLVGTGLR YGLTGNTDIY
101  GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151  TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201  YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251  AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10

20

30

40

50

60

916

```

m587.pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
                ||||||||||||||||:|||||||||||||||||||||||||||||||
g587           MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENSRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587.pep      TGATSFIPTEIQENGSTNDMLVGTGLGLRYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                ||||||||||||||||:|||||||||||||||||||||||||||||||
g587           TGATSFIPTEIQENGSTNDMLAGTGLGLRYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

                130     140     150     160     170     180
m587.pep      NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
                |||||:| ||||||||| |||||||||||||||||||||
g587           NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKKRGLCPFYNLIRINYEY
                130     140     150     160     170     180

                190     200     210     220     230     240
m587.pep      LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587           X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587.seq
1   ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAAGTGG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTAT
201 CCCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGGCG TACGGACTGA CCGGAATAC CGACATTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCACCG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATGTA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

```

a587.pep
1   MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENN
51  AELAAPVYIQ TGATSFIPTE IQENGSTND DMLVGTGLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

m587/a587 95.2% identity in 289 aa overlap

```

                10      20      30      40      50      60
m587.pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
                ||||||||||||||||:|||||||||||||||||||||||||||||||
a587           MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587.pep      TGATSFIPTEIQENGSTNDMLVGTGLGLRYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                ||||||||||||||||:|||||||||||||||||||||||||||||||
a587           TGATSFIPTEIQENGSTNDMLVGTGLGLRYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

```

917

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLKGQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1  atgcttaaac atctcgcat cctactgccc gccatgatgt tcgccctccc
51  cgccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaaaagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaag gcttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCGTCCTGA CTTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTTCG TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAAC
401 TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1  MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAKGKTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMK EVKLPPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVKGDKGPAGKGTWRCQDGRNYTGS
g588        MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGLP SGKGIWRCRDGRGYTGS
              10      20      30      40      50      60

              70      80      90     100     110     120
m588.pep    FKNGKFDGQGVYTVAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
g588        FKNGKFDGQGVYTVAAGREVLFEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
              70      80      90     100     110     120

              130     139
m588.pep    IMKCENGMIKEVKLPKNKX
g588        YYEMRTRHDX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51 CGCCGCGTCC GCCGTTCTGA CTTCCTATCA AGAACCCGGC TGCACCTACG
101 AAGGCGATGT CGGCAAAGAC GGTAACCCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTTCG TTTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAA GAAGTGAAGC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1  MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKL PKNK*

m588/a588    96.4% identity in 138 aa overlap

              10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVKGDKGPAGKGTWRCQDGRNYTGS
a588        MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKDGPAGKGTWRCQDGRNYTGS
              10      20      30      40      50      60

              70      80      90     100     110     120
m588.pep    FKNGKFDGQGVYTVAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
a588        FKNGKFDGQGVYTVAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
              70      80      90     100     110     120

              130     139
m588.pep    IMKCENGMIKEVKLPKNKX
a588        IMKCENGMIKEVKLPKNKX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1  atgcaacaaa aaatccgttt ccaaatcgag gcgatgacct gtcaggcatg
51  tgcttcgcgc attgaaaaag tgttgaacaa aaaagatttt gtcgaatcgg
101 cgggagtgaa ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcgagggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcggtcg gcggttggtg cttttgctga ccatcaatat cccgttcctt

```

```

301 atcgggtatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgaac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaaggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgtcgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgatgcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggcgtga tgggtgatcg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgccgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttacc
751 cgaccaacc acggcgaacg catcgctgcc gacggcatta tcgaaagcgg
801 cagcggttgg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggc gggcggcaaa gtgttggcgg gcgcgtgat gaccgaaggc
901 agcgtggtgt accgcgcgcg gcagctcggc agccaaacc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcatac
1051 gcgcttctga cttttatcgt tgcttggctg attaagggcg attggacggg
1101 cgcactgatg cacgcggttg ccgttttgtt gattgcctgc ccgtgcgcgc
1151 tcggtctggc gacccctgcc gcgattatgg tcggcatggg caaagcggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtatttg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc cgcggtttat tacgttcccg acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgcgc cccaccgcgt
1401 cgccgcgcgc atcgtctccg ccgcacaagc gcgcggtttg gagattcccg
1451 ctgcacaaaa tgcgcaaac gttgtcggag caggcattac cgccgaagtg
1501 gaaggcgttg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgg atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccaagc cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccg tggcgatggt
1851 cggcgacggc atcaacgacg cgcccgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgttcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct attttctgcc ttcttctaca
2051 atatatggg cattccgctc gccgcgctcg gctttttaa tcccgtcata
2101 gcaggcgcgg caatggcggc aagctcgggt tcggtattgg gcaatgcctt
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE  AMTCQACASR  IEKVLNKKDF  VESAGVNFAS  EEAQVTFDGS
51  KTSVADIAKI  IEKTYGAKE  KTEDTLQPE  AEHHIGWRLW  LLLTINIPFL
101  IGMVGMMLKG  LNWTRHDWMI  PPVWQFVLAS  IVQLWLAIPF  YKSAWASIKG
151  GLANMDVLVT  IGTVSIYLYS  VYMLFFSSHA  AHGMAHVYFE  AGVMVIGFVS
201  LGKFLEHRTK  KSSLNSLGLL  LKLTPTQVNV  QRNGEWKQLP  IDQVQIGDLI
251  RTNHGERIAA  DGIIESGSGW  ADESHLTGES  NPEKKKAGGK  VLAGALMTEG
301  SVVYRAAQLG  SQTLLGDMMN  ALSEAQGSKA  PIARVADKAA  AVFVPTVVGI
351  ALLTFIVAWL  IKGDWTVAlM  HAVAVLVIAc  PCALGLATPA  AIMVGMGKAV
401  KHGIWFKDAA  AMEEAAHVDA  VVLDKTGTLT  EGRPQVAAYV  YVPDSGFDED
451  ALYRIAAAVE  QNAAHPLARA  IVSAAQARGL  EIPAAQNAQT  VVGAGITAEV
501  EGVGLVKSgK  AEFAELTLPK  FSDGVWEIAS  AVTVSVNGKP  IGAFALSDAL
551  KADTAEAIgR  LKKHNIDVYI  MSGDNQSTVE  YVAKQLGIAH  AFGNMSPCDK
601  AAEVQKLKAA  GKTVMVGDG  INDAPALAAA  NVSFAMKGGA  DVAETASAT
651  LMQHSVNQLA  DALLISQATL  ENIKQNLFFA  FFYNILGIPL  AALGFLNPVI
701  AGAAMAASSV  SVLGNALRLK  WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA  AAATCCGTTT  CCAAATCGAA  GGCATGACCT  GCCAGGCCTG
51  CGCTTCGCGC  ATTGAAAAAG  TGTGTAACAA  AAAAGATTTT  GTCGAATCGG
101  CGGGGGTAAA  CTTGCCAGC  GAAGAGGCGC  AGGTAGTGTT  TGACGACAGC
151  AAAACCTCAG  TAGCCGACAT  TGCCAAAATC  ATTGAGAAAA  CCGGTTACGG
201  CGCGAAGGAA  AAAACGGAAG  ATACATTGCC  GCAACCCGAA  GCAGAACACC
251  ATATCGGCTG  GCGGCTGTGG  CTGCTGTTCa  CCATCAACGT  CCCGTTTCCT

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920

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301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTACAA AAGCGCGTGG GCGAGCATTA AGGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGCTACTGGG TAAATTTTTG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTT GGCGGCGCGG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCAGCTC GGCGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TGCGCGCGTA GCCGATAAAG
1001 CGGCTGCGGT ATTCGTGCCT GCCGTCTGGT GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CGCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTTAAACA CGGTATTTGG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCCAGCTCG ATGCCGTCGT
1251 GTTGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCCG
1301 TTTATTGCGT TCCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCCGCCG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCCGCC CAAGCGCGCG GTTTGGACAT TCCCGCCGCA CAAAACGCAC
1451 AAACCGTTGT CGGCGCAGGC ATTACCGCCG AAGTGGAAAG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTTG TGCGGTCTCA GTCGATAACA
1601 AACCACATCG CGCATTCGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCTT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAAGTCAAAG CCGCCGGCAA AACCGTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCG
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAACAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTG
2051 CTCTCGCCGC GCTTGCTTTT TTAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAAACGGGT
2151 AAAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

```

m589.pep..
  1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
 51  KTSVADIANK IEKTGYGAKE KTEDTLPOPE AEHHIGWRLW LLFTINVPFLL
101  IGMAGMMIGR HDWMIPPLWQ FALASVVQLW LAIPFYKSAW ASIKGGLANMM
151  DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVYFEVGMV IGFBVSLGKFL
201  EHRTKKSSLN SLGLLLKLTP TQVNVQRNGE WKQLPIDQVQ IGDILIRANHG
251  ERIAADGIEE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSSVYR
301  ATQLGSQTQL GDMMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTFF
351  IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401  FKDAAMEEEA AHVDAVVLDK TGTLTEGSPQ VAAVYCVFDS GFDEDALYRI
451  AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501  VKAGKAEFAE LALPKFLDGV WDIASIVAVS VDNKPIGAFD LADALKADTA
551  EAIGRLKKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601  KLKAAGKTVA MVGDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651  VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701  AASSVSVLSN ALRLKRVKID *

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Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

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              10      20      30      40      50      60
m589.pep      MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANKI
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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921

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g589      MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIAKI
           10          20          30          40          50          60

           70          80          90         100         110
m589.pep  IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMMLKGLNWTRHDWMI
           70          80          90         100         110         120

           120         130         140         150         160         170
m589.pep  PPLWQFALASVVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      PPVWQFVLASIVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
           130         140         150         160         170         180

           180         190         200         210         220         230
m589.pep  AYGMAHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           190         200         210         220         230         240

           240         250         260         270         280         290
m589.pep  IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           250         260         270         280         290         300

           300         310         320         330         340         350
m589.pep  SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLT FIVTWL
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVGIALLT FIVAWL
           310         320         330         340         350         360
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922

	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKGTGLTEGSPQVAAYVCVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKGTGLTEGRPQVAAYVYPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEEVGVLVKAGKAFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEEVGVLVKSGKAFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEAIGRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLSNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

a589.seq	1	ATGCAACAAA	AAGTCCGTTT	CCAAATCGAA	GGCATGACCT	GCCAGGCATG
	51	TGCTTCGCGC	ATTGAAAAAG	TGTTGAACAA	AAAAGATTTT	GTCGAATCGG
	101	CGGGGGTAAA	CTTCGCCAGC	GAAGAGGCTC	AGGTAGTGTT	TGACGACAGC
	151	AAAACCTCAG	TAGCCGACAT	TGCCAAAATC	ATTGAGAAAA	CCGGTTACGG
	201	CGCGAAGGAA	AAAACGGAAG	ATACATTGCC	GCAACCCGAA	GCAGAACACC
	251	ATATCGGCTG	GAGGTTGTGG	CTTTTGCTGG	CCATCAATAT	CCCGTTCCTT
	301	ATCGGTATGG	TAGGGATGAT	GCTAAAAGGG	CTGAATTGGA	CACGGCATGA
	351	TTGGATGTTG	TCGCCCTTGT	TGCAGTTTGC	ATTGGCGAGT	GTGGTGCAGC
	401	TTTGGCTGGC	GGTGCCATTT	TACAAAAGCG	CGTGGGCGAG	CATTAAAGGC
	451	GGGCTGGCGA	ATATGGACGT	ACTCGTTACC	ATCGGCACGG	TCTCGATTTA
	501	CCTGTATTCC	GTCTATATGC	TGTTTTTCAG	CCCGCACGCG	GCGTACGGTA
	551	TGGCGCATGT	GTATTTTGAA	GTAGGCATAA	TGGTGATTGG	TTTTGTGTCA
	601	CTGGGTAAAT	TTTTGGAACA	CCGCACCAAA	AAATCCAGCC	TGAACAGCTT
	651	GGGCTTGCTG	CTCAAACCTCA	CGCCAACCCA	AGTCAACGTG	CAACGCGATG
	701	GCGAATGGCG	GCAGCTACCC	ATCGACCAAG	TGCAAATCGG	CGACCTAATC
	751	CGCGCCAATC	ACGGCGAACG	CATTGCCGCC	GACGGCATCA	TAGAAAGCGG
	801	CAGCGGCTGG	GCGGACGAAA	GCCATCTTAC	CGGCGAATCC	AATCCCGAAG
	851	AGAAAAAGGC	AGGCGGCAAA	GTATTGGCGG	GCGCGCTGAT	GA CTGAAGGC
	901	AGCGTGGTGT	ACCGCGCCGC	GCAGCTCGGC	AGCCAAACCC	TGCTCGGCGA
	951	CATGATGAAC	GCGCTCTCCG	AAGCGCAAGG	CAGTAAAGCA	CCGATTGCGC
	1001	GTGTGGCGGA	CAAGGCGGCG	GCGGTATTCT	TGCCTGCCGT	TGTGGGCATC
	1051	GCACTTTTGA	CTTTTATCGC	TACTTGCTGT	ATTAAGGGCG	ATTGGACGCT
	1101	CGCATTGATG	CACGCCGTCG	CCGTTTTGGT	GATTGCCTGC	CCGTGTGCAC

923

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1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCCAGGC GCGCGGTTTG GAGATTCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTTGGTAAA AGCAGGCAAA GCCGAATTG CCGAAGTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAG CGGCAAACTT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCCGCCGAAG TGCAGAAACT CAAAGCCGCC GGCAAAACCG TGGCGATGGT
1851 CCGCGACGGC ATCAACGACG CGCCCGCGCT CGCCCGCGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCGCTC GCGCGCTCG GCTTTTAAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGGTAAAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

a589.pep

```

1  MQQKVRFAQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIANKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMLKGL LNWTRHDWML SPLLOFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSGW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIA PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGLT EGKPOVAAVY CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVVG DG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

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m589/a589 94.9% identity in 725 aa overlap

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          10      20      30      40      50      60
m589.pep  MQQKIRFAQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSDKTSVADIANKI
          ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      MQQKVRFAQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSDKTSVADIANKI
          10      20      30      40      50      60

          70      80      90      100     1      110
m589.pep  IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVFPFLIGMAGMMIG-----RHDWMI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLAINIPFLIGMVGMMMLKGLNWTRHDWML
          70      80      90      100     110     120

          120     130     140     150     160     170
m589.pep  PPLWQFALASVVQLWLAIIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      SPLLOFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          130     140     150     160     170     180

          180     190     200     210     220     230
m589.pep  AYGMHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWRQLP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      AYGMHVYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWRQLP
          190     200     210     220     230     240

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924

m589.pep	240	250	260	270	280	290
	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
a589	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
	250	260	270	280	290	300
m589.pep	300	310	320	330	340	350
	SVVYRATQLGSQTQLGDMMNALSEAQSGKAPIARVADKAAAVFVPVAVVGIALLTFIIVTWL					
a589	SVVYRAAQLGSQTLLGDMMNALSEAQSGKAPIARVADKAAAVFVPVAVVGIALLTFIATWL					
	310	320	330	340	350	360
m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
a589	IKGDWTLALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
m589.pep	420	430	440	450	460	470
	VVLDKTGTLTGEGSPQVAAYVCVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
a589	VVLDKTGTLTGEGKPQVAAYVCVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAFAELALPKFLDGVWDIASIVAVSVDNKP					
a589	EIPTAQNQITVVGAGITAEVKGAGLVKAGKAFAELTLPKFSDGVWEIASVAVSVNGKP					
	490	500	510	520	530	540
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAEAIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
a589	IGAFALADALKADTAEAIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
	550	560	570	580	590	600
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
a589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLSNALRLK					
a589	DALSVSRATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLSNALRLK					
	670	680	690	700	710	720
m589.pep	720					
	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:

g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcgttgcttt
51  ggggtacacct tattatttgg gtgtcaaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacgggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtgttgga acagccggtt acgctggtaa accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgctgaa acggaaaaag ttttggaacg ctttttggg aaacaagttc
401 cggtttcctt tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtgttc ccgctttcga ttatgaagaa ctgtcgggca tcaggctgca

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925

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501 ctgggaaggc ctgacggggg aaacggttta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttgttca aaatcaagct ggcagacaaa
601 ggcgatgccg cgtttgaaaa agcgcatttc gattcggaaa cttcagacgg
651 catcaatccg cttgcttttg gcagcagcaa tctgactttg gaaaaathtt
701 cgctcgaatg gaaagagggt gtcgattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccgggga atcgggcgcg tttatcgaca gcgaaggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaaaaatac ggcccgctgg acatccatat
951 cgctgccgaa cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgagg cagtcaaagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaatht tccgtttcac cctgcctcag ggaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcctcaaaaa atgttggaag atttgccggt aagttaggct ggaaatattt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatggtggac agtacggctc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgccctg aagttaaacg ggaaaacgct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttcgggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1  M KKPLISVAA VLLGVALGTP YYLGVKAEES LTQQQKILQK TGFLTVESHQ
51  YDRGWFTSTE TTIVIRLKPEL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVVGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKG MKKEDLN
401 QLGLMLKKEH ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIAD
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1  ..TGGTTACCT CTATGAAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51  GAATAATGCC CGAAATACC TGCCGGATAA CCTGAAACA GTGTTGGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCACGC AGCGGTACAT TGAAACCGAG TTCAAATACG CGCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCTC
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG .CTGCACT GGGAAKGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
401 ATGATGCCCC CTTGTTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCATTTTCA TTCGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAATCGT CAATCTTGTT
601 ACCGATTTCG AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCAAATATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGCGAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTTACC AACAAATCCG TATTGGACAT
951 TAAACTTTTC CGATTACGC TGCCATCGGG AAAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1   ATGAAAAAAC CTTTGATTTT GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTTGCCGGCG GATTGCGGAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTTGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451 GTCAGTGTTT CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCATTTC GATTTCGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGCT
751 GTCAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGACG ATTAATACTT TCCGATTACG GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGCGCGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAGAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
1501 CCGGAGCCCG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1   MKKPLISVAA ALLGVALGTP YYLGVKAEEs LTQQQKILQE AGFLTVESHQ
51  YERGWFSTTE TTVIRLKP EL LHNAQKYL PD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAAE HLDASALTVL KKKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTLNGDQID TAISLKNNQL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*
```

m590/a590 97.8% identity in 462 aa overlap

```
m590.pep
10 20 30
WFTSMETT VIRLKP ELLNNARKYLPDNLKT
|||||
a590 VKAESL TQQQKILQEAGFLT VESHQYERGWFTSTETT VIRLKP ELLHNAQKYL PDNLKT
30 40 50 60 70 80

40 50 60 70 80 90
VLEQPV TLVNHITHGPFAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFN
|||||
a590 VLEQPV TLVNHITHGPFAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFN
90 100 110 120 130 140

100 110 120 130 140 150
GSGKMEV SVPAFDYEE LSGIXLHWEXLTGETVYQKG FKSyrNGYDAPL FKIKLADKGDAA
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928

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|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKLNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGV DYNVKLNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLA FSTKTGESGAFINSEGGQFRFDLTVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLA FSTKTGESGAFIDSEGGQFRFGTLVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTEE QIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSPGKID
          |||||
a590      SALTVLKRKFARISAKKMTEE QIRNDLIAAVKGEASGLFTHNPVLDIKTFRFTLPSPGKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLT LNGDQIDTAISLKNQKLKNGKTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLT LNGDQIDTAISLKNQKLKNGKTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEFPQQX
          |||||
a590      FDEGGMVSEFPQQX
          510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTTCGCGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101  AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151  TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGTCTGAA
201  ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251  CAGTGTGGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301  TTCGCCGCGG GATTCCGGAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351  CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401  CGGCTTCCTT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451  GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501  CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551  ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601  GGCAGATGCC CGTTTGAAAA AGTGCATTTC GATTGCGAAA CTTGAGACGG
651  CATCAATCCG CTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701  CCTAGAAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACGT
751  GTCAATCTTG TTACCGATTG GCAGATTGGC GCGTTTATCA ATCCCAACGG
801  CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851  AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901  GATACACTGG TGTACGGCGA TGAAAAATAC GGCCCGCTGG ACATCCATAT
951  CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001  TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051  TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACAATCC
1101  CGTATTGGAC ATTAAACTT TCCGATTCAC GCTGCCATCG GAAAAATCG
1151  ATGTGGGCGG AAAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAT
1201  CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

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1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
 1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
 1351 ATCAACGAGA CTTTGGCCTT GATGGTGGAC AGTACGGTTC AGAGTATGGC
 1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
 1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAAAGTT GCAAAACGAA
 1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
 1551 A

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

1 MKKPLISVAA ALLGVALGTP YYLGVKAEEES LTQQQKILQE TGFLTVESHQ
 51 YERGWFSTME TTIVRLKPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
 101 FAGGFGTOAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
 151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
 201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
 251 VNLVTDLQIG AFINPNNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
 301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
 351 LIAAVKGEAS GLFTNNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
 401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
 451 INETLRMLVD STVQSMAREK YLTNGDQID TAISLKNQNL KLNKTLQNE
 501 PEPDFDEGGM VSEPPQ*

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAA	ALLGVALGTP	YYLGVKAEEES	LTQQQKILQE	TGFLTVESHQ	YERGWFSTME
g590	MKKPLISVAA	VLLGVALGTP	YYLGVKAEEES	LTQQQKILQKT	TGFLTVESHQ	YDRGWFTSTE
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTIVRLKPEL	LNNARKYLPD	NLKTVLEQPV	TLVNHITHGP	PFAGGFGTQAY	IETEFKYAPE
g590	TTIVRLKPEL	LHNAQKYL	PDNLKIVLEQ	QPVTLVNHITH	GP	PFAGGFGTQAH
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFG	KQVPASLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
g590	TEKVLERFFG	KQVPVSLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDA	PLFKIKLADK	GDAAFEKVHF	DSETSDGINP	LALGSSNLTL	EKFSLEWKEG
g590	FKSYRNSYDA	PLFKIKLADK	GDAAFEKAHF	DSETSDGINP	LALGSSNLTL	EKFSLEWKEG
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNEL	VNLVTDLQIG	AFINPNNGSIA	PSKIEVGKLA	FSTKTGESGA	FINSEGQFRF
g590	VDYNVKLNEL	VNLVTDLQIG	AFINPNNGSIA	PSKIEVGKLA	FSTKTGESGA	FIDSEGRFRF
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KRKFAQISAK	KMTEEQIRND	LIAAVKGEAS
g590	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KRKFAQISAK	KMTEEQIRND	LIAAVKGDAS
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVLD	IKTFRFTLPS	GKIDVGGKIM	FKDMKKEDLN	QLGLMLKKTE	ADIRMSIPQK
g590	GLFTHDPVNI	KIFRFTLPQ	GKIDVGGKIM	FKGMKKEDLN	QLGLMLKKTE	ANIRMSIPQK
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQA	GNIFSVNAED	EAEGRASLDD	INETLRMLVD	STVQSMAREK	YLTNGDQID
g590	MLEDLAVSQA	GNIFSVNAED	EAERASIADIN	ETLRMLVDST	VQSMAREKYL	TDGNQID
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQNL	KLNKTLQNE	PEPDFDEGGM	VSEPPQX		

g591.seq

```
1      TTGCAAACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51     GCACGAATTC GGACACATACA TCGTCGCCAG GTTGTGCGCG GTCAAGGTTG
101    TCGCTTTTTC GCCTCGGCTTC GGCAAACCGT TTTTCAACCG AAAGCGCGGG
151    GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGCT ACGTCAAAAT
201    GGTGATACG CGCGAAGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251    TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTGCg CGCCGGTCCG
301    CTGACCAACC TCGCActggc ggTTTGTCTG TACGGACTGa gctTttctct
351    cggcgtaaCC GAACTGCGGC Cctatgtcgg cacagtcqaa cccqacacc
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401 ttgccgCCCC CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGA
1001 CAACCCCTCA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCGG GGCCGCTGAC CATTGCCGAC ATTGCCGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CAAAACATC GGTTCGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1  LQTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKR
51 DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVLNLL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFGALMM LMMAAAFFND VTRLIG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1  TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51 GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
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1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
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1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

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This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..